

1		5		10		15									
Ser	Glu	Ile	Ile	Phe	Leu	Asp	Ser	Tyr	Pro	Gln	Ile	Ala	Ser	Ser	Arg
		20						25					30		
Ser	Asp	Ile	Ser	Thr	Tyr	Phe	Asp	Ile	Ala	Pro	Ser	Leu	Arg	Asn	Phe
		35					40					45			
Tyr	Ala	Ser	Leu	Thr	Gln	Ala	Lys	Ala	Leu	Asn	Ile	Ser	Val	Ser	Met
		50				55					60				
Phe	Ser	Pro	Asn	Thr	Lys	Gln	Gly	Gln	Cys	Ser	Asp	Cys	Trp	Gly	Leu
65					70				75						80
Gly	Tyr	Gln	Trp	Ile	Asp	Arg	Ala	Phe	Tyr	Ala	Met	Glu	Lys	Arg	Pro
			85						90					95	
Cys	Pro	Thr	Cys	Gly	Gly	Phe	Arg	Val	Gln	Pro	Leu	Ile	Gln	Glu	Val
		100						105					110		
Val	Tyr	Glu	Gly	Lys	His	Phe	Gly	Gln	Leu	Leu	Gln	Ala	Ser	Leu	Asn
		115					120					125			
Glu	Val	Ala	Glu	Thr	Phe	Ser	Phe	Leu	Lys	Lys	Ile	Gln	Lys	Pro	Leu
		130				135					140				
His	Thr	Leu	Ile	Thr	Asn	Gly	Leu	Gly	Tyr	Leu	Ser	Leu	Gly	Gln	Asn
145					150				155						160
Met	Ala	Ser	Leu	Ser	Leu	Ser	Glu	Lys	Ile	Ala	Ile	Lys	Leu	Thr	Lys
			165						170					175	
His	Leu	Phe	Leu	Pro	Pro	Lys	His	Pro	Thr	Leu	Phe	Leu	Leu	Asp	Glu
		180						185					190		
Ile	Ala	Thr	Ser	Leu	Asp	Asn	Gln	Gln	Gln	Ser	Ala	Leu	Leu	Val	Gln
		195				200					205				
Leu	Asn	Thr	Leu	Val	Ser	Leu	Gly	His	Thr	Val	Val	Ile	Ile	Glu	Asn
		210				215					220				
His	Pro	Ala	Phe	Ser	Gln	Gln	Ala	Asp	Phe	Trp	Ile	Gln	Met	Gly	Arg
225					230				235						240
Lys	Thr	Asp	Asn	His	Ile	Leu	Phe	Ala	Gly	Pro	Asn	Pro	Asn	Leu	Ser
			245						250					255	
Phe	Thr														

(2) INFORMATIONS POUR LA SEQ ID NO: 98:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 189 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(94071..94637)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 98:

Ile	Gly	Leu	Leu	Asp	Arg	Val	Gly	Leu	Gly	Tyr	Val	Ile	Leu	Gly	Gln
1			5					10					15		
Glu	Gln	Gln	Ser	Leu	Ser	Asp	Gly	Glu	His	Tyr	Arg	Leu	Leu	Leu	Ala
		20					25					30			
Lys	Ala	Phe	Ser	Ser	Gly	Leu	Thr	Asp	Val	Ile	Tyr	Leu	Leu	Glu	Asp
		35				40					45				
Pro	Leu	Ala	Gly	Ile	His	Pro	Glu	Asp	Ala	Pro	Cys	Leu	Leu	Ala	Val
		50			55					60					
Ile	Lys	Lys	Leu	Val	Thr	Asn	His	Asn	Thr	Val	Ile	Val	Thr	Asp	Arg
65					70					75					80

Glu	Gly	Ser	Leu	Ala	Glu	His	Ala	Asp	Tyr	Leu	Leu	His	Leu	Gly	Pro
				85					90					95	
Glu	Pro	Gly	Pro	Asn	Gly	Gly	Tyr	Leu	Leu	Ser	Thr	Ser	Ala	Leu	Lys
			100					105					110		
Gln	Ser	Gln	Pro	Val	Leu	Cys	Asn	Thr	Arg	Ser	Ser	Glu	Glu	Thr	Pro
		115					120					125			
Gln	Leu	Ser	Val	Ser	Val	Ser	Thr	Ser	Met	Ile	Gln	Ile	Glu	Asn	Leu
		130				135					140				
Ala	Phe	Pro	Leu	Gln	Arg	Leu	Ser	Thr	Ile	Ser	Gly	Val	Ser	Gly	Ser
145					150					155					160
Gly	Lys	Thr	Thr	Leu	Leu	Asn	Ser	Ile	Tyr	Glu	His	Ala	Ala	Leu	Phe
				165					170					175	
Leu	Lys	Arg	Ile	Leu	Leu	Tyr	Ser	Gln	Lys	Leu	Phe	Phe			
				180				185							

(2) INFORMATIONS POUR LA SEQ ID NO: 99:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1224 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(94628..98299)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 99:

Asn	Ser	Cys	His	Ser	Arg	Trp	Asn	Ser	Thr	Asp	Phe	Ala	Arg	Ser	Ser
1				5					10					15	
Ser	Arg	Gln	Asp	Val	Leu	Thr	Val	Arg	Glu	Cys	Leu	Arg	Gln	Gly	Phe
			20					25					30		
Thr	Lys	Val	Leu	Ile	Asp	Glu	Glu	Val	Val	Pro	Ile	His	Lys	Phe	Leu
		35				40						45			
Thr	Thr	Gly	Ile	Pro	Val	Pro	Gly	Gln	Leu	Ile	Val	Asp	Thr	Leu	Ile
		50				55					60				
Lys	Asn	Thr	Ser	Asn	Thr	Pro	Arg	Leu	Lys	Val	Ser	Leu	Phe	Thr	Thr
65				70					75						80
Leu	Asp	Ile	Gly	His	Gly	Glu	Cys	Ser	Leu	His	Phe	Asp	Asn	Gln	Lys
				85					90					95	
Arg	Val	Phe	Ser	Thr	Gln	Ala	Thr	Leu	Pro	Glu	Thr	Gln	Gln	Thr	Tyr
			100					105					110		
Ala	Pro	Leu	Ser	Pro	Asp	Leu	Phe	Ser	Ser	His	Ser	His	Lys	Asp	Arg
		115					120					125			
Cys	Pro	Gln	Cys	Gln	Gly	Ser	Gly	Ile	Phe	Ile	Ser	Ile	Asp	Asp	Pro
		130				135					140				
Cys	Ile	Ile	Gln	Gln	Thr	Leu	Ser	Ile	Glu	Asp	Asn	Cys	Cys	Pro	Phe
145					150					155					160
Ala	Gly	Asn	Cys	Ser	Thr	Phe	Leu	Tyr	Arg	Thr	Ile	Tyr	Gln	Ser	Leu
				165					170					175	
Ala	Asp	Ser	Leu	Gly	Phe	Ser	Leu	Ser	Thr	Pro	Trp	Gln	Asn	Leu	Ser
			180					185					190		
Pro	Glu	Ile	Gln	His	Ile	Phe	Leu	Tyr	Gly	Lys	Glu	Gly	Leu	Ser	Ile
		195					200					205			
Pro	Val	Lys	Leu	Phe	Asp	Gly	Thr	Leu	Gly	Lys	Lys	Thr	Gln	Thr	His
		210				215					220				
Lys	Gln	Trp	Lys	Gly	Val	Leu	Asn	Glu	Ile	Gly	Glu	Lys	Ile	Arg	Phe



225					230					235					240
Ser	Asn	Lys	Pro	Ala	Arg	Tyr	Leu	Pro	Lys	Gly	Thr	Ser	Tyr	Thr	Val
				245					250					255	
Cys	Pro	Arg	Cys	Asn	Lys	Thr	Gly	Leu	Ser	Asp	Tyr	Ala	Asn	Ala	Thr
			260					265					270		
Arg	Trp	His	Gly	Lys	Ser	Phe	Ala	Asp	Phe	Gln	Gln	Met	Ser	Leu	Gln
		275					280					285			
Glu	Leu	Phe	Ile	Phe	Leu	Asn	Gln	Leu	Pro	Lys	Lys	Glu	Leu	Ala	Ile
	290					295					300				
Glu	Glu	Val	Ile	Gln	Gly	Phe	Lys	Ser	Arg	Leu	Ala	Ile	Leu	Ile	Asp
305					310					315					320
Leu	Gly	Leu	Pro	Tyr	Leu	Ser	Pro	Glu	Arg	Ala	Ile	Asp	Thr	Leu	Ser
				325					330					335	
Gly	Gly	Glu	Arg	Glu	Arg	Thr	Ala	Leu	Ala	Lys	His	Leu	Gly	Ala	Glu
			340				345						350		
Leu	Ile	Gly	Val	Met	Tyr	Ile	Leu	Asp	Glu	Pro	Ser	Ile	Gly	Leu	His
		355					360					365			
Pro	Gln	Asp	Thr	His	Lys	Leu	Met	Asn	Val	Ile	Arg	Arg	Leu	Arg	Asp
	370					375					380				
Gln	Gly	Asn	Thr	Val	Leu	Leu	Val	Glu	His	Asp	Glu	Gln	Met	Ile	Ser
385					390					395					400
Leu	Ala	Asp	Arg	Val	Ile	Asp	Ile	Gly	Pro	Gly	Ala	Gly	Ile	Phe	Gly
				405					410					415	
Gly	Glu	Val	Val	Phe	Asn	Gly	Ser	Pro	Arg	Glu	Phe	Leu	Ala	Lys	Ser
			420					425					430		
Asp	Ser	Leu	Thr	Ala	Gln	Tyr	Leu	Arg	Gln	Glu	Gln	His	Ile	Ser	Val
		435					440					445			
Pro	Ala	Lys	Arg	Thr	Asn	Ser	Leu	Gly	Thr	Ile	Thr	Leu	Ser	Lys	Ala
	450					455					460				
Asn	Lys	His	Asn	Leu	Lys	Asp	Leu	Thr	Val	Ser	Ile	Pro	Leu	Gly	Gln
465					470					475					480
Met	Thr	Val	Val	Thr	Gly	Val	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Ile
				485					490					495	
Asn	Asp	Thr	Leu	Val	Pro	Cys	Val	Glu	Glu	Phe	Ile	Glu	Gln	Gly	Phe
			500					505					510		
Cys	Ser	Thr	Leu	Ser	Ile	Gln	Gly	Ala	Leu	Ser	Arg	Leu	Val	His	Ile
		515					520					525			
Asn	Arg	Asp	Leu	Pro	Gly	Arg	Ser	Gln	Arg	Ser	Ile	Pro	Leu	Thr	Tyr
	530				535						540				
Ile	Lys	Ala	Phe	Asp	Glu	Val	Arg	Gln	Leu	Phe	Ala	Glu	Gln	Pro	Arg
545					550					555					560
Cys	Lys	Thr	Leu	Gly	Leu	Thr	Lys	Ser	His	Phe	Ser	Phe	Asn	Thr	Pro
				565					570					575	
Leu	Gly	Ala	Cys	Ala	Glu	Cys	Gly	Gly	Leu	Gly	Ser	Ile	Thr	Thr	Thr
			580				585						590		
Asp	Asn	Arg	Asp	Ser	Ile	Thr	Cys	Pro	Ser	Cys	Leu	Gly	Lys	Arg	Phe
	595						600					605			
Leu	Pro	Gln	Val	Leu	Glu	Val	Arg	Tyr	Lys	Asn	Lys	Thr	Ile	Ala	Asp
	610					615					620				
Ile	Leu	Glu	Met	Thr	Ala	Tyr	Glu	Ala	Lys	Asn	Phe	Phe	Leu	Asp	Glu
625					630					635					640
Pro	Ser	Ile	His	Gln	Lys	Ile	Glu	Thr	Leu	Cys	Thr	Leu	Gly	Leu	Gln
				645					650					655	
Tyr	Leu	Pro	Leu	Gly	Arg	Pro	Leu	Tyr	Ser	Leu	Ser	Gly	Gly	Glu	Ile
			660				665						670		
Gln	Arg	Leu	Lys	Leu	Ala	Tyr	Glu	Leu	Leu	Ala	Pro	Val	Lys	His	Pro
	675						680					685			
Thr	Leu	Tyr	Val	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	His	Thr	His	Asp
	690					695					700				

Val Lys Gln Leu Ile Tyr Val Val Gln Ser Leu Ile His Gln Gly His  
 705 710 715 720  
 Ser Val Ile Ile Ile Glu His Asn Met His Val Val Lys Val Ala Asp  
 725 730 735  
 Tyr Ile Leu Glu Leu Gly Pro Glu Gly Gly Asn Lys Gly Gly Tyr Leu  
 740 745 750  
 Ile Ala Ser Cys Ser Pro Glu Glu Leu Ile His Lys His Thr Pro Thr  
 755 760 765  
 Ala Ile Ala Leu Arg Pro Phe Leu Ser Ser Pro Gln Glu Leu Pro Tyr  
 770 775 780  
 Leu Pro Asp Pro Ser Pro Lys Pro Pro Val Pro Ala Ala Ile Thr Ile  
 785 790 795 800  
 Ala Asn Ala His Gln Tyr Asn Leu Lys His Ile Asp Leu Ser Ile Pro  
 805 810 815  
 Arg Tyr Ala Leu Thr Ala Val Thr Gly Pro Ser Ala Ser Gly Lys His  
 820 825 830  
 Ser Leu Val Phe Asp Ile Leu His Ala Ala Gly Asn Ile Ala Tyr Ala  
 835 840 845  
 Glu Leu Phe Pro Pro Tyr Ile Arg Gln Ala Leu Ile Lys Lys Thr Pro  
 850 855 860  
 Leu Pro Ala Val Asp Lys Val Thr Gly Leu Ser Pro Val Ile Ala Ile  
 865 870 875 880  
 Glu Lys Thr Ser Ala Ser Arg Asn Ser Asn His Ser Val Ala Ser Ala  
 885 890 895  
 Leu Glu Ile Ser Glu Met Leu Glu Ser Leu Phe Thr Arg Ile Gly His  
 900 905 910  
 Pro Tyr Ser Pro Ile Ser Gly Asp Ala Leu Arg Thr Ile Ser Pro Glu  
 915 920 925  
 Thr Ile Ala Glu Glu Leu Leu Thr His Tyr Thr Lys Gly Tyr Val Thr  
 930 935 940  
 Ile Thr Val Pro Phe Pro Lys Glu Glu Glu Phe Phe Ser Tyr Thr Gln  
 945 950 955 960  
 Glu Met Leu Gln Glu Gly Phe Leu Lys Leu Tyr Ala Asn Glu Gln Phe  
 965 970 975  
 Tyr Asp Leu Asp Gly Pro Phe Pro Thr Ser Leu Glu Asn Pro Ala Leu  
 980 985 990  
 Val Ile His His Val Lys Ile Leu Glu Lys Asn Leu Pro Ser Leu Leu  
 995 1000 1005  
 Ala Ser Leu Thr Leu Ala Phe Ser Lys Ala Ser Ser Val Cys Leu His  
 1010 1015 1020  
 Ile Glu Tyr Ala Gly Thr Ser Leu Ser Lys Thr Tyr Arg Gln Gly Leu  
 1025 1030 1035 1040  
 Gln Asp Ala Ser Gly Asn Leu Phe Pro Asn Ile Glu Thr Pro Ser Ile  
 1045 1050 1055  
 Leu Asn His Glu Ser Tyr Leu Cys Pro Leu Cys His Gly Lys Gly Phe  
 1060 1065 1070  
 Leu Ser Thr Cys Ser Ile Leu Pro His Lys Lys Arg Phe Ala Gln His  
 1075 1080 1085  
 Thr Pro Ile Ser Leu Phe Thr Ser Leu Phe Pro Asn Gln Asp Pro Ser  
 1090 1095 1100  
 Pro Ile Tyr Pro Leu Leu Asn Glu Leu Gly Ile Pro Ser Ile Ala Leu  
 1105 1110 1115 1120  
 Phe Gln Glu Ile Asp Val Leu Ser Phe Glu Ser Leu Cys Leu Gly Thr  
 1125 1130 1135  
 Gln Gln His Leu Gly Leu Asn Ala Leu Cys Thr Lys Ala Met Leu Met  
 1140 1145 1150  
 Glu Ser Glu Glu Asp Phe Pro Pro Asp Leu Ile Ser Lys Thr Pro Cys  
 1155 1160 1165  
 Asn Gln Cys Gln Gly Leu Gly Val Tyr Thr Tyr Lys His Cys Ile Arg

```

1170          1175          1180
Ile His Ser Ile Ser Leu Ser Glu Ile Tyr Gln Ser Asn Val Ala Phe
1185          1190          1195          1200
Leu Lys Lys Leu Leu Leu Ser Val Glu Glu Glu Pro Ser Leu Val Gln
          1205          1210          1215
Asp Ile Leu Ser Arg Leu Ala Phe
          1220

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 100:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 201 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(98113..98715)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 100:

```

Met Ser Ser Ile Val Arg Leu Ser Gly Ile Thr Val Arg Asn Leu Lys
1          5          10          15
Asn Ile Thr Val Glu Phe Cys Pro Arg Glu Ile Val Leu Phe Thr Gly
          20          25          30
Val Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe Asn Thr Ile Tyr Ala
          35          40          45
Ala Gly Arg Lys Arg Tyr Leu Ala Thr Leu Pro Ser Phe Phe Ala Thr
          50          55          60
Lys Leu Asp Ser Leu Pro Asp Pro Ser Val Lys Lys Ile Glu Gly Leu
65          70          75          80
Ser Pro Thr Val Ala Val Lys Gln Asn Phe Phe Glu Gln His Val His
          85          90          95
Ala Thr Val Gly Ser Thr Thr Glu Ile Asn Ser Tyr Leu Ala Leu Leu
          100          105          110
Phe Ser Leu Glu Gly Gln Ala Tyr Asp Pro Val Thr Leu His Pro Leu
          115          120          125
Thr Leu Tyr Ser Lys Glu Lys Ile Leu Ser Glu Ile Ala Ala Ile Pro
          130          135          140
Asp Gly Thr Gln Leu Thr Leu Leu Ala Pro Leu Pro Ala Arg Met Phe
145          150          155          160
Leu Pro Phe Glu Asn Val Ser Val Lys Gly Leu Pro Lys Ser Ser Leu
          165          170          175
Met Lys Arg Leu Phe Leu Phe Ile Ser Phe Leu Gln Gln Ala Phe Leu
          180          185          190
Phe Pro Val Asn Ser Leu Ser Ile Arg
          195          200

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 101:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 496 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(98741..100228)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 101:

Ile	Phe	Tyr	Ser	Leu	Ile	Pro	Val	Ser	Arg	Phe	Met	Ile	Ala	Arg	Thr
1				5					10					15	
Lys	Ile	Ile	Cys	Thr	Ile	Gly	Pro	Ala	Thr	Asn	Thr	Pro	Glu	Met	Leu
			20					25					30		
Glu	Lys	Leu	Leu	Asp	Ala	Gly	Met	Asn	Val	Ala	Arg	Leu	Asn	Phe	Ser
		35					40					45			
His	Gly	Thr	His	Glu	Ser	His	Gly	Arg	Thr	Ile	Ala	Ile	Leu	Lys	Glu
	50					55					60				
Leu	Arg	Glu	Lys	Arg	Gln	Val	Pro	Leu	Ala	Ile	Met	Leu	Asp	Thr	Lys
65					70					75					80
Gly	Pro	Glu	Ile	Arg	Leu	Gly	Gln	Val	Glu	Ser	Pro	Ile	Lys	Val	Gln
				85					90					95	
Pro	Gly	Asp	Arg	Leu	Thr	Leu	Val	Ser	Lys	Glu	Ile	Leu	Gly	Ser	Lys
			100					105					110		
Glu	Ser	Gly	Val	Thr	Leu	Tyr	Pro	Ser	Cys	Val	Phe	Pro	Tyr	Val	Arg
		115					120					125			
Glu	Arg	Ala	Pro	Val	Leu	Ile	Asp	Asp	Gly	Tyr	Ile	Gln	Ala	Val	Val
	130					135					140				
Val	Asn	Ala	Gln	Glu	His	Met	Val	Glu	Ile	Glu	Phe	Gln	Asn	Ser	Gly
145					150					155					160
Glu	Ile	Lys	Ser	Asn	Lys	Ser	Leu	Ser	Ile	Lys	Asp	Ile	Asp	Val	Ala
				165					170					175	
Leu	Pro	Phe	Met	Thr	Glu	Lys	Asp	Ile	Ala	Asp	Leu	Lys	Phe	Gly	Val
			180					185					190		
Glu	Gln	Glu	Leu	Asp	Leu	Ile	Ala	Ala	Ser	Phe	Val	Arg	Cys	Asn	Glu
		195					200					205			
Asp	Ile	Asp	Ser	Met	Arg	Lys	Val	Leu	Glu	Ser	Phe	Gly	Arg	Pro	Asn
	210					215					220				
Met	Pro	Ile	Ile	Ala	Lys	Ile	Glu	Asn	His	Leu	Gly	Val	Gln	Asn	Phe
225					230					235					240
Gln	Glu	Ile	Ala	Arg	Ala	Ala	Asp	Gly	Ile	Met	Ile	Ala	Arg	Gly	Asp
				245					250					255	
Leu	Gly	Ile	Glu	Leu	Ser	Ile	Val	Glu	Val	Pro	Gly	Leu	Gln	Lys	Phe
			260					265					270		
Met	Ala	Arg	Ala	Ser	Arg	Glu	Thr	Gly	Arg	Phe	Cys	Ile	Thr	Ala	Thr
		275					280					285			
Gln	Met	Leu	Glu	Ser	Met	Ile	Arg	Asn	Pro	Leu	Pro	Thr	Arg	Ala	Glu
	290					295					300				
Val	Ser	Asp	Val	Ala	Asn	Ala	Ile	Tyr	Asp	Gly	Thr	Ser	Ala	Val	Met
305					310					315					320
Leu	Ser	Gly	Glu	Thr	Ala	Ser	Gly	Ala	His	Pro	Val	His	Ala	Val	Lys
				325					330					335	
Thr	Met	Arg	Ser	Ile	Ile	Gln	Glu	Thr	Glu	Lys	Thr	Phe	Asp	Tyr	His
			340					345					350		
Ala	Phe	Phe	Gln	Leu	Asn	Asp	Lys	Asn	Ser	Ala	Leu	Lys	Val	Ser	Pro
		355					360					365			
Tyr	Leu	Glu	Ala	Ile	Gly	Phe	Ser	Gly	Ile	Gln	Ile	Ala	Glu	Lys	Ala
	370					375					380				
Ser	Ala	Lys	Ala	Ile	Ile	Val	Tyr	Thr	Gln	Thr	Gly	Gly	Ser	Pro	Met
385					390					395					400
Phe	Leu	Ser	Lys	Tyr	Arg	Pro	Tyr	Leu	Pro	Ile	Ile	Ala	Val	Thr	Pro
				405					410					415	
Asn	Arg	Asn	Val	Tyr	Tyr	Arg	Leu	Ala	Val	Glu	Trp	Gly	Val	Tyr	Pro

			420					425					430			
Met	Leu	Thr	Leu	Glu	Ser	Asn	Arg	Thr	Val	Trp	Arg	His	Gln	Ala	Cys	
			435					440					445			
Val	Tyr	Gly	Val	Glu	Lys	Gly	Ile	Leu	Ser	Asn	Tyr	Asp	Lys	Ile	Leu	
			450				455					460				
Val	Phe	Ser	Arg	Gly	Ala	Gly	Met	Gln	Asp	Thr	Asn	Asn	Leu	Thr	Leu	
465					470					475					480	
Thr	Thr	Val	His	Asp	Ala	Leu	Ser	Pro	Ser	Leu	Asp	Glu	Ile	Val	Pro	
				485					490					495		

(2) INFORMATIONS POUR LA SEQ ID NO: 102:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(100337..101347)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 102:

Lys	Arg	Pro	Ile	Arg	Tyr	His	Gly	Val	Lys	Ala	His	Phe	Gln	Asn	Thr	
1			5					10					15			
Ser	Leu	Lys	Lys	Thr	Ser	Gly	Asn	Val	Glu	Leu	Gln	Thr	Pro	Ile	Ser	
			20					25					30			
Phe	Pro	Gln	His	Ala	Gly	Asn	Ile	Leu	Cys	Arg	Leu	Gly	Lys	Lys	Tyr	
		35				40						45				
Pro	Gln	Leu	Gln	Val	Val	Thr	Pro	Ala	Met	Ser	Leu	Gly	Ser	Cys	Leu	
		50				55				60						
Glu	Asp	Phe	Arg	Lys	Gln	Phe	Pro	Asp	Arg	Phe	Thr	Asp	Val	Gly	Ile	
65				70					75					80		
Ala	Glu	Gly	His	Ala	Val	Thr	Phe	Ser	Ala	Gly	Ile	Ala	Arg	Ser	Gly	
			85					90						95		
Thr	Pro	Val	Cys	Cys	Ser	Ile	Tyr	Ser	Thr	Phe	Leu	His	Arg	Ala	Met	
			100					105					110			
Asp	Asn	Val	Phe	His	Asp	Val	Cys	Met	Gln	Glu	Leu	Pro	Val	Ile	Phe	
		115					120					125				
Ala	Ile	Asp	Arg	Ala	Gly	Leu	Ala	Phe	His	Asp	Gly	Arg	Ser	His	His	
	130					135					140					
Gly	Ile	Tyr	Asp	Leu	Gly	Phe	Leu	Cys	Ser	Met	Pro	Asn	Met	Val	Ile	
145				150						155				160		
Cys	Gln	Pro	Arg	Asn	Ala	Leu	Val	Leu	Glu	Arg	Leu	Phe	Phe	Ser	Ser	
			165					170						175		
Leu	Leu	Trp	Lys	Ser	Pro	Cys	Ala	Ile	Arg	Tyr	Pro	Asn	Ile	Pro	Ala	
		180						185					190			
Asn	Glu	Lys	Ala	Ser	Asn	Ser	Ser	Phe	Pro	Phe	Ser	Pro	Ile	Leu	Pro	
		195					200					205				
Gly	Glu	Ala	Glu	Ile	Leu	Cys	Gln	Gly	Asp	Asp	Leu	Leu	Leu	Ile	Ala	
	210					215					220					
Leu	Gly	His	Met	Cys	Asn	Thr	Ala	Leu	Thr	Val	Lys	Glu	His	Leu	Leu	
225				230						235				240		
Asp	Tyr	Gly	Ile	Ser	Thr	Thr	Val	Val	Asp	Pro	Ile	Phe	Ile	Lys	Pro	
			245						250					255		
Leu	Asp	Arg	Lys	Leu	Leu	Gln	Ser	Leu	Leu	Thr	His	His	Ser	Lys	Val	
			260					265					270			

```

Ile Ile Leu Glu Glu His Ser Ile His Gly Gly Leu Gly Ser Glu Phe
      275                280                285
Leu Leu Phe Leu Asn Gln His Asn Ile Lys Ala Asp Val Leu Ser Leu
      290                295                300
Gly Val Pro Asp Met Xaa Ile Pro His Gly Asn Pro Glu Leu Phe Lys
305                310                315                320
Phe Asp Trp Thr His Gln Arg Ser His His Ser Thr Asn Pro Phe Ser
      325                330                335
Phe

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 103:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 296 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(101323..102210)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 103:

```

Met Thr Tyr Ser Leu Leu Pro His Ile His Ser Pro Gln Asp Leu His
1      5      10      15
Ala Leu Ser Leu Asp Lys Leu Pro Val Leu Cys Asp Glu Ile Arg Asn
      20      25      30
Lys Ile Ile Glu Ser Leu Ser Leu Thr Gly Gly His Leu Ala Ser Asn
      35      40      45
Leu Gly Gly Val Glu Leu Thr Val Ala Leu His Tyr Val Phe Ser Ser
50      55      60
Pro Asp Asp Gln Phe Ile Phe Asp Val Gly His Gln Ser Tyr Val His
65      70      75      80
Lys Leu Leu Thr Gly Arg Asn Thr Glu Ala Phe Ser Asn Ile Arg His
      85      90      95
Asp Asn Gly Leu Ser Gly Phe Thr Thr Pro Gln Glu Ser Asn His Asp
      100     105     110
Ile Phe Phe Ser Gly His Ala Gly Asn Ala Leu Ser Leu Ala Leu Gly
      115     120     125
Leu Ala Lys Gly Ser Ser Asn Ser Ser Ser His Ile Leu Pro Ile Leu
130     135     140
Gly Asp Ala Ala Phe Ser Cys Gly Leu Thr Leu Glu Ala Leu Asn Asn
145     150     155     160
Ile Pro Ala Asp Leu Ser Lys Phe Ile Ile Val Leu Asn Asp Asn Gln
      165     170     175
Met Ser Ile Ser Glu Asn Val Gly Asn Ile Pro Gln Gly Ile Ser Gln
      180     185     190
Trp Ile Tyr Pro Gln Lys Ile Ser Lys Leu Ser Gln Lys Ile His Ser
      195     200     205
Trp Ile Gln Asn Leu Pro Ser Phe Leu His Lys Lys Lys Thr Leu Ser
210     215     220
His Lys Val Asp Ile Ala Leu Lys Ser Leu Ser His Pro Leu Phe Glu
225     230     235     240
Gln Phe Gly Leu His Tyr Val Gly Pro Ile Asp Gly His Asn Val Lys
      245     250     255
Lys Leu Val Gln Ala Leu Gln Met Ile Lys Asp Gln Pro Gln Pro Ile

```

(2) INFORMATION POUR LA SEQ ID NO: 104:

(A) LONGUEUR: 92 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(102210..102485)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 104:

Pro	Val	Met	Gln	Glu	Ile	Ser	Val	Pro	Glu	Ala	Ser	His	Leu	Asp	Thr
1				5					10					15	
Val	Ile	Gln	Arg	Leu	Leu	Val	Leu	Gln	Lys	Ala	Leu	Glu	Asp	Cys	His
			20					25					30		
Ser	Val	Glu	Ala	Ile	Leu	Ala	Ile	Tyr	Glu	Glu	Met	Phe	Ser	Leu	Ile
			35				40					45			
Gln	Glu	Gly	Glu	Thr	Asn	Leu	Asn	His	Val	Glu	Gln	Leu	Ser	Phe	Gln
			50			55					60				
Leu	Gln	Leu	Asn	Pro	Asp	Gly	Ser	Val	Ala	Val	Asp	Thr	Ser	Gly	Asn
65					70					75					80
Pro	Ile	Lys	His	Pro	Phe	Ile	Pro	Gly	Glu	Ser	Val				
				85					90						

(2) INFORMATION POUR LA SEQ ID NO: 105:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 504 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(102726..104237)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 105:

Met	Ser	Ile	Thr	Ser	Pro	Pro	Ile	Glu	Val	Ser	Val	Leu	Thr	Asp	Ser
1				5					10					15	
Ile	Lys	Asn	Leu	Leu	Glu	Lys	Asn	Phe	Leu	Arg	Val	Val	Val	Lys	Gly
			20					25					30		
Glu	Leu	Ser	Asn	Val	Ser	Leu	Gln	Thr	Ser	Gly	His	Leu	Tyr	Phe	Ala
		35					40					45			
Ile	Lys	Asp	Ser	Lys	Ala	Val	Leu	Asn	Gly	Ala	Phe	Phe	His	Phe	Arg
	50					55					60				
Ser	Lys	Tyr	Phe	Asp	Arg	Lys	Pro	Lys	Asp	Gly	Asp	Tyr	Val	Ile	Leu
65					70					75					80

His	Gly	Lys	Leu	Thr	Val	Tyr	Ala	Pro	Arg	Gly	Gln	Tyr	Gln	Ile	Val
			85						90					95	
Ala	Tyr	Ala	Leu	Thr	Phe	Ser	Gly	Glu	Gly	Asn	Leu	Leu	Gln	Gln	Phe
			100					105					110		
Glu	Glu	Arg	Lys	Gln	Arg	Leu	Ala	Ala	Glu	Gly	Tyr	Phe	Asp	Pro	Lys
		115					120					125			
Arg	Lys	Lys	Pro	Leu	Pro	Ser	Gly	Ala	Arg	Val	Ile	Gly	Val	Ile	Thr
	130					135					140				
Ser	Pro	Thr	Gly	Ala	Val	Ile	Gln	Asp	Ile	Leu	Arg	Val	Leu	Ser	Arg
145					150					155					160
Arg	Cys	His	Gln	Phe	Gln	Val	Ile	Leu	Tyr	Pro	Val	Thr	Val	Gln	Gly
			165						170					175	
Ala	Thr	Ala	Ala	Gln	Glu	Ile	Ser	Gln	Ala	Ile	Gln	Phe	Phe	Asn	Gln
			180					185						190	
Asn	Ser	Met	Arg	Val	His	Ala	Leu	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser
		195					200					205			
Ile	Glu	Asp	Leu	Trp	Ala	Phe	Asn	Glu	Glu	Glu	Leu	Val	Lys	Ser	Ile
	210					215					220				
Val	Ala	Ser	Ser	Ile	Pro	Ile	Ile	Ser	Ala	Val	Gly	His	Glu	Thr	Asp
225					230					235					240
Phe	Thr	Leu	Cys	Asp	Phe	Ala	Ser	Asp	Val	Arg	Ala	Pro	Thr	Pro	Ser
			245						250					255	
Ala	Ala	Ala	Glu	Ile	Val	Cys	Lys	Ser	Ser	Asp	Gln	Tyr	Arg	Gln	Glu
			260					265					270		
Leu	Gln	Asn	Leu	Arg	Arg	Tyr	Val	Ser	Ser	His	Ala	Arg	Gln	Phe	Ile
		275					280					285			
Ala	Ala	Lys	Lys	Asn	Leu	Leu	Thr	His	Trp	Gln	Arg	His	Leu	Ala	Ser
	290				295						300				
Val	Asp	Phe	Tyr	His	Thr	Ala	Gln	Gln	Thr	Leu	Asp	Tyr	Thr	Arg	Ala
305					310					315					320
Ala	Leu	Glu	Arg	Gly	Ile	Glu	Thr	Lys	Leu	Glu	Tyr	Tyr	Lys	Gln	Arg
			325						330					335	
Phe	Ala	Gln	Tyr	Arg	Arg	Trp	Leu	Lys	Ser	Asp	Val	Leu	Ile	Arg	Ile
		340						345					350		
Glu	Lys	His	Leu	Ala	Asp	Leu	Asn	Gln	Ser	Leu	Met	Leu	Ser	Ile	Lys
		355					360				365				
Asn	Lys	Ile	Tyr	Thr	Lys	Lys	Thr	Ser	Leu	Asn	Gln	Leu	Tyr	Thr	Ser
	370					375					380				
Cys	Leu	Lys	Asn	Glu	Leu	Leu	Asn	Leu	Gln	His	Arg	Thr	Gln	His	Ser
385					390					395					400
Arg	Asn	Ile	Leu	Ser	Gln	Leu	Ser	Arg	Arg	Leu	His	Ile	Ala	Ile	Ala
			405						410					415	
Ser	Ser	Gln	Gln	Thr	His	Gln	Glu	Cys	Leu	Val	Arg	Leu	Gln	Asn	Glu
		420						425					430		
Leu	Ser	Phe	Thr	Ile	Gln	His	Leu	Leu	Thr	Lys	Ala	Lys	Glu	Arg	Cys
		435					440					445			
Gln	Ala	Ile	Gln	Glu	Gln	Ala	Ser	Ser	Leu	Asn	Pro	Lys	Asn	Val	Leu
	450					455					460				
Lys	Arg	Gly	Phe	Ala	Gln	Leu	Phe	Asp	Phe	Asn	Lys	His	Phe	Val	Ile
465					470					475					480
Ile	Ser	Ala	Glu	Ser	Leu	Lys	Gln	Ser	Asp	Leu	Val	Arg	Ser	Ala	Ser
			485						490					495	
Lys	Thr	Val	Lys	Gln	Leu	Tyr	Gln								
			500												

(2) INFORMATIONS POUR LA SEQ ID NO: 106:

(i) CARACTERISTIQUES DE LA SEQUENCE:



(A) LONGUEUR: 252 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(104254..105009)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 106:

Pro	Ser	Lys	Gln	Phe	Val	Phe	Gly	Asn	Trp	Lys	Met	Asn	Lys	Thr	Leu	1	5	10	15
Thr	Glu	Ala	Gln	Thr	Phe	Leu	Lys	Ser	Phe	Leu	Ser	Ser	Asp	Ile	Leu	20	25	30	
Ser	Asn	Pro	Gln	Ile	Ile	Thr	Gly	Ile	Ile	Pro	Pro	Phe	Thr	Leu	Leu	35	40	45	
Ser	Ala	Cys	Gln	Gln	Ala	Val	Ser	Asp	Ser	Pro	Ile	Phe	Leu	Gly	Ala	50	55	60	
Gln	Thr	Thr	His	Glu	Ala	Asp	Ser	Gly	Ala	Phe	Thr	Gly	Glu	Ile	Ser	65	70	75	80
Ala	Pro	Met	Leu	Lys	Asp	Ile	Gly	Val	Asp	Phe	Val	Leu	Ile	Gly	His	85	90	95	
Ser	Glu	Arg	Arg	His	Ile	Phe	His	Glu	Gln	Asn	Pro	Val	Leu	Ala	Glu	100	105	110	
Lys	Ala	Ala	Ala	Ala	Ile	His	Ser	Gly	Met	Ile	Pro	Val	Leu	Cys	Ile	115	120	125	
Gly	Glu	Thr	Leu	Glu	Glu	Gln	Glu	Ser	Gly	Ala	Thr	Gln	Asp	Ile	Leu	130	135	140	
Leu	Asn	Gln	Leu	Thr	Ile	Gly	Leu	Ser	Lys	Leu	Pro	Glu	Gln	Ala	Ser	145	150	155	160
Phe	Ile	Leu	Ala	Tyr	Glu	Pro	Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	Val	165	170	175	
Ala	His	Pro	Asp	Leu	Val	Gln	Glu	Thr	His	Ala	Phe	Cys	Arg	Lys	Thr	180	185	190	
Ile	Ala	Ser	Leu	Phe	Ser	Lys	Asp	Ile	Ala	Glu	Arg	Thr	Pro	Ile	Leu	195	200	205	
Tyr	Gly	Gly	Ser	Val	Lys	Ala	Asp	Asn	Ala	Arg	Ser	Leu	Ser	Leu	Cys	210	215	220	
Pro	Asp	Val	Asn	Gly	Leu	Leu	Val	Gly	Gly	Ala	Ser	Leu	Ser	Ser	Glu	225	230	235	240
Asn	Phe	Leu	Ser	Ile	Ile	Gln	Gln	Ile	Asp	Ile	Pro					245	250		

(2) INFORMATIONS POUR LA SEQ ID NO: 107:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 212 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 105259..105894

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 107:

```

Pro Leu Cys Cys Met Lys Val Lys Ile Cys Gly Ile Thr His Pro Asp
1      5      10      15
Asp Ala Arg Glu Ala Ala Lys Ala Gly Ala Asp Tyr Ile Gly Met Ile
      20      25      30
Phe Ala Lys Asp Ser Arg Arg Cys Val Ser Glu Glu Lys Ala Lys Tyr
      35      40      45
Ile Val Glu Ala Ile Gln Glu Gly Asn Ser Glu Pro Val Gly Val Phe
      50      55      60
Pro Glu His Ser Val Glu Glu Ile Leu Ala Ile Thr Glu Ala Thr Gly
65      70      75      80
Ile Thr Ser Ile Gln Leu Ser Gly Glu Asp Ile Leu Phe Lys Phe Ser
      85      90      95
Gln Leu Arg Glu His Phe Ser Ile Phe Tyr Val Val Ser Val Tyr Ser
      100     105     110
Asn Gly Gln Pro Ser Ala Ala Leu Pro Pro Met Asn Asp Ala Val Thr
      115     120     125
Val Val Tyr Asp His Ile Gly Gly Glu Arg Gly Ser Pro Phe Asp Trp
      130     135     140
Lys Ala Phe Ser Pro Phe Gln His Asn Asn Trp Met Leu Gly Gly Gly
145     150     155     160
Val Asn Leu Trp Asn Ile Lys Glu Gly Ile Ser Leu Leu Asn Pro Arg
      165     170     175
Gly Ile Asp Val Ser Ser Gly Val Glu Arg Pro Gly Ile Leu Arg Lys
      180     185     190
Asp Ile Phe Leu Met Gln Ala Leu Ile Asn Ser Ala Lys Glu Leu Ser
      195     200     205
Ser Ser Thr Leu
      210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 108:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 344 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 107429...108460

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 108:

```

Arg Thr Arg Gly Gly Gly Leu Phe Ser Asn Phe Cys Ser Ser Pro Thr
1      5      10      15
Val Gln Ala Leu Leu Arg Ala Trp Asp Arg Phe Phe Ser Arg Val Ser
      20      25      30
Asp Gly Arg Phe Leu Gln Ile Tyr Gly Asp Gly Gly Leu Phe Val
      35      40      45
Glu Arg Ala Leu Gln Leu Ile Ser Cys Pro Leu Gln Arg Ala Arg Ile
      50      55      60
Arg Val Val Gly Ile Asn Pro Ser Phe Phe Val Thr Val Ser Asp Asn
65      70      75      80
Arg His Phe Tyr Thr Ser Pro Gly Ser Cys Gly Arg Ile Leu Asp Met
      85      90      95
Ser Gly Tyr Leu Ser Ala Arg Arg Asp Gly Cys Val Ser His Val Pro
      100     105     110
Phe Ser Pro His Ser Gln Ser Ile Thr Pro Gly Val Gly Asp Ala Cys

```

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 97 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 108665..108955

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 109:

[illegible]

## (2) INFORMATIONS POUR LA SEQ ID NO: 110:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 149 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(109013..109459)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 110:

```

Thr Met Ile Leu Thr Thr Pro Ser Glu His Lys Ala Cys Leu Glu Lys
1           5           10           15
Gln Glu Lys Ala Val Ala Leu Leu Phe Pro Glu Asn Phe Val Lys Asp
          20           25           30
Thr Phe Tyr Lys Gln Leu Leu Gln Ile Gly Arg Thr Ala Lys Pro Phe
          35           40           45
Pro Lys Glu Phe Leu Thr Lys Glu Asn Leu Val Leu Gly Cys Gln Ser
          50           55           60
Asp Leu Tyr Leu His Gly Glu Phe Lys Asn Asn Ala Val Phe Phe Phe
65           70           75           80
Thr Tyr Thr Glu Ala Leu Ile Ser Ser Gly Val Ala Val Leu Phe Ser
          85           90           95
Asp Ile Tyr Ser Gly Glu Thr Pro Glu Thr Ile Leu Thr Cys Lys Pro
          100          105          110
Leu Phe Phe Glu Lys Leu Ser Arg His Leu Ser Met Gly Arg Ser Arg
          115          120          125
Gly Gly Glu Ser Leu Phe Leu Asn Met Gln Arg Ile Ala Val Gln Tyr
          130          135          140
Leu Ala Arg Lys Thr
145

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 111:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 221 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(109704..110366)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 111:

```

Ala Met Val Lys Ala Ala His Pro Leu His Ser Ser Ile Ser Gly Ala
1           5           10           15
Leu Pro Leu His Ser Ser Arg Gly Gly Ala Tyr His Asp Ser Leu Gly
          20           25           30
Asp Leu His Ser Pro Ile Ser Leu Thr Pro Pro Ala Leu Ser Val Leu
          35           40           45
Thr Pro Glu Pro Ala Gln Ser Lys Ser Arg Val Gln Ala Val Ala Asn

```

50		55		60											
Thr	Ile	Gly	Asp	Phe	Leu	Gln	Arg	Asn	Trp	Lys	His	Leu	Leu	Leu	Tyr
65					70					75					80
Ile	Leu	Ala	Trp	Ser	Leu	Ile	Leu	Ile	Cys	His	Ser	Ser	Val	Ala	Leu
				85					90					95	
Val	Leu	Ser	Ile	Trp	Leu	Gly	Ile	Gly	Phe	Gly	Ala	Gly	Val	Val	Leu
			100					105					110		
Gly	Ile	Ile	Ser	Ala	Asn	Phe	Leu	Asp	Lys	Glu	Asn	Lys	Tyr	Pro	His
		115					120					125			
Leu	Asn	Ser	Leu	Trp	Asn	Ile	Thr	Asn	His	Gly	Leu	Gln	Gln	Leu	Asp
	130					135					140				
Pro	Asn	Gly	Thr	Arg	Gln	Val	Leu	Leu	Ala	Thr	Val	Ile	Ala	Ser	Ile
145					150					155					160
Ser	Ala	Leu	Ile	Tyr	Ala	Ser	Pro	Gln	Ala	Ile	Gly	Phe	Ile	Ile	Gly
				165					170					175	
Ala	Phe	Leu	Gly	His	Gln	Thr	Ser	Ser	Leu	Ala	Val	Tyr	Gly	Tyr	Arg
			180					185					190		
Phe	Lys	Ser	Gly	Gln	Asp	Ile	Leu	Gln	Ile	Arg	Asn	Cys	Leu	Ile	Asn
	195					200					205				
Lys	Lys	Asn	Glu	Phe	Asp	Lys	Pro	Ser	Cys	Ser	Val	Gly			
	210					215					220				

(2) INFORMATIONS POUR LA SEQ ID NO: 112:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 392 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 111345..112520

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 112:

Met	Ser	Lys	Glu	Thr	Phe	Gln	Arg	Asn	Lys	Pro	His	Ile	Asn	Ile	Gly
1				5					10					15	
Thr	Ile	Gly	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Ile
			20					25					30		
Thr	Arg	Thr	Leu	Ser	Gly	Asp	Gly	Leu	Ala	Asp	Phe	Arg	Asp	Tyr	Ser
		35					40					45			
Ser	Ile	Asp	Asn	Thr	Pro	Glu	Glu	Lys	Ala	Arg	Gly	Ile	Thr	Ile	Asn
	50					55				60					
Ala	Ser	His	Val	Glu	Tyr	Glu	Thr	Ala	Asn	Arg	His	Tyr	Ala	His	Val
65				70					75						80
Asp	Cys	Pro	Gly	His	Ala	Asp	Tyr	Val	Lys	Asn	Met	Ile	Thr	Gly	Ala
			85						90					95	
Ala	Gln	Met	Asp	Gly	Ala	Ile	Leu	Val	Ser	Ala	Thr	Asp	Gly	Ala	
		100						105				110			
Met	Pro	Gln	Thr	Lys	Glu	His	Ile	Leu	Leu	Ala	Arg	Gln	Val	Gly	Val
	115						120					125			
Pro	Tyr	Ile	Val	Val	Phe	Leu	Asn	Lys	Ile	Asp	Met	Ile	Ser	Glu	Glu
	130					135					140				
Asp	Ala	Glu	Leu	Val	Asp	Leu	Val	Glu	Met	Glu	Leu	Ala	Glu	Leu	Leu
145					150					155					160
Glu	Glu	Lys	Gly	Tyr	Lys	Gly	Cys	Pro	Ile	Arg	Gly	Ser	Ala	Leu	
			165						170					175	

Lys Ala Leu Glu Gly Asp Ala Ala Tyr Ile Glu Lys Val Arg Glu Leu  
 180 185 190  
 Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp  
 195 200 205  
 Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg  
 210 215 220  
 Gly Thr Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser Asp  
 225 230 235 240  
 Lys Val Gln Leu Val Gly Arg Asp Thr Lys Glu Thr Ile Val Thr Gly  
 245 250 255  
 Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly Glu Asn  
 260 265 270  
 Val Gly Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu Arg Gly  
 275 280 285  
 Met Val Val Cys Leu Pro Asn Ser Val Lys Pro His Thr Arg Phe Lys  
 290 295 300  
 Cys Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His Lys Pro  
 305 310 315 320  
 Phe Phe Thr Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr Asp Val  
 325 330 335  
 Thr Gly Val Val Thr Leu Pro Glu Gly Val Glu Met Val Met Pro Gly  
 340 345 350  
 Asp Asn Val Glu Phe Glu Val Gln Leu Ile Ser Pro Val Ala Leu Glu  
 355 360 365  
 Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile Gly Ala  
 370 375 380  
 Gly Thr Ile Ser Lys Ile Ile Ala  
 385 390

(2) INFORMATIONS POUR LA SEQ ID NO: 113:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 112915...113463

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 113:

Phe Met Phe Lys Trp Tyr Val Val Gln Val Phe Thr Ala Gln Glu Lys  
 1 5 10 15  
 Lys Val Lys Lys Ser Leu Glu Asp Phe Lys Glu Ala Ser Gly Met Ser  
 20 25 30  
 Asp Phe Ile Gln Gln Ile Ile Leu Pro Ser Glu Asn Val Met Glu Val  
 35 40 45  
 Lys Lys Gly Glu His Lys Ile Val Glu Lys Tyr Ile Trp Pro Gly Tyr  
 50 55 60  
 Leu Leu Val Lys Met His Leu Thr Asp Glu Ser Trp Ser Tyr Val Lys  
 65 70 75 80  
 Lys Thr Gln Gly Val Val Glu Phe Leu Gly Gly Gly Ala Pro Val Ala  
 85 90 95  
 Leu Ser Glu Glu Glu Ile Lys Asn Ile Leu Ala Asp Leu Glu Lys  
 100 105 110  
 Lys Ser Gly Val Val Gln Lys His Lys Phe Glu Val Gly Ser Gln Val

```

          115              120              125
Lys Ile Asn Asp Gly Val Phe Val Asn Phe Val Gly Val Val Ser Glu
    130              135              140
Val Phe His Asp Lys Gly Arg Leu Ser Val Met Val Ser Ile Phe Gly
    145              150              155              160
Arg Glu Thr Arg Val Asp Asp Leu Glu Phe Trp Gln Val Glu Glu Val
          165              170              175
Val Pro Gly Gln Glu Ser Glu
          180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 114:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 141 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 113572..113994

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 114:

```

Met Ser Asn Lys Lys Ile Ile Lys Ile Ile Lys Leu Gln Ile Pro Gly
1      5      10      15
Gly Lys Ala Asn Pro Ala Pro Pro Ile Gly Pro Ala Leu Gly Ala Ala
    20      25      30
Gly Val Asn Ile Met Gly Phe Cys Lys Glu Phe Asn Ala Ala Thr Gln
    35      40      45
Asp Arg Pro Gly Asp Leu Leu Pro Val Val Ile Thr Val Tyr Ser Asp
    50      55      60
Lys Thr Xaa Ser Phe Val Met Lys Gln Ser Pro Val Ser Ser Leu Ile
    65      70      75      80
Lys Lys Ala Leu Gly Leu Glu Ser Gly Ser Lys Ile Pro Asn Arg Asn
    85      90      95
Lys Val Gly Lys Leu Thr Arg Ala Gln Ile Thr Ala Ile Ala Glu Gln
    100     105     110
Lys Met Lys Asp Met Asp Val Val Leu Leu Glu Ser Ala Glu Arg Met
    115     120     125
Val Glu Gly Thr Ala Arg Ser Met Gly Val Asp Val Glu
    130     135     140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 115:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 195 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 114020..114604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 115:





130		135		140											
Gly	Leu	Ile	Ala	Ala	Pro	Met	Ser	Gln	Val	Val	Gly	Ile	Met	Asn	Ser
145				150				155							160
Val	Leu	Ser	Gly	Val	Val	Ser	Cys	Val	Asp	Gln	Lys	Ala	Glu	Lys	Thr
			165					170						175	
Gln	Glu														

## (2) INFORMATIONS POUR LA SEQ ID NO: 117:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 115362..115676

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 117:

Lys	Ile	Ile	Gly	Arg	Lys	Val	Gly	Arg	Tyr	Ala	Ala	Ala	Pro	Val	Val
1				5					10					15	
Ala	Val	Ala	Gly	Ala	Ala	Ala	Ala	Gly	Asp	Ala	Pro	Ala	Ser	Ala	Glu
			20					25					30		
Pro	Thr	Glu	Phe	Ala	Val	Ile	Leu	Glu	Asp	Val	Pro	Ser	Asp	Lys	Lys
		35					40					45			
Ile	Gly	Val	Leu	Lys	Val	Val	Arg	Glu	Val	Thr	Gly	Leu	Ala	Leu	Lys
	50					55					60				
Glu	Ala	Lys	Glu	Met	Thr	Glu	Gly	Leu	Pro	Lys	Thr	Val	Lys	Glu	Lys
65				70					75					80	
Thr	Ser	Lys	Ser	Asp	Ala	Glu	Asp	Thr	Val	Lys	Lys	Leu	Gln	Glu	Ala
			85					90						95	
Gly	Ala	Lys	Ala	Val	Ala	Lys	Gly	Leu							
			100					105							

## (2) INFORMATIONS POUR LA SEQ ID NO: 118:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1258 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 116022..119795

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 118:

Ser	Leu	Arg	Arg	Ala	Arg	Met	Phe	Lys	Cys	Pro	Glu	Arg	Val	Ser	Val
1				5					10					15	
Lys	Lys	Lys	Glu	Asp	Ile	Leu	Asp	Leu	Pro	Asn	Leu	Val	Glu	Val	Gln
			20					25					30		
Ile	Lys	Ser	Tyr	Lys	Gln	Phe	Leu	Gln	Ile	Gly	Lys	Leu	Ala	Glu	Glu
		35					40					45			

Arg	Glu	Asn	Ile	Gly	Leu	Glu	Glu	Val	Phe	Arg	Glu	Ile	Phe	Pro	Ile
50						55					60				
Lys	Ser	Tyr	Asn	Glu	Ala	Thr	Ile	Leu	Glu	Tyr	Leu	Ser	Tyr	Asn	Leu
65					70					75					80
Gly	Val	Pro	Lys	Tyr	Ser	Pro	Glu	Glu	Cys	Ile	Arg	Arg	Gly	Ile	Thr
				85					90					95	
Tyr	Ser	Val	Thr	Leu	Lys	Val	Arg	Phe	Arg	Leu	Thr	Asp	Glu	Thr	Gly
			100					105					110		
Ile	Lys	Glu	Glu	Glu	Val	Tyr	Met	Gly	Thr	Ile	Pro	Ile	Met	Thr	Asp
	115						120					125			
Lys	Gly	Thr	Phe	Ile	Ile	Asn	Gly	Ala	Glu	Arg	Val	Val	Val	Ser	Gln
	130					135					140				
Val	His	Arg	Ser	Pro	Gly	Ile	Asn	Phe	Glu	Gln	Glu	Lys	His	Ser	Lys
145					150					155					160
Gly	Asn	Val	Leu	Phe	Ser	Phe	Arg	Ile	Ile	Pro	Tyr	Arg	Gly	Ser	Trp
				165					170					175	
Leu	Glu	Ala	Val	Phe	Asp	Ile	Asn	Asp	Leu	Ile	Tyr	Ile	His	Ile	Asp
			180					185					190		
Arg	Lys	Lys	Arg	Arg	Arg	Lys	Ile	Leu	Ala	Met	Thr	Phe	Ile	Arg	Ala
	195						200					205			
Leu	Gly	Tyr	Ser	Thr	Asp	Ala	Asp	Ile	Ile	Glu	Glu	Phe	Phe	Ser	Val
	210				215						220				
Glu	Glu	Arg	Ser	Leu	Arg	Ser	Glu	Lys	Asp	Phe	Val	Ala	Leu	Val	Gly
225					230					235					240
Lys	Val	Leu	Ala	Asp	Asn	Val	Val	Asp	Ala	Asp	Ser	Ser	Leu	Val	Tyr
				245					250					255	
Gly	Lys	Ala	Gly	Glu	Lys	Leu	Ser	Thr	Ala	Met	Leu	Lys	Arg	Ile	Leu
		260						265					270		
Asp	Thr	Gly	Val	Gln	Ser	Leu	Lys	Ile	Ala	Val	Gly	Ala	Asp	Glu	Asn
	275					280						285			
His	Pro	Ile	Ile	Lys	Met	Leu	Ala	Lys	Asp	Pro	Thr	Asp	Ser	Tyr	Glu
	290					295					300				
Ala	Ala	Leu	Lys	Asp	Phe	Tyr	Arg	Arg	Leu	Arg	Pro	Gly	Glu	Pro	Ala
305					310					315					320
Thr	Leu	Ala	Asn	Ala	Arg	Ser	Thr	Ile	Met	Arg	Leu	Phe	Phe	Asp	Ala
			325						330					335	
Lys	Arg	Tyr	Asn	Leu	Gly	Arg	Val	Gly	Arg	Tyr	Lys	Leu	Asn	Lys	Lys
		340						345					350		
Leu	Gly	Phe	Pro	Leu	Asp	Asp	Glu	Thr	Leu	Ser	Gln	Val	Thr	Leu	Arg
	355					360					365				
Lys	Glu	Asp	Val	Ile	Gly	Ala	Leu	Lys	Tyr	Leu	Ile	Arg	Leu	Arg	Met
	370					375					380				
Gly	Asp	Glu	Lys	Thr	Ser	Ile	Asp	Asp	Ile	Asp	His	Leu	Ala	Asn	Arg
385					390					395					400
Arg	Val	Arg	Ser	Val	Gly	Glu	Leu	Ile	Gln	Asn	His	Cys	Arg	Ser	Gly
			405						410					415	
Leu	Ala	Arg	Met	Glu	Lys	Ile	Val	Arg	Glu	Arg	Met	Asn	Leu	Phe	Asp
		420						425					430		
Phe	Ser	Ser	Asp	Thr	Leu	Thr	Pro	Gly	Lys	Ile	Ile	Ser	Ala	Lys	Gly
	435						440					445			
Leu	Val	Ser	Val	Leu	Lys	Asp	Phe	Phe	Ser	Arg	Ser	Gln	Leu	Ser	Gln
	450					455					460				
Phe	Met	Asp	Gln	Thr	Asn	Pro	Val	Ala	Glu	Leu	Thr	His	Lys	Arg	Arg
465					470					475					480
Leu	Ser	Ala	Leu	Gly	Pro	Gly	Gly	Leu	Asn	Arg	Glu	Arg	Ala	Gly	Phe
			485						490					495	
Glu	Val	Arg	Asp	Val	His	Ala	Ser	His	Tyr	Gly	Arg	Ile	Cys	Pro	Ile
		500						505					510		
Glu	Thr	Pro	Glu	Gly	Pro	Asn	Ile	Gly	Leu	Ile	Thr	Ser	Leu	Ser	Ser

		515					520					525				
Phe	Ala	Lys	Ile	Asn	Glu	Phe	Gly	Phe	Ile	Glu	Thr	Pro	Tyr	Arg	Val	
	530					535					540					
Val	Arg	Asp	Gly	Ile	Val	Thr	Asp	Glu	Ile	Glu	Tyr	Met	Thr	Ala	Asp	
545					550					555						560
Val	Glu	Glu	Glu	Cys	Val	Ile	Ala	Gln	Ala	Ser	Ala	Glu	Leu	Asp	Glu	
				565				570						575		
Tyr	Asn	Met	Phe	Lys	Thr	Pro	Val	Cys	Trp	Ala	Arg	Tyr	Lys	Gly	Glu	
			580					585					590			
Ala	Phe	Glu	Ala	Asp	Thr	Ser	Thr	Val	Thr	His	Met	Asp	Val	Ser	Pro	
		595					600					605				
Lys	Gln	Leu	Val	Ser	Val	Val	Thr	Gly	Leu	Ile	Pro	Phe	Leu	Glu	His	
	610					615					620					
Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ser	Asn	Met	Gln	Arg	Gln	Ala	
625					630					635						640
Val	Pro	Leu	Leu	Lys	Thr	Glu	Ala	Ala	Ile	Val	Gly	Thr	Gly	Leu	Glu	
				645					650					655		
Gly	Arg	Ala	Ala	Lys	Asp	Ser	Gly	Ala	Ile	Ile	Val	Ala	Gln	Glu	Asp	
			660					665					670			
Gly	Val	Val	Glu	Tyr	Val	Asp	Ser	Tyr	Glu	Ile	Val	Val	Ala	Lys	Lys	
		675					680					685				
Asn	Asn	Pro	Thr	Leu	Lys	Asp	Arg	Tyr	Gln	Leu	Lys	Lys	Phe	Leu	Arg	
	690					695					700					
Ser	Asn	Ser	Gly	Thr	Cys	Ile	Asn	Gln	Thr	Pro	Leu	Cys	Ser	Val	Gly	
705					710					715					720	
Asp	Val	Val	Thr	His	Gly	Asp	Val	Leu	Ala	Asp	Gly	Pro	Ala	Thr	Asp	
			725						730					735		
Lys	Gly	Glu	Leu	Ala	Leu	Gly	Lys	Asn	Val	Leu	Val	Ala	Phe	Met	Pro	
			740					745					750			
Trp	Tyr	Gly	Tyr	Asn	Phe	Glu	Asp	Ala	Ile	Ile	Ile	Ser	Glu	Arg	Leu	
		755					760					765				
Ile	Lys	Gln	Asp	Ala	Tyr	Thr	Ser	Ile	Tyr	Ile	Glu	Glu	Phe	Glu	Leu	
	770					775					780					
Thr	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Lys	Glu	Glu	Ile	Thr	Arg	Asp	Ile	
785					790					795					800	
Pro	Asn	Val	Ser	Glu	Glu	Val	Leu	Ala	Asn	Leu	Gly	Glu	Asp	Gly	Ile	
				805					810					815		
Val	Arg	Ile	Gly	Ala	Glu	Val	Lys	Pro	Gly	Asp	Ile	Leu	Val	Gly	Lys	
			820					825					830			
Ile	Thr	Pro	Lys	Ser	Glu	Thr	Glu	Leu	Ala	Pro	Glu	Glu	Arg	Leu	Leu	
		835					840					845				
Arg	Ala	Ile	Phe	Gly	Glu	Lys	Ala	Ala	Asp	Val	Lys	Asp	Ala	Ser	Leu	
		850				85										

Glu Val Asn Tyr Lys Thr Glu Ala Glu His Ile Lys Glu Gly Asp Ala  
 995 1000 1005  
 Asp Leu Asp His Gly Val Ile Arg Gln Val Lys Val Tyr Val Ala Ser  
 1010 1015 1020  
 Lys Arg Lys Leu Gln Val Gly Asp Lys Met Ala Gly Arg His Gly Asn  
 1025 1030 1035 1040  
 Lys Gly Val Val Ser Lys Ile Val Pro Glu Ala Asp Met Pro Phe Leu  
 1045 1050 1055  
 Ala Asn Gly Glu Thr Val Gln Met Ile Leu Asn Pro Leu Gly Val Pro  
 1060 1065 1070  
 Ser Arg Met Asn Leu Gly Gln Val Leu Glu Thr His Leu Gly Tyr Ala  
 1075 1080 1085  
 Ala Lys Thr Ala Gly Ile Tyr Val Lys Thr Pro Val Phe Glu Gly Phe  
 1090 1095 1100  
 Pro Glu Ser Arg Ile Trp Asp Met Met Ile Glu Gln Gly Leu Pro Glu  
 1105 1110 1115 1120  
 Asp Gly Lys Ser Tyr Leu Phe Asp Gly Lys Thr Gly Glu Arg Phe Asp  
 1125 1130 1135  
 Ser Lys Val Val Gly Tyr Ile Tyr Met Leu Lys Leu Ser His Leu  
 1140 1145 1150  
 Ile Ala Asp Lys Ile His Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val  
 1155 1160 1165  
 Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Met Gly Gly Gln Arg Phe  
 1170 1175 1180  
 Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Val Ala His Met  
 1185 1190 1195 1200  
 Leu Gln Glu Ile Leu Thr Val Lys Ser Asp Asp Val Ser Gly Arg Thr  
 1205 1210 1215  
 Arg Ile Tyr Glu Ser Ile Val Lys Gly Glu Asn Leu Leu Arg Ser Gly  
 1220 1225 1230  
 Thr Pro Glu Ser Phe Asn Val Leu Ile Lys Glu Met Gln Gly Leu Gly  
 1235 1240 1245  
 Leu Asp Val Arg Pro Met Val Val Asp Ala  
 1250 1255

(2) INFORMATIONS POUR LA SEQ ID NO: 119:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1396 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui \_

(viii) POSITION DANS LE GENOME: 119823..124010

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 119:

Met Phe Arg Glu Gly Ser Arg Asp Asp Ala Ala Leu Val Lys Glu Gly  
 1 5 10 15  
 Leu Phe Asp Lys Leu Glu Ile Gly Ile Ala Ser Asp Val Thr Ile Arg  
 20 25 30  
 Asp Lys Trp Ser Cys Gly Glu Ile Lys Lys Pro Glu Thr Ile Asn Tyr  
 35 40 45  
 Arg Thr Phe Lys Pro Glu Lys Gly Gly Leu Phe Cys Glu Lys Ile Phe  
 50 55 60  
 Gly Pro Thr Lys Asp Trp Glu Cys Tyr Cys Gly Lys Tyr Lys Lys Ile

65					70					75					80
Lys	His	Lys	Gly	Ile	Val	Cys	Asp	Arg	Cys	Gly	Val	Glu	Val	Thr	Leu
				85					90					95	
Ser	Lys	Val	Arg	Arg	Glu	Arg	Met	Ala	His	Ile	Glu	Leu	Ala	Val	Pro
			100					105					110		
Ile	Val	His	Ile	Trp	Phe	Phe	Lys	Thr	Thr	Pro	Ser	Arg	Ile	Gly	Asn
		115					120					125			
Val	Leu	Gly	Met	Thr	Ala	Ser	Asp	Leu	Glu	Arg	Val	Ile	Tyr	Tyr	Glu
	130					135				140					
Glu	Tyr	Val	Val	Ile	Asp	Pro	Gly	Asn	Thr	Asp	Leu	Val	Lys	Lys	Gln
145					150					155					160
Leu	Leu	Asn	Asp	Ala	Lys	Tyr	Arg	Glu	Val	Val	Glu	Lys	Trp	Gly	Lys
				165				170						175	
Asp	Ala	Phe	Val	Ala	Lys	Met	Gly	Gly	Glu	Ala	Val	Tyr	Asp	Leu	Leu
			180				185					190			
Lys	Ser	Glu	Asp	Leu	Glu	Ser	Leu	Leu	Gly	Glu	Leu	Lys	Asp	Arg	Leu
		195					200					205			
Arg	Lys	Thr	Lys	Ser	Gln	Gln	Ala	Arg	Met	Lys	Leu	Ala	Lys	Arg	Leu
	210				215						220				
Lys	Ile	Val	Glu	Gly	Phe	Val	Ser	Ser	Ser	Asn	Arg	Pro	Glu	Trp	Met
225					230					235					240
Val	Leu	Lys	Asn	Ile	Pro	Val	Val	Pro	Pro	Asp	Leu	Arg	Pro	Leu	Val
			245					250						255	
Pro	Leu	Asp	Gly	Gly	Arg	Phe	Ala	Thr	Ser	Asp	Leu	Asn	Asp	Leu	Tyr
			260				265						270		
Arg	Arg	Val	Ile	Asn	Arg	Asn	Asn	Arg	Leu	Lys	Ala	Ile	Leu	Arg	Leu
		275				280						285			
Lys	Thr	Pro	Glu	Val	Ile	Val	Arg	Asn	Glu	Lys	Arg	Met	Leu	Gln	Glu
	290				295					300					
Ala	Val	Asp	Ala	Leu	Phe	Asp	Asn	Gly	Arg	His	Gly	His	Pro	Val	Met
305					310					315					320
Gly	Ala	Gly	Asn	Arg	Pro	Leu	Lys	Ser	Leu	Ser	Glu	Met	Leu	Lys	Gly
			325						330					335	
Lys	Asn	Gly	Arg	Phe	Arg	Gln	Asn	Leu	Leu	Gly	Lys	Arg	Val	Asp	Tyr
			340				345					350			
Ser	Gly	Arg	Ser	Val	Ile	Ile	Val	Gly	Pro	Glu	Leu	Lys	Phe	Asn	Gln
	355				360							365			
Cys	Gly	Leu	Pro	Lys	Glu	Met	Ala	Leu	Glu	Leu	Phe	Glu	Pro	Phe	Ile
	370				375					380					
Ile	Lys	Arg	Leu	Lys	Asp	Gln	Gly	Ser	Val	Tyr	Thr	Ile	Arg	Ser	Ala
385					390				395						400
Lys	Lys	Met	Ile	Gln	Arg	Gly	Ala	Pro	Glu	Val	Trp	Asp	Val	Leu	Glu
			405					410						415	
Glu	Ile	Ile	Lys	Gly	His	Pro	Val	Leu	Leu	Asn	Arg	Ala	Pro	Thr	Leu
			420				425					430			
His	Arg	Leu	Gly	Ile	Gln	Ala	Phe	Glu	Pro	Val	Leu	Ile	Glu	Gly	Lys
	435					440						445			
Ala	Ile	Arg	Val	His	Pro	Leu	Val	Cys	Ala	Ala	Phe	Asn	Ala	Asp	Phe
	450				455					460					
Asp	Gly	Asp	Gln	Met	Ala	Val	His	Val	Pro	Leu	Ser	Ile	Glu	Ala	Gln
465					470				475						480
Leu	Glu	Ala	Lys	Val	Leu	Met	Met	Ala	Pro	Asp	Asn	Ile	Phe	Leu	Pro
			485					490						495	
Ser	Ser	Gly	Lys	Pro	Val	Ala	Thr	Pro	Ser	Lys	Asp	Met	Thr	Leu	Gly
			500				505					510			
Ile	Tyr	Tyr	Leu	Met	Ala	Asp	Pro	Thr	Tyr	Phe	Pro	Glu	Glu	His	Gly
	515					520					525				
Gly	Lys	Thr	Lys	Ala	Phe	Lys	Asp	Glu	Val	Glu	Val	Leu	Arg	Ala	Leu
	530					535					540				

Asn	Ala	Gly	Gly	Phe	Ile	Leu	Lys	Asp	Glu	Ile	Cys	Gly	Ser	Arg	Arg	
545					550					555					560	
Asp	Glu	Thr	Gly	Arg	Gly	Ile	His	Ile	His	Glu	Lys	Ile	Lys	Val	Arg	
				565					570					575		
Ile	Asp	Gly	Gln	Ile	Ile	Glu	Thr	Thr	Pro	Gly	Arg	Val	Phe	Phe	Asn	
			580					585					590			
Thr	Ile	Val	Pro	Lys	Glu	Leu	Gly	Phe	Gln	Asn	Tyr	Ser	Met	Pro	Ser	
		595					600					605				
Lys	Arg	Ile	Ser	Glu	Leu	Ile	Leu	Gln	Cys	Tyr	Lys	Lys	Val	Gly	Leu	
	610					615					620					
Glu	Ala	Thr	Val	Arg	Phe	Leu	Asp	Asp	Leu	Lys	Glu	Leu	Gly	Phe	Val	
625					630					635					640	
Gln	Ser	Thr	Lys	Ala	Ala	Ile	Ser	Met	Gly	Leu	Lys	Asp	Val	Lys	Ile	
				645					650					655		
Pro	Glu	Ile	Lys	Lys	Glu	Ile	Leu	Lys	Asp	Ala	Tyr	Asp	Lys	Val	Ala	
			660					665					670			
Ile	Val	Lys	Lys	Gln	Tyr	Glu	Asp	Gly	Ile	Ile	Thr	Asp	Gly	Glu	Arg	
		675					680					685				
His	Ser	Lys	Thr	Ile	Ser	Ile	Trp	Thr	Glu	Val	Ser	Asp	Leu	Leu	Ser	
	690					695					700					
Asn	Ala	Leu	Tyr	Ser	Glu	Ile	Lys	Lys	Gln	Thr	Asn	Ser	Lys	His	Asn	
705					710					715					720	
Pro	Leu	Phe	Leu	Met	Val	Xaa	Ser	Gly	Ala	Arg	Gly	Asn	Lys	Ser	Gln	
				725					730					735		
Leu	Lys	Gln	Leu	Gly	Ala	Leu	Arg	Gly	Leu	Met	Ala	Lys	Pro	Asn	Gly	
			740					745					750			
Ala	Ile	Ile	Glu	Ser	Pro	Ile	Thr	Ser	Asn	Phe	Arg	Glu	Gly	Leu	Thr	
		755					760					765				
Val	Leu	Glu	Tyr	Ser	Ile	Ser	Ser	His	Gly	Ala	Arg	Lys	Gly	Leu	Ala	
	770					775					780					
Asp	Thr	Ala	His	Lys	Thr	Ala	Asp	Ser	Gly	Tyr	Leu	Thr	Arg	Arg	Leu	
785					790					795					800	
Val	Asp	Val	Ala	Gln	Asp	Val	Ile	Ile	Thr	Glu	Arg	Asp	Cys	Gly	Thr	
				805					810					815		
Leu	Asn	His	Ile	Glu	Val	Ser	Thr	Ile	Arg	Gln	Gly	Ser	Glu	Glu	Leu	
			820					825					830			
Leu	Pro	Leu	Lys	Asp	Arg	Val	Tyr	Gly	Arg	Thr	Val	Ser	Glu	Asn	Ile	
		835					840					845				
Tyr	Gln	Pro	Gly	Asp	Lys	Ser	Asn	Val	Leu	Ala	Tyr	Ala	Gly	Asp	Val	
	850					855					860					
Leu	Thr	Ser	Ala	Gln	Ala	Glu	Ala	Ile	Asp	Asp	Ala	Gly	Ile	Glu	Ser	
865					870					875					880	
Val	Lys	Ile	Arg	Ser	Thr	Leu	Thr	Cys	Glu	Ser	Arg	Arg	Gly	Val	Cys	
				885					890					895		
Ala	Lys	Cys	Tyr	Gly	Leu	Asn	Leu	Ala	Asn	Gly	His	Leu	Ile	Gly	Leu	
			900					905					910			
Gly	Glu	Ala	Val	Gly	Ile	Ile	Ala	Ala	Gln	Ser	Ile	Gly	Glu	Pro	Gly	
		915					920						925			
Thr	Gln	Leu	Thr	Met	Arg	Thr	Phe	His	Leu	Gly	Gly	Val	Ala	Ala	Thr	
	930					935						940				
Ser	Ser	Thr	Pro	Glu	Ile	Val	Ala	Glu	Cys	Asp	Gly	Ile	Leu	Val	Tyr	
945					950					955					960	
Leu	Asp	Leu	Arg	Val	Val	Val	Asp	Gln	Glu	Gly	Asn	Asn	Leu	Val	Leu	
				965					970					975		
Asn	Lys	Met	Gly	Ala	Leu	His	Leu	Val	Gln	Asp	Glu	Gly	Arg	Ser	Leu	
			980					985					990			
Ser	Glu	Tyr	Lys	Lys	Leu	Leu	Ser	Thr	Lys	Ser	Ile	Glu	Ser	Leu	Ala	
		995					1000					1005				
Thr	Phe	Pro	Val	Glu	Leu	Gly	Ala	Lys	Ile	Leu	Val	Asn	Asp	Gly	Ala	

1010	1015	1020
Ala Val Thr Ala Gly Gln Arg Ile Ala Glu Val Glu Leu His Asn Ile		
1025	1030	1035
Pro Ile Ile Cys Asp Lys Pro Gly Phe Val His Tyr Glu Asp Leu Val		1040
	1045	1050
Glu Gly Val Ser Thr Glu Lys Val Ala Asn Lys Asn Thr Gly Leu Val		1055
	1060	1065
Glu Leu Ile Val Lys Gln His Arg Gly Glu Leu His Pro Gln Ile Ala		1070
	1075	1080
Ile Tyr Ala Asp Ala Asn Met Lys Glu Leu Val Gly Thr Tyr Ala Ile		1085
	1090	1095
Pro Ser Gly Ala Ile Ile Ser Val Glu Glu Gly Gln Arg Ile Ala Pro		1100
1105	1110	1115
Gly Met Leu Leu Ala Arg Leu Pro Arg Gly Ala Ile Lys Thr Lys Asp		1120
	1125	1130
Ile Thr Gly Gly Leu Pro Arg Val Ala Glu Leu Val Glu Ala Arg Lys		1135
	1140	1145
Pro Glu Asp Ala Ala Asp Ile Ala Lys Ile Asp Gly Val Val Asp Phe		1150
	1155	1160
Lys Gly Ile Gln Lys Asn Lys Arg Ile Leu Val Val Arg Asp Glu Ile		1165
	1170	1175
Thr Gly Met Glu Glu Glu His Leu Ile Ser Leu Thr Lys His Leu Ile		1180
1185	1190	1195
Val Gln Arg Gly Asp Ser Val Ile Lys Gly Gln Gln Leu Thr Asp Gly		1200
	1205	1210
Leu Val Val Pro His Glu Ile Leu Ala Ile Cys Gly Val Arg Glu Leu		1215
	1220	1225
Gln Lys Tyr Leu Val Asn Glu Val Gln Glu Val Tyr Arg Leu Gln Gly		1230
	1235	1240
Val Asp Ile Asn Asp Lys His Ile Glu Ile Ile Val Arg Gln Met Leu		1245
	1250	1255
Gln Lys Val Arg Ile Thr Asp Pro Gly Asp Thr Thr Leu Leu Phe Gly		1260
1265	1270	1275
Glu Asp Val Asp Lys Lys Glu Phe Tyr Glu Glu Asn Arg Arg Thr Glu		1280
	1285	1290
Glu Asp Gly Gly Lys Pro Ala Gln Ala Val Pro Val Leu Leu Gly Ile		1295
	1300	1305
Thr Lys Ala Ser Leu Gly Thr Glu Ser Phe Ile Ser Ala Ala Ser Phe		1310
	1315	1320
Gln Asp Thr Thr Arg Val Leu Thr Asp Ala Ala Cys Ser Ser Lys Thr		1325
	1330	1335
Asp Tyr Leu Leu Gly Phe Lys Glu Asn Val Ile Met Gly His Met Ile		1340
1345	1350	1355
Pro Gly Gly Thr Gly Phe Asp Thr His Lys Arg Ile Lys Gln His Leu		1360
	1365	1370
Glu Lys Glu Gln Glu Asp Leu Val Phe Asp Phe Asp Ser Glu Phe Glu		1375
	1380	1385
Ser Val Ala Gly		1390
	1395	

(2) INFORMATIONS POUR LA SEQ ID NO: 120:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 124095..124988

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 120:

His	Leu	Glu	Ser	Lys	Ile	Asp	Lys	Val	Phe	Met	Ser	Ser	Gln	Phe	Asp	1	5	10	15
Gln	Phe	Lys	Leu	Trp	Ser	Val	Leu	Val	Gly	Asp	Thr	Gly	Asp	Pro	Ala	20	25	30	
Leu	Ile	Lys	Thr	Leu	Gly	Val	Gln	Asp	Ala	Thr	Thr	Asn	Pro	Ser	Leu	35	40	45	
Ile	Leu	Lys	Val	Ala	Gln	Glu	Pro	Lys	Tyr	Gln	Ser	Met	Leu	Thr	Glu	50	55	60	
Ala	Ile	Ser	Trp	Gly	Ile	Arg	Gln	Asn	Gly	Asp	Asp	Val	Gln	Thr	Leu	65	70	75	80
Thr	Phe	Val	Leu	Asp	Lys	Ile	Gln	Val	Asn	Leu	Gly	Leu	Glu	Ile	Leu	85	90	95	
Lys	His	Val	Pro	Gly	Arg	Val	Ser	Leu	Glu	Ile	Asp	Ala	Arg	Leu	Ser	100	105	110	
Phe	Asn	Thr	Glu	Ala	Met	Val	Gln	Arg	Ala	Ile	Phe	Leu	Ser	Gln	Leu	115	120	125	
Phe	Glu	Lys	Met	Gly	Gly	Asp	Lys	Lys	Arg	Leu	Leu	Val	Lys	Ile	Pro	130	135	140	
Gly	Thr	Trp	Glu	Gly	Ile	Cys	Ala	Ala	Glu	Val	Leu	Glu	Ser	Gln	Gly	145	150	155	160
Ile	Ala	Cys	Asn	Val	Thr	Leu	Ile	Phe	Asn	Leu	Val	Gln	Ala	Ile	Ala	165	170	175	
Ala	Ala	Lys	Ala	Lys	Val	Thr	Leu	Val	Ser	Pro	Phe	Val	Gly	Arg	Ile	180	185	190	
Tyr	Asp	Trp	Trp	Ile	Ala	Ala	Tyr	Gly	Ala	Glu	Gly	Tyr	Ser	Ile	Glu	195	200	205	
Ala	Asp	Pro	Gly	Val	Ala	Ser	Val	Ala	Asn	Ile	Tyr	Ser	Tyr	Tyr	Lys	210	215	220	
Lys	Phe	Asp	Ile	Pro	Thr	Gln	Ile	Met	Ala	Ala	Ser	Phe	Arg	Thr	Lys	225	230	235	240
Glu	Gln	Val	Leu	Ala	Leu	Ala	Gly	Cys	Asp	Phe	Leu	Thr	Val	Ser	Pro	245	250	255	
Lys	Leu	Leu	Glu	Leu	Lys	Lys	Asp	Gln	Gln	Pro	Val	Glu	Arg	Lys		260	265	270	
Leu	Ser	Val	Glu	Glu	Ala	Lys	Lys	Ile	Arg	Tyr	Ser	Thr	Cys	Gly	Val	275	280	285	
Val	Arg	Glu	Cys	Ile	Ser	Val	Leu	Asn	Glu							290	295		

(2) INFORMATIONS POUR LA SEQ ID NO: 121:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 78 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 124873..125106

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 121:



```

Lys Asn Ser Arg Lys Ile Ser Ser Leu Leu Lys Glu Ser Leu Ala Trp
1           5           10           15
Lys Lys Arg Lys Lys Leu Asp Ile Gln Pro Val Glu Leu Ser Glu Ser
20           25           30
Val Phe Arg Phe Leu Met Asn Glu Asp Ala Met Ala Thr Glu Lys Leu
35           40           45
Ala Glu Gly Ile Arg Ile Phe Ser Gly Asp Thr Gln Ile Leu Glu Ser
50           55           60
Ala Val Thr Glu Phe Ile Arg Gln Ile Ala Ala Gln Glu Ala
65           70           75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 122:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 242 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(125536..126261)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 122:

```

Asn Gln Thr Leu Asn Leu Met Lys Arg Val Ile Leu Cys Ser Leu Leu
1           5           10           15
Phe Ala Ser Phe Pro Ile Val Ser Lys Ala Ala Ala Glu Gly Lys Pro
20           25           30
Leu Ser Arg Ala Ala Gln Leu Arg Glu Lys Arg Lys Asp Leu His Val
35           40           45
Ser Arg Lys Pro Ser Pro Arg Tyr Ala Leu Lys Lys Arg Ala Leu Glu
50           55           60
Ala Lys Lys Asn Arg Pro Ser Ile Ser Trp Ile Thr Tyr Ser Asn Ala
65           70           75           80
Thr Tyr Ser Phe Leu Ile Pro Asn Thr Trp Gln Cys Ile Asp Asp Lys
85           90           95
Thr Gln Leu Pro Glu Lys Leu Asp Val Leu Phe Ile Gly Lys Gly Ala
100          105          110
Gly Gly Leu Thr Pro Thr Ile Asn Ser Ala His Glu Ile Ile His Lys
115          120          125
Thr Glu Asp Ala Tyr Ile Glu Glu Ile Leu Asp Tyr His Arg Ala Asn
130          135          140
Glu Asn Thr Leu Glu Ser Ser Ile Phe Ala His Ile Gln Ala Pro Ser
145          150          155          160
Gly Lys Phe Thr Ile Ile Lys Thr Glu Lys Asn Thr Ser Trp Gly Arg
165          170          175
Val Phe Cys Leu Gln Gly Val Thr Val Ile Asp His Thr Ala Tyr Ile
180          185          190
Phe Thr Ser Thr Ser Thr Ile Asp Asp Tyr Pro Asn Val Ser Leu Ala
195          200          205
Leu Leu Lys Ala Ala Ser Ser Phe Lys Leu Ser Glu Lys Glu Glu Ala
210          215          220
Ala Arg Gly Asp Ala Ile Leu Glu Lys Ala Leu Lys Asp Leu Gln Asn
225          230          235          240
Gly Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 123:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 201 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 126328..126930

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 123:

Thr	Leu	Phe	Phe	Leu	Val	Ser	Asp	Met	Ala	Asp	Leu	Ser	Ala	Gln	Asp
1			5						10					15	
Lys	Leu	Lys	Gln	Ile	Cys	Asp	Ala	Leu	Arg	Glu	Glu	Thr	Leu	Lys	Pro
			20					25					30		
Ala	Glu	Glu	Glu	Ala	Gly	Ser	Ile	Val	His	Asn	Ala	Arg	Glu	Gln	Ala
			35				40					45			
Lys	Arg	Ile	Val	Glu	Glu	Ala	Lys	Glu	Glu	Ala	Gln	Arg	Ile	Ile	Arg
	50						55				60				
Ser	Ala	Glu	Glu	Thr	Ala	Asp	Gln	Thr	Leu	Lys	Lys	Gly	Glu	Ala	Ala
65					70					75				80	
Leu	Val	Gln	Ala	Gly	Lys	Arg	Ser	Leu	Glu	Asn	Leu	Lys	Gln	Ala	Val
				85					90				95		
Glu	Thr	Lys	Ile	Phe	Arg	Glu	Ser	Leu	Gly	Glu	Trp	Leu	Asp	His	Val
			100					105					110		
Ala	Thr	Asp	Pro	Glu	Val	Ser	Ala	Lys	Leu	Val	Gln	Ala	Leu	Val	Gln
			115				120					125			
Ala	Val	Asp	Ala	Gln	Gly	Ile	Ser	Gly	Asn	Leu	Ser	Ala	Tyr	Ile	Gly
	130					135					140				
Lys	His	Val	Ser	Ala	Arg	Ala	Val	Asn	Glu	Ala	Leu	Gly	Lys	Glu	Ile
145					150					155				160	
Thr	Ser	Lys	Leu	Lys	Glu	Lys	Gly	Val	Ser	Val	Gly	Lys	Phe	Ser	Gly
				165				170					175		
Gly	Ala	Gln	Leu	Lys	Val	Glu	Glu	Arg	Asn	Trp	Val	Leu	Asp	Met	Ser
			180					185					190		
Ser	Glu	Val	Leu	Leu	Asp	Phe	Ile	Asp							
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 124:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 127138..127785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 124:

Glu Arg Val Met Asn Gln Tyr Tyr Phe Leu Ser Ser Phe Leu Ser Pro

1				5						10					15
Gln	Gln	Pro	Glu	Ser	Ser	Pro	Leu	Tyr	Ser	Phe	Gln	Glu	Ile	Asn	Asp
			20					25					30		
Leu	Leu	Ala	Leu	Asn	Phe	Thr	Asp	Lys	Asp	Trp	Arg	Ser	Tyr	Val	Ile
		35					40					45			
Leu	Arg	Arg	Phe	Phe	Asp	Leu	Glu	Asn	Phe	Ala	Phe	Phe	Trp	Ala	Gly
	50					55					60				
Lys	Ser	Ile	Pro	Phe	Ser	Phe	Gly	Thr	Val	Thr	Asn	Ser	Asn	Val	Glu
65					70					75				80	
Ser	Leu	Leu	Arg	Leu	Gln	Met	Trp	Ser	Asp	Glu	Trp	Glu	Phe	Glu	Asp
				85				90						95	
Phe	Phe	Lys	Asp	Phe	Leu	Leu	Arg	Tyr	Lys	Thr	Pro	Arg	Glu	Arg	Leu
			100					105					110		
Thr	His	Phe	Ser	Glu	Leu	Val	Arg	Asp	Phe	Leu	Asp	His	Tyr	Gln	Asp
		115					120					125			
Tyr	Pro	Ser	Glu	Phe	Leu	Arg	Thr	Tyr	Phe	Arg	Phe	Lys	Gln	Asp	Leu
	130					135					140				
Arg	Ile	Ile	Leu	Ala	Gly	Phe	Arg	Ala	Arg	Val	Met	Gln	Lys	Asp	Val
145					150					155				160	
Ser	Phe	Val	Leu	Arg	Asp	Glu	Asp	Ser	Ser	Asn	Pro	Ile	Val	Leu	His
				165				170						175	
Val	Leu	Met	Gln	Lys	Asp	Ser	Pro	Asn	Tyr	Glu	Leu	Pro	Asp	Glu	Phe
			180					185					190		
Phe	Glu	Leu	Arg	Asp	Val	Leu	Gly	Arg	Leu	Arg	Ala	Ser	Ser	Thr	His
		195				200						205			
Val	Glu	Ser	Asp	Ser	Leu	Phe	Leu								
	210					215									

(2) INFORMATIONS POUR LA SEQ ID NO: 125:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 597 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 127924..129714

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 125:

Asp	Gly	Glu	Arg	Asn	Gln	Met	Val	Ala	Thr	Ser	Lys	Gln	Thr	Thr	Gln
1				5					10					15	
Gly	Tyr	Val	Val	Glu	Ala	Tyr	Gly	Asn	Leu	Leu	Arg	Val	His	Val	Asp
			20					25				30			
Gly	His	Val	Arg	Gln	Gly	Glu	Val	Ala	Tyr	Val	Ser	Val	Asp	Asn	Thr
		35					40					45			
Trp	Leu	Lys	Ala	Glu	Ile	Ile	Glu	Val	Val	Gly	Met	Lys	Leu	Arg	Phe
	50					55					60				
Gln	Val	Phe	Glu	Glu	Thr	Gln	Gly	Ile	Ser	Arg	Gly	Ala	Leu	Val	Thr
65					70					75				80	
Phe	Ser	Gly	His	Leu	Leu	Glu	Ala	Glu	Leu	Gly	Pro	Gly	Leu	Leu	Gln
				85				90					95		
Gly	Ile	Phe	Asp	Gly	Leu	Gln	Asn	Arg	Leu	Glu	Ile	Leu	Ala	Asp	Thr
			100				105					110			
Ser	Leu	Phe	Leu	Arg	Arg	Gly	Glu	Tyr	Val	Asn	Ala	Ile	Cys	Arg	Glu
		115					120					125			

Thr	Val	Trp	Ala	Tyr	Thr	Gln	Lys	Ala	Ser	Val	Gly	Ser	Val	Leu	Ser	130	135	140
Arg	Gly	Asp	Val	Leu	Gly	Thr	Val	Lys	Glu	Gly	Arg	Phe	Asp	His	Lys	145	150	155
Ile	Met	Val	Pro	Phe	Ser	Cys	Phe	Glu	Glu	Val	Thr	Ile	Thr	Trp	Val	165	170	175
Ile	Ser	Ser	Gly	Asn	Tyr	Thr	Val	Asp	Thr	Val	Val	Ala	Lys	Gly	Arg	180	185	190
Thr	Ser	Thr	Gly	Glu	Glu	Leu	Glu	Phe	Thr	Met	Val	Gln	Lys	Trp	Pro	195	200	205
Ile	Lys	Gln	Ala	Phe	Leu	Glu	Gly	Glu	Lys	Val	Pro	Ser	His	Glu	Ile	210	215	220
Met	Asp	Val	Gly	Leu	Arg	Val	Leu	Asp	Thr	Gln	Ile	Pro	Val	Leu	Lys	225	230	235
Gly	Gly	Thr	Phe	Cys	Thr	Pro	Gly	Pro	Phe	Gly	Ala	Gly	Lys	Thr	Val	245	250	255
Leu	Gln	His	His	Leu	Ser	Lys	Tyr	Ala	Ala	Val	Asp	Ile	Val	Val	Leu	260	265	270
Cys	Ala	Cys	Gly	Glu	Arg	Ala	Gly	Glu	Val	Val	Glu	Ile	Leu	Gln	Glu	275	280	285
Phe	Pro	His	Leu	Lys	Asp	Pro	His	Thr	Gly	Gln	Ser	Leu	Met	His	Arg	290	295	300
Thr	Cys	Ile	Ile	Cys	Asn	Thr	Ser	Ser	Met	Pro	Val	Ala	Ala	Arg	Glu	305	310	315
Ser	Ser	Ile	Tyr	Leu	Gly	Ile	Thr	Ile	Ala	Glu	Tyr	Tyr	Arg	Gln	Met	325	330	335
Gly	Leu	His	Ile	Leu	Leu	Leu	Ala	Asp	Ser	Thr	Ser	Arg	Trp	Ala	Gln	340	345	350
Ala	Leu	Arg	Glu	Ile	Ser	Gly	Arg	Leu	Glu	Glu	Ile	Pro	Gly	Glu	Glu	355	360	365
Ala	Phe	Pro	Ala	Tyr	Leu	Ala	Ser	Arg	Ile	Ala	Ala	Phe	Tyr	Glu	Arg	370	375	380
Gly	Gly	Ala	Val	Lys	Met	Lys	Asp	Gly	Ser	Glu	Gly	Ser	Leu	Thr	Ile	385	390	395
Cys	Gly	Ala	Val	Ser	Pro	Ala	Gly	Gly	Asn	Phe	Glu	Glu	Pro	Val	Thr	405	410	415
Gln	Ala	Thr	Leu	Ser	Val	Val	Gly	Ala	Phe	Cys	Gly	Leu	Ser	Lys	Ala	420	425	430
Arg	Ala	Asp	Ala	Arg	Arg	Tyr	Pro	Ser	Ile	Asp	Pro	Met	Ile	Ser	Trp	435	440	445
Ser	Lys	Tyr	Leu	Asp	Ser	Val	Ala	Glu	Ile	Leu	Glu	Lys	Lys	Val	Pro	450	455	460
Gly	Trp	Gly	Glu	Ser	Val	Lys	Gln	Ala	Ser	Arg	Phe	Leu	Glu	Glu	Gly	465	470	475
Ala	Glu	Ile	Gly	Lys	Arg	Ile	Glu	Val	Val	Gly	Glu	Glu	Gly	Ile	Ser	485	490	495
Met	Glu	Asp	Met	Glu	Ile	Phe	Leu	Lys	Ser	Glu	Leu	Tyr	Asp	Phe	Cys	500	505	510
Tyr	Leu	Gln	Asn	Ala	Phe	Asp	Ala	Glu	Asp	Cys	Tyr	Cys	Pro	Phe		515	520	525
Asp	Arg	Gln	Ile	Glu	Leu	Phe	Ser	Leu	Met	Asn	His	Ile	Phe	Asn	Ser	530	535	540
Arg	Phe	Cys	Phe	Asp	Cys	Pro	Asp	Asn	Ala	Arg	Ser	Phe	Phe	Leu	Glu	545	550	555
Leu	Gln	Ser	Lys	Ile	Lys	Thr	Leu	Asn	Gly	Gln	Lys	Phe	Leu	Ser	Glu	565	570	575
Glu	Tyr	Gln	Lys	Gly	Leu	Glu	Val	Ile	Tyr	Lys	Leu	Leu	Glu	Ser	Lys	580	585	590
Met	Val	Gln	Thr	Ala														

595

(2) INFORMATIONS POUR LA SEQ ID NO: 126:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 129720..131033

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 126:

Met	Gln	Thr	Ile	Tyr	Thr	Lys	Ile	Thr	Asp	Ile	Lys	Gly	Asn	Leu	Ile
1			5					10					15		
Thr	Val	Glu	Ala	Glu	Gly	Ala	Ser	Leu	Gly	Glu	Leu	Val	Gln	Ile	Glu
		20					25						30		
Arg	Ala	Asp	Gly	Arg	Ser	Ser	Tyr	Ala	Ser	Val	Leu	Arg	Phe	Asp	Ala
		35					40					45			
Arg	Lys	Val	Thr	Leu	Gln	Val	Phe	Gly	Gly	Thr	Ser	Gly	Leu	Ser	Thr
	50					55				60					
Gly	Asp	Lys	Val	Ile	Phe	Leu	Gly	Arg	Pro	Met	Glu	Val	Ile	Tyr	Gly
65				70					75					80	
Asp	Ser	Leu	Leu	Gly	Arg	Arg	Phe	Asn	Gly	Thr	Gly	Lys	Pro	Ile	Asp
			85					90						95	
His	Glu	Asp	Glu	Cys	Phe	Gly	Glu	Pro	Ile	Pro	Ile	Thr	Thr	Pro	Ser
		100						105					110		
Phe	Asn	Pro	Val	Cys	Arg	Ile	Val	Pro	Arg	Glu	Met	Val	Arg	Thr	Asn
		115					120					125			
Ile	Pro	Met	Ile	Asp	Met	Phe	Asn	Cys	Leu	Val	Lys	Ser	Gln	Lys	Ile
	130					135					140				
Pro	Ile	Phe	Ser	Ser	Ser	Gly	Glu	Asn	His	Asn	Ala	Leu	Leu	Met	Arg
145				150					155					160	
Ile	Ala	Ala	Gln	Thr	Asp	Ala	Asp	Ile	Val	Ile	Ile	Gly	Gly	Met	Gly
			165					170						175	
Leu	Thr	Phe	Val	Asp	Tyr	Asn	Phe	Phe	Val	Glu	Glu	Ser	Gln	Arg	Leu
		180					185						190		
Gly	Phe	Ala	Asp	Lys	Cys	Val	Lys	Phe	Ile	His	Lys	Ala	Val	Asp	Ala
	195						200					205			
Pro	Val	Glu	Cys	Val	Leu	Ile	Pro	Asp	Met	Ala	Leu	Ala	Cys	Ala	Glu
	210					215				220					
Arg	Phe	Ala	Leu	Glu	Gln	Gln	Lys	Asn	Val	Leu	Val	Leu	Leu	Thr	Asp
225				230					235					240	
Met	Thr	Ala	Phe	Ala	Asp	Ala	Leu	Lys	Glu	Ile	Ala	Ile	Thr	Met	Asp
			245					250						255	
Gln	Ile	Pro	Ala	Asn	Arg	Gly	Tyr	Pro	Gly	Ser	Leu	Tyr	Ser	Asp	Leu
		260						265					270		
Ala	Val	Arg	Tyr	Glu	Lys	Ala	Val	Asp	Ile	Ala	Gln	Gly	Gly	Ser	Ile
	275						280					285			
Thr	Leu	Ile	Ser	Val	Thr	Thr	Met	Pro	Gly	Asp	Asp	Ile	Thr	His	Pro
	290					295					300				
Val	Pro	Asp	Asn	Thr	Gly	Phe	Ile	Thr	Glu	Gly	Gln	Phe	Tyr	Leu	Lys
305				310					315					320	
Asp	Asn	Arg	Ile	Asp	Pro	Phe	Gly	Ser	Leu	Ser	Arg	Leu	Lys	Gln	Leu
			325						330					335	

Val Ile Gly Lys Lys Thr Arg Glu Asp His Gly Asp Leu Ala Asn Ala  
                   340                  345                  350  
 Leu Ile Arg Leu Tyr Ala Asp Ser Arg Lys Ser Ala Glu Arg Met Ser  
                   355                  360                  365  
 Met Gly Phe Lys Leu Ser Asn Trp Asp Lys Lys Leu Leu Ala Phe Ser  
                   370                  375                  380  
 Glu Leu Phe Glu Ala Arg Leu Met Ser Leu Glu Val Asn Ile Pro Leu  
 385                  390                  395                  400  
 Glu Glu Ala Leu Asp Ile Gly Trp Lys Ile Leu Ser Gln Ser Phe His  
                   405                  410                  415  
 Ser Glu Glu Val Gly Ile Lys Glu Gln Leu Ile Gln Lys Tyr Trp Pro  
                   420                  425                  430  
 Lys Ala Cys Leu His Lys  
                   435

(2) INFORMATIONS POUR LA SEQ ID NO: 127:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 131018..131629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 127:

Ser Met Ser Ser Gln Ile Lys Leu Thr Lys Asn Ser Tyr Arg Ala Glu  
 1                  5                  10                  15  
 Lys Gln Lys Leu Asn Met Leu Gly Met Tyr Leu Pro Thr Leu Lys Leu  
                   20                  25                  30  
 Lys Lys Ala Leu Leu Gln Ala Glu Val Gln Ser Ala Ile Arg Leu Ala  
                   35                  40                  45  
 Ala Glu Ser Thr Ala Thr Asn Glu Gln Ala Arg Asp Arg Met Tyr Ala  
                   50                  55                  60  
 Phe Ala Glu Leu Phe Ser Ile Pro Leu Tyr Thr Asp Ala Val Glu Gln  
 65                  70                  75                  80  
 Cys Phe Ser Val Asp Ile Leu Glu Lys Asp Val Glu Asn Ile Ala Gly  
                   85                  90                  95  
 Val Glu Val Pro Leu Leu Lys Arg Val Val Leu Thr Ser Pro Glu Tyr  
                   100                  105                  110  
 Ser Leu Leu Asp Thr Pro Ile Trp Leu Asp Ser Leu Leu Ala Ser Val  
                   115                  120                  125  
 Lys Glu Tyr Val Val Ser Lys Ile Tyr Ala Glu Asn Ala Gln Glu Arg  
                   130                  135                  140  
 Leu Leu Leu Leu Glu Glu Leu Arg Arg Val Ser Ile Arg Val Asn  
 145                  150                  155                  160  
 Leu Phe Glu Lys Lys Leu Ile Pro Thr Thr Ser Gln Thr Leu Lys Lys  
                   165                  170                  175  
 Ile Ala Ile Phe Leu Ser Asp Arg Ser Ile Thr Asp Val Gly Gln Met  
                   180                  185                  190  
 Lys Met Ala Lys Lys Lys Ile Gln Gln His Lys Glu  
                   195                  200

(2) INFORMATIONS POUR LA SEQ ID NO: 128:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 441 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 131834..133156

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 128:

Ser	Thr	Lys	Ser	Gly	Tyr	Leu	Val	Thr	Glu	Gln	Leu	Leu	Gln	Glu	Ile	1	5	10	15
Phe	Asp	Leu	Asn	Gln	Glu	Ile	Thr	Thr	Leu	Thr	Glu	Ser	Leu	Lys	Ala	20	25	30	
Leu	Gly	Lys	Xaa	Ile	Val	Arg	Val	Lys	Pro	Leu	Gly	Asp	Phe	Ser	Ser	35	40	45	
Glu	Glu	Ile	Arg	Glu	Leu	Thr	Leu	Lys	Thr	Gly	Leu	Ala	Val	Arg	Phe	50	55	60	
Phe	Tyr	Lys	Arg	His	Ile	Glu	Gly	Ala	Pro	Leu	Glu	Val	Glu	Glu	Glu	65	70	75	80
Asn	Val	Phe	Tyr	Leu	Ala	Thr	Ala	Tyr	Asn	Tyr	Asp	Tyr	Tyr	Ala	Val	85	90	95	
Ile	Gly	Ile	Val	Ser	Leu	Ser	Lys	Asp	Ile	Phe	Thr	Glu	Ile	Glu	Ala	100	105	110	
Pro	Arg	Ser	Val	Asn	Glu	Leu	Arg	Glu	Glu	Ala	Gly	His	Leu	Gln	Ala	115	120	125	
Leu	Leu	Arg	Lys	Lys	Lys	Ala	Arg	Val	Cys	Glu	Leu	Tyr	Ala	Tyr	Arg	130	135	140	
Glu	Asp	Leu	Leu	Glu	Ala	Leu	Cys	Glu	Gln	Cys	Asn	Glu	Gln	Ser	Leu	145	150	155	160
Gln	His	Ala	Glu	Ala	Ser	Ala	Glu	Asp	Leu	Phe	Asp	Asp	Lys	Val	Phe	165	170	175	
Ser	Ala	Leu	Gly	Trp	Val	Ile	Val	Asp	Arg	Leu	Asp	Glu	Val	Lys	Lys	180	185	190	
Leu	Cys	Asp	Ser	Leu	Gly	Ile	Tyr	Leu	Glu	Arg	Val	Gln	Pro	Asp	Pro	195	200	205	
Asp	Glu	Val	Ile	Pro	Thr	Tyr	Leu	Glu	Asn	His	Gly	Leu	Gly	Ala	Leu	210	215	220	
Gly	Glu	Ser	Leu	Val	Asn	Ile	Tyr	Asp	Thr	Pro	Ala	Ser	Thr	Asp	Lys	225	230	235	240
Asp	Pro	Ser	Leu	Trp	Val	Phe	Phe	Ser	Phe	Phe	Val	Phe	Phe	Ser	Met	245	250	255	
Ile	Ile	Asn	Asp	Ala	Gly	Tyr	Gly	Leu	Val	Phe	Leu	Ala	Thr	Ser	Leu	260	265	270	
Phe	Leu	Ser	Phe	Lys	Ala	Arg	Lys	Gln	Ile	Lys	Arg	Ser	Ile	Ala	Leu	275	280	285	
Lys	Arg	Phe	Leu	Gln	Met	Phe	Met	Ile	Leu	Gly	Leu	Gly	Cys	Val	Cys	290	295	300	
Trp	Gly	Gly	Ala	Thr	Thr	Ser	Phe	Phe	Gly	Val	Ser	Val	Ser	Tyr	Thr	305	310	315	320
Ser	Pro	Phe	Arg	Glu	Tyr	Ser	Leu	Thr	His	Phe	Leu	Ala	Leu	Lys	Lys	325	330	335	
Ala	Glu	Tyr	Tyr	Leu	Lys	Glu	Arg	Pro	Lys	Gly	Tyr	Lys	Glu	Leu	Val	340	345	350	
His	Asp	Tyr	Pro	Ile	Leu	Lys	Glu	Lys	Lys	Thr	Pro	Lys	Glu	Phe	Leu	355	360	365	

Leu Ala Gln Ser Thr Ser Ser Gly Asp Ser Val Tyr Lys Ala Val Val  
 370 375 380  
 Tyr Asp Lys Phe Ile Asp Asn Ile Leu Met Glu Ile Ala Leu Leu Val  
 385 390 395 400  
 Gly Val Val His Leu Ser Leu Gly Met Leu Arg Tyr Cys Arg Gln Arg  
 405 410 415  
 Tyr Ser Ser Ile Gly Trp Val Ile Phe Met Cys Gly Asp Ile Cys Ile  
 420 425 430  
 Cys Leu Ser Ile Cys Lys Pro Tyr Leu  
 435 440

(2) INFORMATIONS POUR LA SEQ ID NO: 129:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 133075..133584

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 129:

Thr Ala Val Phe Phe Tyr Arg Met Gly Asn Leu Tyr Val Arg Arg Tyr  
 1 5 10 15  
 Met Tyr Leu Pro Ile Tyr Leu Gln Ala Val Ser Leu Ile His Tyr Ala  
 20 25 30  
 Leu His Ile Pro Tyr Glu Leu Gly Gly Leu Val Gly Tyr Tyr Val Thr  
 35 40 45  
 Phe Ile Gly Leu Gly Val Ala Ile Leu Gly Gly Val Ile Gln Arg Gly  
 50 55 60  
 Leu Arg Gly Leu Asp Glu Ile Thr Ala Val Ile Gln Val Phe Ser Asp  
 65 70 75 80  
 Val Leu Ser Tyr Leu Arg Leu Tyr Ala Leu Ser Leu Ala Gly Glu Met  
 85 90 95  
 Val Gly Asn Thr Val Met Val Met Ser Glu Arg Phe Ser Pro Ala Val  
 100 105 110  
 Gly Ile Leu Ile Ile Ile Phe Gly His Thr Val Asn Ile Ala Leu Ser  
 115 120 125  
 Ile Met Gly Gly Val Ile His Gly Leu Arg Leu Asn Phe Ile Glu Trp  
 130 135 140  
 Tyr His Tyr Ser Phe Asp Gly Gly Gly Lys Phe Leu His Pro Leu Lys  
 145 150 155 160  
 Lys Val Ile Tyr Gln Lys Ser Gln Asn Leu  
 165 170

(2) INFORMATIONS POUR LA SEQ ID NO: 130:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: 133625..133999

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 130:

Glu	Met	Ser	Ser	Glu	Arg	Lys	Tyr	Met	Ile	Asp	Val	Ser	Val	Val	Gly
1				5					10					15	
Pro	Val	Leu	Ala	Met	Ala	Leu	Ala	Met	Ile	Gly	Ser	Ala	Val	Gly	Cys
			20					25					30		
Gly	Met	Ala	Gly	Val	Ala	Ser	His	Ala	Val	Met	Ser	Arg	Ile	Asp	Glu
		35					40					45			
Gly	His	Gly	Lys	Ile	Ile	Gly	Leu	Ser	Ala	Met	Pro	Ser	Ser	Gln	Ser
	50					55					60				
Ile	Tyr	Gly	Leu	Ile	Phe	Met	Leu	Leu	Leu	Asn	Asp	Ala	Ile	Lys	Asp
65					70					75				80	
Gly	Lys	Val	Ser	Ala	Val	Ser	Gly	Ile	Val	Met	Gly	Ile	Ala	Val	Gly
				85					90					95	
Ser	Ala	Leu	Leu	Leu	Ser	Ala	Phe	Met	Gln	Gly	Lys	Cys	Cys	Val	Ser
			100					105					110		
Ala	Ile	Gln	Ala	Tyr	Ala	Arg	Ser	Ser	Ala	Asn	Ile	Trp			
		115					120					125			

(2) INFORMATIONS POUR LA SEQ ID NO: 131:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 133861..134508

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 131:

Gly	Trp	Lys	Ser	Leu	Cys	Ser	Gln	Trp	Tyr	Arg	Asn	Gly	Tyr	Ser	Cys
1				5					10					15	
Arg	Ile	Cys	Val	Ile	Ala	Phe	Cys	Phe	Tyr	Ala	Arg	Glu	Val	Leu	Cys
			20					25					30		
Glu	Cys	Tyr	Ser	Ser	Leu	Cys	Ala	Phe	Leu	Cys	Lys	Tyr	Met	Val	Asn
		35					40					45			
His	Leu	Leu	Arg	Leu	Gly	Leu	Leu	Ser	Leu	Leu	Arg	Tyr	Leu	Leu	Ser
	50					55					60				
Phe	Leu	Arg	Tyr	Cys	Tyr	Ser	Lys	Trp	Xaa	Ala	Ala	Ala	Phe	Ser	Ala
65					70					75				80	
Leu	Cys	Leu	Gly	Gly	Cys	Ser	Gln	Pro	Ala	Leu	Ser	Ser	Phe	Leu	Glu
			85						90					95	
Phe	Ile	Asp	Asn	Asp	Tyr	Thr	Ala	Ala	Ala	His	Leu	Gly	Ile	Asp	Arg
			100					105					110		
Gly	Cys	Val	Thr	Glu	Ser	Val	Gly	Gln	Gln	Leu	Val	Val	Thr	Trp	Gly
		115					120					125			
Leu	Pro	Ser	Arg	Phe	Arg	Asp	Ser	Leu	Pro	Met	Val	Leu	His	Val	Trp
	130					135					140				
Val	Tyr	Tyr	Gly	Asn	Gly	Glu	Ala	Ala	Lys	Phe	Ser	Tyr	Asp	Val	Gln
145					150					155				160	
His	Leu	Ser	Gly	Tyr	Gln	Val	Tyr	Thr	Leu	Lys	Glu	Asn	Asp	Tyr	Gln
			165						170					175	

Asp Arg Gln Gly Ile Xaa Ser Tyr Lys Val Ser Leu Thr Lys Asp Gly  
                   180                                  185                  190  
 Lys Glu Ile Leu Ser Arg Ser His His Leu Trp Met Glu Val Ile Ser  
                   195                                  200                  205  
 Leu Lys Ala Phe Ser Gln Leu Ser  
                   210                                  215

(2) INFORMATIONS POUR LA SEQ ID NO: 132:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 939 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 134638..137454

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 132:

Met Asn Glu Asp Gln Phe Pro Lys Ala Tyr Asp Pro Lys Ser Ser Glu  
 1                  5                                  10                  15  
 Thr Gly Val Tyr Ser Phe Trp Glu Arg Ser Gly Met Phe Val Ala Asn  
                   20                                  25                  30  
 Ala Ser Ser Glu Lys Pro Ala Tyr Ser Ile Val Met Pro Pro Pro Asn  
                   35                                  40                  45  
 Val Thr Gly Ile Leu His Met Gly His Ala Leu Val Asn Thr Leu Gln  
                   50                                  55                  60  
 Asp Thr Leu Ile Arg Tyr Lys Arg Met Gln Gly Phe Glu Val Cys Trp  
 65                  70                                  75                  80  
 Val Pro Gly Thr Asp His Ala Gly Ile Ala Thr Gln Thr Val Val Glu  
                   85                                  90                  95  
 Arg His Leu Lys Ala Ser Leu Gly Lys Arg Arg Thr Asp Phe Ser Arg  
                   100                                  105                  110  
 Glu Glu Phe Leu Lys His Val Trp Asp Trp Lys Glu Lys Ser Gln Asn  
                   115                                  120                  125  
 Val Ile Leu Ser Gln Leu Arg Gln Leu Gly Cys Ser Cys Asp Trp Ser  
                   130                                  135                  140  
 Arg Gln Arg Phe Thr Met Asp Pro Gly Ala Asn Arg Ala Val Lys Lys  
 145                  150                                  155                  160  
 Ala Phe Lys Ile Leu Phe Asp Lys Gly Val Ile Tyr Arg Gly Tyr Tyr  
                   165                                  170                  175  
 Leu Val Asn Trp Asp Pro Ile Leu Gln Thr Ala Leu Ala Asp Asp Glu  
                   180                                  185                  190  
 Val Glu Tyr Glu Glu Arg Asp Gly Trp Leu Tyr Tyr Ile Arg Tyr Gln  
                   195                                  200                  205  
 Val Val Asn Ser Glu Glu Phe Ile Thr Val Ala Thr Thr Arg Pro Glu  
                   210                                  215                  220  
 Thr Leu Leu Gly Asp Thr Ala Ile Ala Val Ser Pro Glu Asp Gln Arg  
 225                  230                                  235                  240  
 Tyr Ser His Leu Ile Gly Ala Lys Val Val Val Pro Phe Val Asn Arg  
                   245                                  250                  255  
 Glu Ile Pro Ile Ile Gly Asp Phe Ser Val Asp Ala Ser Phe Gly Thr  
                   260                                  265                  270  
 Gly Ala Val Lys Ile Thr Pro Ala His Asp Lys Asp Asp Tyr Lys Thr  
                   275                                  280                  285  
 Gly Met Asn His Gln Leu Pro Met Ile Asn Ile Leu Thr Ser Thr Gly

290		295		300
Glu Ile Asn Glu Asn Gly Gly Ile Phe Thr Gly Leu Ser Arg Glu Val				
305		310		315
Ala Arg Glu Asn Ile Ile Thr Ser Leu Glu Ala Leu Gly Leu Phe Val				
	325		330	335
Lys Lys Glu Ala Tyr Ser Ser Arg Val Gly Val Ser Tyr Arg Ser Gly				
	340		345	350
Ala Ile Ile Glu Pro Tyr Leu Ser Lys Gln Trp Phe Val Ser Val Asp				
	355	360		365
Ser Phe Arg Asp Ser Leu Arg Glu Phe Val Asn Ser Glu Glu Ile Arg				
	370	375		380
Ile Phe Pro Pro Glu Phe Val Arg Asn Tyr Leu Thr Trp Val Asn Asn				
385		390		395
Leu Lys Asp Trp Cys Ile Ser Arg Gln Leu Trp Trp Gly His Arg Ile				
	405		410	415
Pro Val Trp His Asn Lys His Asp Glu Asn Val Ile Cys Phe Asp Gly				
	420		425	430
Glu Gly Gly Pro Glu Glu Val Met Arg Asp Pro Glu Ser Trp Tyr Gln				
	435	440		445
Asp Pro Asp Val Leu Asp Thr Trp Phe Ser Ser Gly Leu Trp Pro Leu				
	450	455		460
Thr Cys Phe Gly Trp Pro Asp Glu Asp Ser Leu Asp Leu Lys Lys Phe				
465		470		475
Tyr Pro Thr Ala Val Leu Val Thr Gly His Asp Ile Leu Phe Phe Trp				
	485		490	495
Val Thr Arg Met Val Leu Met Cys Ser Ala Met Val Asp Thr Glu Pro				
	500		505	510
Phe Ser Asp Val Phe Leu His Gly Leu Ile Phe Gly Lys Ser Tyr Arg				
	515	520		525
Glu Tyr Asp Glu Lys Gly Glu Trp Phe Tyr Val Ser Gly Glu Arg Lys				
	530	535		540
Arg Asp Tyr Asp Lys Gly Lys Ala Leu Pro Lys Asn Val Val Ala Lys				
545		550		555
Trp Glu Lys Leu Ser Lys Ser Lys Gly Asn Val Ile Asp Pro Ile Glu				
	565		570	575
Met Ile Glu Ala Tyr Gly Ala Asp Ala Val Arg Leu Thr Leu Cys Ser				
	580		585	590
Cys Ala Asn Arg Gly Glu Gln Ile Asp Leu Asp Tyr Arg Leu Phe Glu				
	595	600		605
Glu Tyr Lys Asn Phe Ile Asn Lys Leu Trp Asn Gly Ala Arg Phe Ile				
	610	615		620
Phe Gly His Ile Ser Glu Leu Thr Ser Arg Asp Leu Glu Glu Gly Val				
625		630		635
Asn Gln Asp Leu Leu Gly Leu Glu Asp Phe Tyr Ile Leu Asp Arg Phe				
	645		650	655
Asn Glu Leu Leu Asp Leu Ile Asp Gly His Tyr Asn Cys Tyr Ser Phe				
	660		665	670
Asp Lys Ile Ala Ser Leu Ala Tyr Asp Phe Phe Lys Asn Asp Leu Cys				
	675	680		685
Ser Thr Tyr Leu Glu Ile Ile Lys Pro Thr Leu Phe Gly Lys Gln Gly				
	690	695		700
Ser Asp Gln Gln Arg Ala Thr Lys Arg Lys Leu Leu Ala Thr Leu Leu				
705		710		715
Ile Asn Ile Leu Gly Val Leu His Pro Ile Val Pro Tyr Ile Thr Glu				
	725		730	735
Thr Leu Phe Gln Lys Leu Lys Ala Thr Leu Gly Thr Val Glu Asn Gly				
	740		745	750
Lys Gly Asp Ser Val Thr Gly His Ala Val Ser Met Leu Arg Ser Glu				
	755	760		765

Ala Cys Met Val Ala Glu Tyr Pro Lys Pro Ile His Val Ala Phe Pro  
 770 775 780  
 Gln Gly Leu Arg Glu Ser Phe Gly Ile Ala Glu Arg Leu Val Tyr Thr  
 785 790 795 800  
 Ile Arg Asn Ile Arg Gly Glu Met Gln Leu Asp Pro Arg Glu Pro Leu  
 805 810 815  
 Gln Ala Phe Val Ile Ser Ser Glu Lys Lys Glu Leu Val Asp Val Cys  
 820 825 830  
 Ile Pro Ile Met Cys Ala Leu Gly Gly Val Lys Thr Val Glu Gln Leu  
 835 840 845  
 Ala Glu Ala Pro Lys Asp Ser Ile Phe Ser Leu Gly Val Val Glu Gly  
 850 855 860  
 Ile Gln Val Gly Val Ile Leu Pro Pro Glu His Leu Ala Lys Glu Arg  
 865 870 875 880  
 Val Arg Leu Glu Lys Glu Lys Thr Arg Leu Glu Lys Ser Ile Asp Ser  
 885 890 895  
 Val Ser Lys Leu Leu Ala Ser Glu Asp Phe Arg Thr Arg Ala Asn Pro  
 900 905 910  
 Ser Leu Val Gln Ala Lys Lys Asp Ser Leu Arg Asn Ser Gln Arg Glu  
 915 920 925  
 Leu Gln Ser Ile Leu Asp Lys Leu Ala Ser Leu  
 930 935

(2) INFORMATIONS POUR LA SEQ ID NO: 133:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 945 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 137442..140276

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 133:

Thr Arg Ile Ala Leu Lys Glu Ala Val Leu Leu Gln Arg Tyr Glu Leu  
 1 5 10 15  
 Ile Arg Leu Ile Gly Lys Gly Gly Met Gly Glu Val Tyr Leu Ala His  
 20 25 30  
 Asp Lys Ala Cys Ser Arg Arg Val Ala Leu Lys Arg Ile Arg Glu Asp  
 35 40 45  
 Leu Ser Gly Asn Ala Leu Leu Arg Lys Arg Phe Leu Arg Glu Ala Lys  
 50 55 60  
 Ile Ala Ala Asp Leu Ile His Pro Gly Ile Val Pro Val Tyr Ser Ile  
 65 70 75 80  
 Cys Ser Asp Gly Glu Ala Val Tyr Tyr Thr Met Pro Tyr Ile Glu Gly  
 85 90 95  
 Phe Ser Leu Lys Ser Leu Leu Lys Ser Val Trp Gln Lys Glu Val Leu  
 100 105 110  
 Ser Lys Glu Leu Glu Glu Lys Thr Ser Val Lys Ser Phe Leu Pro Ile  
 115 120 125  
 Phe Asp Lys Ile Cys Ala Thr Val Glu Tyr Ile His Ser Lys Gly Val  
 130 135 140  
 Leu His Arg Asp Leu Lys Pro Asp Asn Ile Leu Leu Gly Leu Phe Gly  
 145 150 155 160  
 Glu Val Val Ile Val Asp Trp Gly Ala Ala Ile Phe Lys His Ala Lys

					165					170					175
Glu	Leu	Lys	Leu	Glu	Gln	Asp	Asp	Glu	Ala	Ala	Val	Ser	Phe	Asp	Glu
			180					185					190		
Arg	Asn	Ile	Cys	Tyr	Ser	Ser	Met	Thr	Ile	Pro	Gly	Lys	Ile	Val	Gly
		195					200					205			
Thr	Pro	Asp	Tyr	Met	Ala	Pro	Glu	Ser	Leu	Leu	Gly	Val	Glu	Ala	Ser
	210					215					220				
Glu	Lys	Thr	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Ile	Leu	Tyr	Gln	Met	Leu
225					230					235					240
Thr	Leu	Ala	Phe	Pro	Tyr	Arg	Arg	Lys	Lys	Gly	Arg	Lys	Leu	Ser	Tyr
			245						250					255	
Arg	Asp	Val	Val	Leu	Pro	Pro	Ile	Glu	Met	Ser	Pro	Tyr	Arg	Glu	Ile
			260					265					270		
Pro	Pro	Ser	Leu	Ser	Gln	Ile	Ala	Met	Lys	Ala	Ile	Ala	Ile	Asn	Pro
		275					280					285			
Ala	Asp	Arg	Phe	Ser	Ser	Ile	Gln	Glu	Leu	Arg	Gln	Ala	Leu	Gln	Pro
	290					295					300				
Tyr	Leu	Gln	Gly	Asp	Pro	Glu	Trp	Thr	Val	Lys	Ala	Thr	Leu	Met	Ala
305					310					315					320
Lys	Glu	Lys	Ser	Cys	Trp	Lys	Tyr	Tyr	Asp	Pro	Ile	Leu	Leu	Ser	Arg
			325						330					335	
Tyr	Phe	Pro	Val	Leu	Ala	Ser	Ser	Pro	Ala	Gln	Trp	Tyr	Asn	Phe	Met
			340					345					350		
Leu	Ser	Glu	Val	Glu	Ile	Ser	Ala	Ser	Thr	Arg	Val	Glu	Tyr	Thr	Val
		355					360					365			
Thr	Lys	Ser	Ala	Val	His	Glu	Gly	Met	Gly	Ile	Leu	Phe	Leu	Pro	Ser
	370					375					380				
Lys	Glu	Ala	Glu	Arg	Gly	Glu	Phe	Tyr	Cys	Gly	Tyr	Gly	Leu	Trp	Phe
385					390					395					400
Ser	Val	Gln	Asn	His	Glu	Leu	Thr	Val	Ser	Leu	Ile	Lys	Asn	Gly	Ile
			405						410					415	
Glu	Ile	Gln	Lys	Lys	Ser	Gln	Glu	Met	Ile	Ser	Gln	Gln	Tyr	Arg	Phe
			420					425					430		
Ala	Ile	Leu	Ile	Glu	Lys	Ser	Asp	Asn	Arg	Ile	Ala	Val	Phe	Val	Glu
		435					440					445			
Gln	Ala	Leu	Phe	Ile	Leu	His	Ile	Asp	Tyr	Leu	Pro	Ser	Leu	Gly	Asn
	450					455					460				
Arg	Leu	Gly	Val	Ile	Ile	Gln	Asp	Leu	Gln	Gly	Met	Ser	Asn	Ile	Ala
465					470					475					480
Ile	Ser	Glu	Ser	Ile	Gly	Ala	Leu	Arg	Val	Ser	Cys	Leu	Ala	Val	Pro
				485					490					495	
Asp	Ala	Phe	Leu	Ser	Glu	Lys	Leu	Tyr	Asp	Gln	Ala	Ala	Ile	Phe	Tyr
			500					505					510		
Arg	Lys	Ile	Arg	Asp	Ser	Phe	Pro	Gly	Arg	Lys	Glu	Ser	Tyr	Glu	Ala
		515													

Glu Glu Lys Arg Phe Leu Arg Ile Ile Tyr His Lys Gln Gln Ala Thr  
 645 650 655  
 Leu Phe Cys Gln Val Asp Lys Ala Pro Leu Gln Phe Arg Ser Ser Lys  
 660 665 670  
 Met Glu Leu Phe Leu Ser Phe Trp Thr Ala Phe Ser Leu Phe Leu Pro  
 675 680 685  
 Glu Leu Phe Arg Arg Ala Gly Glu Leu Arg Asp Tyr Gln Ala Leu Ala  
 690 695 700  
 Asp Ile Phe Tyr Val Ala Gly Val Ser Gly Asn Arg Glu Ala Phe Met  
 705 710 715 720  
 Gln Phe Ser Thr Ala Leu Ala Asn Val Ser Asp Glu Ile Thr Phe Pro  
 725 730 735  
 Glu Ser Leu His Asn Gln Lys Val Ala Glu Leu Met Phe Phe Val Lys  
 740 745 750  
 Gly Val Glu Ala Leu Arg Asn Lys Asp Tyr Gln Lys Ala Lys Lys Ala  
 755 760 765  
 Phe Met Gly Lys Thr Pro Phe Thr Leu Gln Leu Tyr Ala Leu Asp Ile  
 770 775 780  
 Phe His Ile Gln Ala Phe Leu Asp Glu Glu Ile Glu Ser Phe Ile Asp  
 785 790 795 800  
 Leu Leu Gln Ala Ile Tyr Asp Pro Ala Ser Glu Glu Glu Arg Asp His  
 805 810 815  
 Ile Leu Val Tyr Ile Ile Gln Thr His Leu Trp Asn Arg Asp Leu Glu  
 820 825 830  
 Arg Ala Tyr Lys Leu Leu Asn Asp Arg Phe Pro Leu Asp Glu Glu Leu  
 835 840 845  
 Ala Glu Tyr Ser Glu Ala Phe Ile Leu Trp Gly Cys Tyr Leu Ala Leu  
 850 855 860  
 Thr Gly Asp Arg Val Ala Val Lys Ala His Phe Ser Arg Cys Arg Tyr  
 865 870 875 880  
 Lys Tyr Gly Lys Ser Ala Leu Ile Gly Lys Cys Val Asp Gly Asp Ile  
 885 890 895  
 Phe Asp Tyr Leu Asp Asn Leu Val Trp Trp Glu Lys Lys Met Thr Leu  
 900 905 910  
 Phe Gln Ser Tyr Phe Leu Leu Arg Cys Leu Asn Glu Ser Pro Arg Arg  
 915 920 925  
 Tyr Glu Lys Tyr Arg Gln Ala Tyr Leu Ser Met Glu Asn Asn Phe Phe  
 930 935 940  
 Asp  
 945

(2) INFORMATIONS POUR LA SEQ ID NO: 134:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(140335..140733)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 134:

Pro Pro Leu Gly Asn Gln Ser Val Ile Cys Thr Gly Pro Ile Phe Leu  
 1 5 10 15  
 Glu Ile Cys Val Met Ser Ser Ile Ser Ser Pro Gly Asn Ile Gln His

(2) INFORMATION POUR LA SEQ ID NO: 135:

(A) LONGUEUR: 226 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(141077..141754)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 135:

Leu 1	Gly	Asn	Ile	Pro 5	Leu	Arg	Leu	Ala	Ser 10	Arg	Gln	Ser	Ser	Leu 15	Ala
Val	Leu	Gln	Ala	His 20	Glu	Cys	Leu	Arg 25	Lys	Leu	Gln	Ile	Phe 30	Phe	Pro
Arg	Leu	Trp 35	Gly	Gln	Ile	Ile	Thr 40	Thr	Thr	Thr	Gln	Gly 45	Asp	Leu	Asp
Gln	Glu 50	Thr	Pro	Leu	Cys	Ala 55	Val	Glu	Asn	Thr	Gly 60	Phe	Phe	Thr	Asp
Asp 65	Val	Asp	Phe	Leu 70	Val	Gln	Ser	Gly	Gln	Cys 75	Asp	Leu	Gly	Ile	His 80
Ser	Ala	Lys	Asp	Leu 85	Pro	Glu	Asn	Pro	Lys 90	Ala	Thr	Val	Val	Ser 95	Ile
Thr	Ala	Ser	Ile 100	Asp	Pro	Arg	Asp	Ile 105	Leu	Val	Phe	His 110	Glu	Lys	Tyr
Leu	Ser	Ile 115	Pro	Leu	Pro	Arg	Arg 120	Leu	Arg	Ile	Gly 125	Ser	Ser	Ser	Val
Arg	Arg	Lys 130	Glu	Leu	Leu	Ser 135	Leu	Leu	Tyr	Pro	Ser 140	Ala	Ile	Ile	Thr
Asp 145	Ile	Arg	Gly	Thr 150	Ile	Gln	Thr	Arg	Leu 155	Lys	Leu	Leu	Glu	Glu	Lys 160
Asn	Phe	Asp	Ala	Ile 165	Val	Met	Ala	Asn 170	Ala	Ala	Val	Ser	Arg	Leu 175	Gly
Leu	Arg	Leu 180	Pro	Cys	Thr	Lys	Ile 185	Leu	Pro	Pro	Pro	Tyr 190	His	Pro	Leu
Gln	Gly	Arg 195	Leu	Ala	Ile	Thr	Ala 200	Ser	Arg	His	Ile 205	Arg	Ser	Trp	Arg
Gly	Leu 210	Phe	Leu	Thr	Cys	Gly 215	Ile	Thr	Glu	Asp	Val 220	Glu	Ile	Met	Cys

(2) INFORMATION POUR LA SEQ ID NO: 136:

(A) LONGUEUR: 454 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(141780..143141)

(xi) DESCRIPTION DE LA SEQUENCE: SEO ID NO: 136:

Met	Thr	Thr	Lys	Ile	Lys	Thr	Gln	Trp	Thr	Cys	Thr	Glu	Cys	Gly	Thr
1				5					10					15	
His	Ser	Pro	Lys	Trp	Leu	Gly	Gln	Cys	Ser	Gly	Cys	Leu	Gln	Trp	Asn
			20					25					30		
Thr	Leu	Val	Glu	Glu	Arg	Thr	Ala	Pro	Lys	Leu	Asn	Thr	Ser	Ser	Tyr
		35					40					45			
Ser	Ser	Ser	Ser	Ser	Ile	Pro	Ile	Pro	Leu	Asn	Asn	Val	Glu	Phe	Gln
	50					55					60				
Glu	Glu	Ile	Arg	Ile	His	Thr	Gln	Ala	Gln	Gly	Trp	Asn	Arg	Leu	Leu
65					70					75					80
Gly	Gly	Gly	Thr	Val	Arg	Gly	Ser	Leu	Ala	Leu	Leu	Gly	Gly	Glu	Pro
				85					90					95	
Gly	Ile	Gly	Lys	Ser	Thr	Leu	Leu	Leu	Gln	Ile	Ser	Ser	Gln	Phe	Ala
			100					105					110		
Ala	Ala	Gly	His	Lys	Val	Leu	Tyr	Val	Cys	Gly	Glu	Glu	Ser	Val	Ser
		115					120					125			
Gln	Thr	Ser	Leu	Arg	Ala	Gln	Arg	Leu	Gln	Ile	Ser	Ser	Asn	Asn	Ile
	130					135					140				
Phe	Leu	Phe	Pro	Glu	Thr	Asn	Leu	Glu	Asp	Ile	Lys	Gln	Gln	Ile	Asp
145					150					155					160
Asn	Ile	Ala	Pro	Asp	Ile	Leu	Val	Ile	Asp	Ser	Ile	Gln	Ile	Ile	Phe
				165					170					175	
Ser	Pro	Ser	Leu	Ser	Ser	Ala	Pro	Gly	Ser	Val	Ala	Gln	Val	Arg	Glu
			180					185					190		
Thr	Thr	Ala	Glu	Leu	Met	His	Ile	Ala	Lys	Gln	Lys	Gln	Ile	Thr	Thr
		195					200					205			
Phe	Ile	Ile	Gly	His	Val	Thr	Lys	Ser	Gly	Glu	Ile	Ala	Gly	Pro	Arg
	210					215					220				
Ile	Leu	Glu	His	Leu	Val	Asp	Thr	Val	Leu	Tyr	Phe	Glu	Gly	Asn	Val
225					230					235					240
His	Ala	Asn	Tyr	Arg	Met	Ile	Arg	Ser	Val	Lys	Asn	Arg	Phe	Gly	Pro
				245					250					255	
Thr	Asn	Glu	Leu	Leu	Ile	Leu	Ser	Met	His	Thr	Asp	Gly	Leu	Arg	Glu
		260						265					270		
Val	Glu	Asn	Pro	Ser	Gly	Leu	Phe	Leu	Gln	Glu	Lys	Ile	Val	Glu	Thr
		275					280					285			
Thr	Gly	Ser	Thr	Ile	Ile	Pro	Ile	Val	Glu	Gly	Ser	Glu	Thr	Leu	Leu
	290					295					300				
Val	Glu	Val	Gln	Ala	Leu	Val	Ser	Ser	Ser	Pro	Phe	Ser	Asn	Pro	Val
305					310					315					320
Arg	Lys	Thr	Ser	Gly	Phe	Asp	Pro	Asn	Arg	Phe	Ser	Leu	Leu	Leu	Ala



				325					330					335			
Val	Leu	Glu	Lys	Arg	Ala	Asn	Ile	Lys	Leu	Tyr	Thr	Ser	Asp	Val	Phe		
			340					345					350				
Leu	Ser	Ile	Ala	Gly	Gly	Leu	Lys	Ile	Thr	Gln	Pro	Ser	Ala	Asp	Leu		
		355					360						365				
Gly	Ala	Val	Leu	Ser	Val	Val	Ser	Ser	Leu	Tyr	Asn	Arg	Tyr	Leu	Pro		
		370					375				380						
Lys	Asn	Tyr	Thr	Tyr	Thr	Gly	Glu	Ile	Gly	Leu	Gly	Gly	Glu	Ile	Arg		
385					390					395					400		
His	Val	Ser	His	Met	Glu	His	Arg	Ile	Lys	Glu	Ser	Ile	Ile	Met	Gly		
				405					410					415			
Phe	Lys	Gly	Ile	Val	Met	Pro	Phe	Gly	Gln	Ile	Lys	Gly	Leu	Pro	Lys		
			420					425					430				
Glu	Phe	Leu	Asp	Gln	Ile	Asp	Ile	Ile	Gly	Val	Lys	Thr	Ile	Lys	Asp		
		435					440					445					
Ala	Val	Arg	Leu	Leu	Gln												
			450														

## (2) INFORMATIONS POUR LA SEQ ID NO: 137:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(143128..143829)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 137:

Lys	Ile	Val	Met	Gln	His	Thr	Val	Asp	Ile	Gln	Ala	Ile	Glu	Ser	Lys		
1				5					10					15			
Leu	Asn	Phe	Thr	Phe	Ser	His	Pro	Arg	Leu	Leu	Ile	Thr	Ala	Leu	Thr		
			20					25					30				
His	Pro	Ser	Tyr	Arg	Asn	Glu	Phe	Pro	Ser	Ala	Glu	Glu	Asp	Ser	Glu		
		35					40					45					
Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val	Leu	Gly	Leu	Val	Val	Thr	Glu		
	50					55					60						
His	Leu	Phe	Leu	Leu	Phe	Pro	Ala	Leu	Asn	Glu	Gly	Leu	Leu	Ser	Thr		
65					70					75					80		
Thr	Arg	Ala	Ala	Leu	Val	Asn	Ala	Glu	Ala	Cys	Phe	Glu	Tyr	Thr	Gln		
				85					90					95			
Lys	Leu	Ser	Leu	Gly	Glu	His	Leu	Leu	Ile	Gly	Arg	Gly	Glu	Lys	Met		
			100					105					110				
Gln	Ser	His	Arg	Gly	Lys	Ile	Ser	Ala	Tyr	Ala	Asn	Leu	Phe	Glu	Ala		
		115					120					125					
Ile	Leu	Gly	Ala	Val	Tyr	Leu	Asp	Gly	Gly	Leu	Ser	Pro	Ala	Arg	Gln		
	130					135					140						
Ile	Ile	Val	Pro	Leu	Leu	Pro	Asp	Lys	Glu	Ser	Ile	Leu	Pro	Leu	Met		
145					150					155					160		
Leu	Val	Asn	Pro	Lys	Asn	Arg	Leu	Gln	Gln	Phe	Thr	Gln	Gln	Thr	Leu		
				165					170					175			
Lys	Val	Leu	Pro	Ser	Tyr	Lys	Ala	Leu	Pro	Trp	Lys	Ser	Glu	Asp	Gly		
			180					185					190				
Ser	Pro	Gly	Tyr	His	Val	Gln	Val	Phe	Val	Asn	Gly	Asp	Leu	Trp	Gly		
		195					200					205					

Glu Gly Phe Ala Gly Ser Lys Lys Glu Ala Glu Lys Leu Ala Ala Lys  
 210 215 220  
 Gln Ala Leu Ser Thr His Asp Asn Lys Asn  
 225 230

(2) INFORMATIONS POUR LA SEQ ID NO: 138:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 143923..144393

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 138:

Val Ser Met Arg Ala Val Leu His Leu Glu His Lys Arg Tyr Phe Gln  
 1 5 10 15  
 Asn His Gly His Ile Leu Phe Glu Gly Leu Ala Pro Val Ser Asp Cys  
 20 25 30  
 Lys Gln Leu Glu Ala Glu Leu Lys Leu Phe Leu Lys Glu Val Ala Val  
 35 40 45  
 Val Lys Asp Arg His Leu Gln Arg Trp Arg Glu Asn Val His Arg Thr  
 50 55 60  
 Leu Pro Gly Val Gln Met Ile Val Lys Arg Val Arg Leu Asp His Leu  
 65 70 75 80  
 Ala Ala Glu Leu Thr His Arg Ser Arg Val Ala Leu Val Arg Asp Leu  
 85 90 95  
 Trp Val Gln Lys Gln Glu Glu Ile Leu Phe Asp Asp Cys Asp Cys Ser  
 100 105 110  
 Val Leu Leu Cys Leu Ser Gly Glu Lys Ala Gly Trp Gly Leu Phe Phe  
 115 120 125  
 Ser Gly Glu Tyr Pro Gln Asp Val Phe Asp Trp Gly Ala Gly Asp Thr  
 130 135 140  
 Ala Ile Ile Leu Arg Phe Ser Ser Ala Gly Phe Pro Asn  
 145 150 155

(2) INFORMATIONS POUR LA SEQ ID NO: 139:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 583 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 144578..146326

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 139:

Met Phe Asp Pro Gln Thr Ala Lys Asn Ile Leu Ser Trp Leu Glu Asp  
 1 5 10 15  
 Val Val Cys Asp His Thr Ser Val Leu Thr Leu Leu Asp Asn Asp Pro

Glu	Arg	Leu	Arg	Glu	Leu	Phe	Ser	Glu	Thr	Leu	Thr	Phe	Gly	Thr	Ala
		35					40					45			
Gly	Leu	Arg	Gly	Leu	Met	Gly	Ile	Gly	Thr	Asn	Arg	Leu	Asn	Val	Phe
	50					55					60				
Thr	Ile	Arg	Arg	Ala	Thr	Gln	Gly	Leu	Ala	Arg	Val	Leu	Lys	Arg	Arg
65					70					75					80
Tyr	Pro	Asp	Glu	Lys	Ile	Ser	Val	Val	Ile	Gly	Tyr	Asp	Thr	Arg	His
				85					90					95	
Asp	Ser	Phe	Glu	Phe	Gly	Gln	Glu	Thr	Ala	Lys	Val	Leu	Ala	Gly	Asn
			100					105						110	
Gly	Ile	Leu	Ala	Tyr	Leu	Phe	Gln	Ile	Pro	Glu	Pro	Leu	Ala	Leu	Val
			115					120						125	
Ser	Tyr	Ser	Val	Arg	Glu	Leu	Gln	Ala	Lys	Ala	Gly	Val	Met	Ile	Thr
	130					135					140				
Ala	Ser	His	Asn	Pro	Pro	Ala	Tyr	Asn	Gly	Tyr	Lys	Val	Tyr	Met	Ser
145					150					155					160
Thr	Gly	Gly	Gln	Val	Leu	Pro	Pro	Met	Asp	Gln	Glu	Ile	Met	Glu	Glu
				165					170					175	
Phe	Gln	Lys	Val	Glu	Met	Val	Ser	Ala	Val	Glu	Ser	Leu	Asp	His	Pro
			180					185						190	
Tyr	Ile	Arg	Met	Ile	Gln	Glu	Asp	Met	Glu	Asn	Tyr	Tyr	Glu	Glu	Thr
			195				200					205			
Leu	His	Lys	Leu	Gln	Leu	Cys	Glu	Glu	Asp	Asn	Arg	Arg	His	Gly	Ser
	210					215					220				
Leu	Leu	Arg	Ile	Ser	Tyr	Ser	Pro	Leu	His	Gly	Thr	Gly	Val	Thr	Met
225					230					235					240
Ile	Pro	Arg	Ile	Leu	Lys	Asp	Trp	Gly	Phe	Ser	Ser	Val	Ser	Leu	Val
				245					250					255	
Glu	Lys	Gln	Met	Val	Pro	Asp	Gly	Asp	Phe	Pro	Thr	Val	Val	Leu	Pro
			260					265						270	
Asn	Pro	Glu	Asp	Pro	Glu	Ala	Leu	Val	Leu	Gly	Ile	Gln	Gln	Met	Val
			275				280					285			
Glu	Gln	Lys	Asp	Asp	Leu	Phe	Ile	Ala	Thr	Asp	Pro	Asp	Ser	Asp	Arg
						295					300				
Ile	Gly	Val	Val	Ser	Leu	Glu	Lys	Glu	Gly	Pro	Tyr	Arg	Phe	Asn	Gly
305					310					315					320
Asn	Gln	Ile	Ala	Cys	Leu	Leu	Ala	Ala	His	Ile	Leu	Ser	Lys	Glu	Ser
				325					330					335	
Gln	Lys	Ala	Pro	Leu	Gly	Ala	Glu	Asp	Lys	Val	Val	Lys	Ser	Leu	Val
			340					345						350	
Thr	Thr	Glu	Leu	Leu	Thr	Ala	Ile	Ser	Glu	Ser	Tyr	Gly	Ala	Asn	Ile
		355					360					365			
Val	Asn	Val	Gly	Ala	Gly	Phe	Lys	Tyr	Ile	Gly	Glu	Lys	Ile	Glu	

Glu Gly Arg Asp Leu Val Thr Asp Ile Thr Tyr Lys Leu Ser Leu Pro  
                   500                  505                  510  
 Lys Met Ser Met Leu Cys Phe Tyr Tyr Glu Gly Asp Cys Arg Val Ile  
                   515                  520                  525  
 Val Arg Pro Ser Gly Thr Glu Pro Lys Met Lys Leu Tyr Phe Glu Ile  
                   530                  535                  540  
 Lys Gln Ser Phe Ser Glu Phe Ser Lys Glu Arg Thr Val Arg Glu Ala  
 545                                  550                  555                  560  
 Arg Glu Lys Glu Ser Phe Glu Ala Leu Gln Gln Phe Ile Lys Glu Thr  
                                   565                  570                  575  
 Lys Ser His Leu Phe Tyr Ser  
                                   580

(2) INFORMATIONS POUR LA SEQ ID NO: 140:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 146413..147078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 140:

Lys Ile Glu Lys Val Ala Arg Ile Val Thr Leu Phe Phe Arg Met Ala  
 1                  5                  10                  15  
 Met Val Phe Ser Ser Tyr Met Leu Pro Ala Leu Pro Tyr Asp Tyr Asp  
                   20                  25                  30  
 Ala Leu Glu Pro Val Ile Ser Ala Glu Ile Met Gln Leu His His Gln  
                   35                  40                  45  
 Lys His His Gln Gly Tyr Ile Asn Asn Leu Asn Glu Ala Leu Lys Ser  
                   50                  55                  60  
 Leu Asp Val Ala Asn Ala Thr Gln Asp Leu Thr Arg Leu Ile Ala Ile  
 65                                  70                  75                  80  
 Asn Pro Ala Leu Arg Phe Asn Gly Gly Gly His Ile Asn His Ser Leu  
                   85                  90                  95  
 Phe Trp Glu Met Leu Ala Pro Gln Gly Lys Gly Gly Gly Val Pro Pro  
                   100                  105                  110  
 Arg His Glu Leu Leu Lys Leu Ile Glu Lys Phe Trp Gly Ser Phe Asp  
                   115                  120                  125  
 Ser Phe Leu Lys Asn Phe Ile Ala Ser Ser Ala Ala Val Gln Gly Ser  
                   130                  135                  140  
 Gly Trp Gly Trp Leu Ala Phe Cys Pro Lys Lys Gln Glu Phe Val Val  
 145                  150                  155                  160  
 Gln Thr Thr Ala Asn Gln Asp Pro Leu Glu Ala Thr Thr Gly Met Ile  
                   165                  170                  175  
 Pro Leu Pro Gly Val Asp Val Trp Glu His Ala Tyr Tyr Leu Gln Tyr  
                   180                  185                  190  
 Lys Asn Val Arg Ile Asp Tyr Leu Lys Ser Phe Pro Ser Ile Ile Asn  
                   195                  200                  205  
 Trp Asp Tyr Ile Glu Asn Arg Phe Val Glu Met Ser Lys Gln  
                   210                  215                  220

(2) INFORMATIONS POUR LA SEQ ID NO: 141:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 312 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 147140..148075

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 141:

Glu	Asp	Gly	Phe	Val	Arg	Leu	Phe	Ser	Tyr	Asp	Lys	Pro	Lys	Ile	Lys	1	5	10	15
Val	Gln	Lys	Ile	Lys	Ala	Asp	Gly	Phe	Ser	Gly	Trp	Leu	Lys	Cys	Thr	20	25	30	
His	Cys	Ser	Glu	Met	Ile	His	Ala	Asn	Glu	Leu	Gly	Gln	Asn	Phe	Asn	35	40	45	
Cys	Cys	Pro	Lys	Cys	Ser	Tyr	His	Tyr	Arg	Ile	Ser	Val	Ser	Glu	Arg	50	55	60	
Ile	Ala	Leu	Leu	Ala	Asp	Lys	Asp	Ser	Trp	Asn	Pro	Leu	Phe	Ser	Asp	65	70	75	80
Leu	Arg	Ser	Gln	Asp	Pro	Leu	Asn	Phe	Val	Asp	Thr	Asp	Thr	Tyr	Pro	85	90	95	
Asn	Arg	Leu	Glu	Lys	Ala	Arg	Lys	Asp	Asn	Pro	Asp	Ser	Glu	Gly	Val	100	105	110	
Leu	Val	Gly	Ala	Cys	Thr	Ile	Gly	Ser	Tyr	Pro	Val	Ala	Leu	Ala	Val	115	120	125	
Met	Asp	Phe	Ser	Phe	Met	Ala	Gly	Ser	Met	Gly	Ala	Val	Val	Gly	Glu	130	135	140	
Lys	Leu	Thr	Arg	Leu	Ile	Glu	Lys	Ala	Ile	Asp	Ser	Arg	Leu	Pro	Val	145	150	155	160
Ile	Ile	Val	Ser	Ala	Ser	Gly	Gly	Ala	Arg	Met	Gln	Glu	Ser	Val	Phe	165	170	175	
Ser	Leu	Met	Gln	Met	Ala	Lys	Thr	Ser	Ala	Ala	Leu	Ala	Lys	Leu	His	180	185	190	
Glu	Ala	Lys	Leu	Pro	Tyr	Ile	Ser	Val	Leu	Thr	Asn	Pro	Thr	Ser	Gly	195	200	205	
Gly	Val	Thr	Ala	Ser	Phe	Ala	Ser	Leu	Gly	Asp	Val	Ile	Ile	Ala	Glu	210	215	220	
Pro	Lys	Ala	Leu	Ile	Cys	Phe	Ala	Gly	Pro	Arg	Val	Val	Ser	Gln	Val	225	230	235	240
Ile	Gly	Glu	Asp	Leu	Pro	Glu	Gly	Ala	Gln	Lys	Ser	Glu	Phe	Leu	Leu	245	250	255	
Glu	His	Gly	Met	Ile	Asp	Lys	Val	Val	Glu	Arg	Lys	Gln	Leu	Lys	Thr	260	265	270	
Thr	Leu	Glu	Ser	Leu	Leu	Ser	Phe	Phe	Ser	Cys	Gln	Ala	Tyr	Ser	Gly	275	280	285	
Gly	Lys	Gly	Asn	Cys	Pro	Arg	Asp	Ile	Ser	Lys	Thr	Ile	Lys	Glu	Ile	290	295	300	
Phe	Leu	Leu	Thr	Asp	Asp	Asn	Lys									305	310		

(2) INFORMATIONS POUR LA SEQ ID NO: 142:

- (i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 148115..148549

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 142:

```

Met Lys Phe Phe Cys Lys Leu Glu Ser Gly Ser Ser Leu Pro Glu Tyr
1      5      10      15
Ala Thr Ser Gly Ala Ser Gly Ala Asp Val Arg Ala Asn Ile Asn Glu
      20      25      30
Pro Ile Ala Ile Leu Pro Gly Gln Arg Ala Leu Ile Pro Thr Gly Ile
      35      40      45
Ser Val Glu Ile Pro His Gly Tyr Glu Ile Gln Val Arg Ser Arg Ser
      50      55      60
Gly Leu Ala Ser Lys Tyr Gly Val Ile Val Leu Gln Ser Pro Gly Thr
65      70      75      80
Val Asp Ala Asp Tyr Arg Gly Glu Ile Arg Val Ile Leu Ala Asn Leu
      85      90      95
Gly Glu Xaa Thr Phe Ile Val Glu Pro Gly Met Arg Ile Ala Gln Leu
      100      105      110
Val Val Ala Lys Val Glu Gln Val Ser Phe Val Glu Thr Gln Glu Glu
      115      120      125
Leu Thr Ala Thr Ala Arg Gly Thr Gly Gly Phe Gly His Thr Gly Glu
      130      135      140
Cys
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 143:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 158 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 148554..149027

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 143:

```

Met Thr Cys Val Ala Asp His Lys Gln Ala Val Thr Leu Ser Ser Leu
1      5      10      15
Leu Ser Ser Asp Leu Ile Thr Phe Leu His Ser Asp Thr Arg Glu Asp
      20      25      30
Ile Leu Phe Glu Leu Ser Glu Leu Ala Ala Arg Ala Gly Leu Leu Glu
      35      40      45
Asp Arg Glu Ala Phe Phe Arg Ala Leu Leu Ala Arg Glu Asn Ile Met
      50      55      60
Ser Thr Gly Ile Gly Met Gly Val Ala Ile Pro His Gly Lys Ile Asp
65      70      75      80
Gly Ser Ala Asp Phe Phe Ile Ala Leu Gly Ile His Ser Glu Gly Ile
      85      90      95
Leu Trp Asp Ala Ile Asp Gly Leu Ser Val Arg Leu Val Phe Leu Ile

```

				100						105						110			
Gly	Gly	Pro	Ser	Asp	Ala	Pro	Ser	Lys	Tyr	Leu	Lys	Leu	Leu	Ser	Ala				
		115						120				125							
Leu	Thr	Gln	Ser	Leu	Arg	Asp	Glu	Ala	Arg	Arg	Ser	Gln	Leu	Leu	Gln				
	130					135					140								
Val	Gln	Thr	Val	Glu	Glu	Val	Met	Ser	Val	Phe	Ser	Gly	Val						
145					150					155									

(2) INFORMATIONS POUR LA SEQ ID NO: 144:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 102 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149000..149305

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 144:

Arg	Ser	Tyr	Glu	Cys	Phe	Phe	Arg	Ser	Leu	Val	Met	Asp	Leu	Arg	Leu				
1				5					10					15					
Asp	Gln	Leu	Ala	Val	Leu	Leu	Asp	Val	Ala	Glu	Asp	Ser	Ile	Arg	Gln				
		20					25						30						
Trp	Val	Ser	Cys	Gly	Gly	Ile	Pro	Ser	Tyr	Thr	Ile	Asn	Asp	Glu	Leu				
	35					40						45							
Arg	Phe	Asn	Arg	Glu	Glu	Val	Glu	Asp	Trp	Leu	Ile	His	Asn	His	Gly				
	50				55					60									
Val	Ile	Pro	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Gly	Glu	Ser	Lys	Asp	Leu				
65				70				75						80					
Ser	Leu	Arg	Tyr	Ser	Leu	Tyr	Arg	Ala	Xaa	Tyr	Xaa	Gly	Arg	Gly	Ser				
			85				90							95					
Lys	Lys	Cys	Ser	Cys	Arg														
				100															

(2) INFORMATIONS POUR LA SEQ ID NO: 145:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149229..149708

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 145:

Pro	Arg	Ile	Cys	His	Leu	Asp	Ile	Ala	Tyr	Ile	Glu	Xaa	Phe	Ile	Xaa				
1			5					10						15					
Gly	Gly	Val	Leu	Lys	Asn	Val	Leu	Val	Asp	Ser	Lys	Glu	Gly	Ala	Leu				
		20					25						30						
Arg	Tyr	Ala	Ala	His	Tyr	Ile	Ala	Asn	Lys	Phe	Glu	Leu	Asp	Pro	Val				
	35					40						45							

```

Val Leu Phe Glu Met Leu Met His Arg Glu Ser Leu Met Ser Thr Gly
 50          55          60
Ile Gly Glu Gly Ile Ala Leu Pro His Ala Lys Asp Phe Leu Ile Asn
65          70          75          80
Val Gly Tyr Asp Ile Ile Val Pro Val Phe Leu Ser Gln Ser Ile Glu
          85          90          95
Tyr Gly Ala Leu Asp Gly Lys Pro Val Asp Thr Leu Phe Phe Leu Phe
          100          105          110
Ala Asn Gln Asp Arg Asn His Leu Asn Leu Val Asn Lys Ile Val His
          115          120          125
Leu Gly Met Ser Ile Gln Ala Arg Leu Phe Leu Lys Glu His Pro Asp
          130          135          140
Gln Pro Gln Leu Leu Ala Phe Val Lys Asn Trp Glu Ala Gln Ile His
145          150          155          160

```

(2) INFORMATIONS POUR LA SEQ ID NO: 146:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149712..150911

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 146:

```

Val Ile Asn Lys Lys Arg Ile Val Arg Pro Ser Cys Glu Lys Ser Phe
1          5          10          15
Asn Val Ala Met Val Ile Pro Lys Val Asp Leu Gly Glu Ser Ala Val
          20          25          30
Met Leu Gly Tyr Lys Leu Thr Ser Gln Leu Ala Met Leu Ser Ile Leu
          35          40          45
Leu Thr Phe Thr His Thr Met Gly His Ala Ser Gln Met Ser Gln Thr
          50          55          60
Leu Pro Thr Ile Met Glu Ala Gln Ala Glu Glu Ala Leu Gln Ala Asp
65          70          75          80
Arg Gly Val Ser Gly Gln Ala Leu Lys Lys Leu Arg Lys Lys Arg Cys
          85          90          95
Ala Ser Arg Lys Ser Ala Trp Lys Ala Ser Phe Glu Lys Lys Asp Phe
          100          105          110
Phe Ser Cys Ile Thr Asn Gly Leu Phe Ser Arg Asn His Glu Gln Arg
          115          120          125
Leu Thr Ala Lys Lys Glu Asn Lys Ala Arg Gly Lys Glu Pro Arg Val
          130          135          140
Val Val Gln Thr Thr Lys Lys Arg Gln Thr Thr Gln Ser Glu Lys Glu
145          150          155          160
Phe Phe Asp Trp Leu Cys Asn Ser Lys Arg Asp Asp Lys Arg Lys Leu
          165          170          175
Leu Lys Lys Lys Pro Val Asn Thr Ser Leu Ala Lys Ser Glu Glu Leu
          180          185          190
Ser Pro Lys Glu Ala Ala Ile Ala Ala Ala Arg Ala Ser Leu Ser Pro
          195          200          205
Glu Glu Lys Arg Gln Leu Ile Arg Glu Trp Leu Ala Glu Glu Lys Thr
          210          215          220
Ala Arg Lys Ser Gly Arg Ala Ala Cys Ala Val Ser Glu Asn Leu Lys

```



225					230					235				240
Arg	Asp	Gly	Ser	Ile	Thr	Ser	Thr	Leu	Arg	Tyr	Asp	Ala	Glu	Lys
				245					250					255
Leu	Thr	Thr	Arg	Val	Lys	Arg	Asn	Glu	Asn	Ser	Val	Asn	Ala	Arg
			260					265					270	
Arg	Gln	Arg	Ala	Ala	Leu	Gln	Lys	Ala	Lys	Lys	Ala	Lys	Thr	Glu
		275					280				285			
Pro	Glu	Ala	Asp	Glu	Lys	Ala	Ala	Glu	Ala	Val	Ala	Ala	Ala	Pro
	290					295					300			
Lys	Gln	Ala	His	Lys	Glu	Pro	Glu	Asn	Tyr	Phe	Ala	Ala	Thr	Ala
305					310					315				320
Thr	Asn	Asn	Thr	Asn	Val	Met	Ser	Tyr	Leu	Asn	Ala	His	Gln	Tyr
				325					330					335
Cys	Asp	Ser	Ser	Glu	Thr	Asp	Trp	Pro	Cys	Ser	Ser	Cys	Val	Thr
			340					345					350	
Arg	Arg	Ala	Asn	Phe	Gly	Ile	Ser	Val	Cys	Thr	Met	Val	Val	Thr
		355					360					365		
Ile	Ala	Met	Ile	Val	Gly	Ala	Val	Ile	Ile	Ser	Asn	Ala	Thr	Asp
	370					375				380				
Thr	Val	Ala	Gly	Ser	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Thr	Gln
385					390				395					400

(2) INFORMATIONS POUR LA SEQ ID NO: 147:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 347 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(151004..152044)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 147:

Asp	Ala	Thr	Lys	Ile	Arg	Trp	Cys	Phe	Phe	Pro	Gln	Ser	Asn	Thr	Leu
1			5					10						15	
Ser	His	Ala	Ser	Arg	Thr	Leu	Tyr	Thr	Val	Leu	Lys	Val	Ala	Leu	Ser
			20					25					30		
Leu	Gly	Val	Leu	Ala	Gly	Val	Ala	Thr	Leu	Val	Val	Phe	Leu	Pro	Pro
		35					40					45			
Ser	Leu	Pro	Phe	Ile	Ala	Val	Ile	Gly	Val	Ser	Ser	Leu	Ala	Leu	Gly
	50					55					60				
Met	Ala	Ser	Phe	Leu	Met	Ile	Arg	Gly	Ile	Lys	Tyr	Leu	Leu	Glu	His
65					70					75				80	
Ser	Pro	Leu	Asn	Arg	Lys	Gln	Leu	Ala	Lys	Asp	Ile	Gln	Lys	Thr	Ile
			85						90					95	
Ser	Pro	Asp	Val	Trp	Ala	Ser	Met	Val	His	Tyr	Gln	His	Gln	Leu	Leu
			100					105					110		
Ser	His	Leu	His	Glu	Thr	Leu	Leu	Asp	Glu	Ala	Ile	Thr	Ala	Arg	Trp
		115					120					125			
Gly	Glu	Pro	Phe	Phe	Ile	Glu	His	Ala	Asn	Leu	Lys	Ala	Lys	Ile	Glu
	130					135					140				
Asp	Leu	Thr	Lys	Gln	Tyr	Asp	Ile	Leu	Asn	Ala	Ala	Phe	Asn	Lys	Ser
145				150						155				160	
Leu	Gln	Gln	Asp	Glu	Ala	Leu	Arg	Ser	Gln	Val	Glu	Lys	Arg	Ala	Tyr
				165					170					175	

```

Leu Phe Pro Ile Pro Asn Asn Asp Glu Asn Ala Lys Thr Lys Glu Ser
      180      185      190
Gln Leu Leu Asp Ser Glu Asn Asp Ser Asn Ser Glu Phe Gln Glu Ile
      195      200      205
Ile Asn Lys Gly Leu Glu Ala Ala Asn Lys Arg Arg Ala Asp Ala Lys
      210      215      220
Ser Lys Phe Tyr Thr Glu Asp Glu Thr Ser Asp Lys Lys Phe Ser Ile
      225      230      235      240
Trp Lys Pro Thr Lys Asn Leu Ala Leu Glu Asp Leu Trp Arg Val His
      245      250      255
Asp Glu Ala Cys Asn Glu Glu Gln Gln Ala Leu Leu Leu Glu Asp Tyr
      260      265      270
Met Ser Tyr Lys Thr Ser Glu Cys Gln Ala Ala Leu Gln Lys Val Ser
      275      280      285
Gln Glu Leu Lys Ala Ala Gln Lys Ser Phe Pro Val Leu Glu Lys His
      290      295      300
Ala Leu Asp Arg Ser Tyr Glu Ser Ser Leu Thr Met Met Asp Leu Ala
      305      310      315      320
Arg Ala Asn Gln Glu Thr His Arg Leu Leu Asn Ile Leu Ser Glu Leu
      325      330      335
Gln Gln Leu Ala Gln Tyr Leu Leu Asp Asn His
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 148:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(151999..152664)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 148:

```

His Thr Pro Lys Thr Phe Pro Leu Lys Val His His Ser Phe Ser Asp
1      5      10      15
Lys His Pro Gln Ile Ala Lys Ala Met Trp Ile Thr Gly Ile Ala Leu
      20      25      30
Ala Ala Leu Ser Leu Leu Ala Val Val Ala Cys Val Ile Ala Val Ser
      35      40      45
Ala Gly Gly Ala Ala Ile Pro Leu Thr Val Val Gly Gly Ile Ala Ala
      50      55      60
Met Ser Gly Leu Leu Ser Ala Ala Thr Ile Ile Cys Ser Ala Lys Lys
      65      70      75      80
Ala Leu Ala Gln Arg Lys Gln Lys Gln Leu Glu Ala Ser Leu Pro Leu
      85      90      95
Asp Asn Ala Thr Glu His Val Asn Tyr Leu Thr Ser Asp Thr Pro Tyr
      100      105      110
Phe Asn Gln Trp Glu Ser Leu Asp Ala Leu Asn Lys Gln Leu Ser Gln
      115      120      125
Ile Asp Leu Thr Ile Gln Ala Pro Glu Lys Lys Leu Leu Lys Glu Val
      130      135      140
Leu Gly Ser Arg Tyr Asp Ser Ile Asn His Ser Ile Glu Glu Ile Ser
      145      150      155      160
Asp Arg Phe Thr Lys Met Leu Ser Leu Leu Arg Leu Arg Glu His Phe

```

				165					170					175			
Tyr	Arg	Gly	Glu	Glu	Arg	Tyr	Thr	Pro	Tyr	Leu	Thr	Pro	Pro	Leu	Leu		
			180					185					190				
Lys	Lys	Asn	Arg	Leu	Leu	Ile	Gln	Ile	Thr	Ser	Asn	Met	Ile	Arg	Met		
		195					200					205					
Leu	Pro	Lys	Phe	Gly	Gly	Val	Phe	Ser	Leu	Lys	Ala	Ile	His				
	210					215					220						

(2) INFORMATIONS POUR LA SEQ ID NO: 149:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 151 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 152900..153352

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 149:

Thr	Lys	Ala	Phe	Ser	Gly	Phe	Ile	Val	Arg	Lys	Thr	Val	Ile	Val	Ala		
1				5					10					15			
Met	Ser	Gly	Gly	Val	Asp	Ser	Ser	Val	Val	Ala	Tyr	Leu	Leu	Lys	Lys		
			20					25					30				
Gln	Gly	Glu	Tyr	Asn	Val	Val	Gly	Leu	Phe	Met	Lys	Asn	Trp	Gly	Glu		
		35					40					45					
Gln	Asp	Glu	Asn	Gly	Glu	Cys	Thr	Ala	Thr	Lys	Asp	Phe	Arg	Asp	Val		
	50					55					60						
Glu	Arg	Ile	Ala	Glu	Gln	Leu	Ser	Ile	Pro	Tyr	Tyr	Thr	Val	Ser	Phe		
	65				70					75					80		
Ser	Lys	Glu	Tyr	Lys	Glu	Arg	Val	Phe	Ser	Arg	Phe	Leu	Arg	Glu	Tyr		
				85					90					95			
Ala	Asn	Gly	Tyr	Thr	Pro	Asn	Pro	Asp	Val	Leu	Cys	Asn	Arg	Glu	Ile		
			100					105					110				
Lys	Phe	Asp	Leu	Leu	Gln	Lys	Lys	Val	Leu	Glu	Leu	Lys	Gly	Asp	Phe		
		115					120					125					
Leu	Ala	Thr	Gly	His	Tyr	Cys	Arg	Gly	Gly	Ala	Asp	Gly	Thr	Gly	Phe		
	130					135					140						
Val	Gln	Arg	Lys	Arg	Pro	Gln											
	145					150											

(2) INFORMATIONS POUR LA SEQ ID NO: 150:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 153389..153997

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 150:

```

Asp Ala Leu Ser Asn Val Leu Phe Pro Leu Gly Gly Met Tyr Lys Thr
1      5      10      15
Glu Val Arg Arg Ile Ala Gln Glu Ala Gly Leu Ala Thr Ala Thr Lys
20      25      30
Lys Asp Ser Thr Gly Ile Cys Phe Ile Gly Lys Arg Pro Phe Lys Ser
35      40      45
Phe Leu Glu Gln Phe Val Ala Asp Ser Pro Gly Asp Ile Ile Asp Phe
50      55      60
Asp Thr Gln Gln Val Val Gly Arg His Glu Gly Ala His Tyr Tyr Thr
65      70      75      80
Ile Gly Gln Arg Arg Gly Leu Asn Ile Gly Gly Met Glu Lys Pro Cys
85      90      95
Tyr Val Leu Ser Lys Asn Met Glu Lys Asn Ile Val Tyr Ile Val Arg
100     105     110
Gly Glu Asp His Pro Leu Leu Tyr Arg Gln Glu Leu Leu Ala Lys Glu
115     120     125
Leu Asn Trp Phe Val Pro Leu Gln Glu Pro Met Ile Cys Ser Ala Lys
130     135     140
Val Arg Tyr Arg Ser Pro Asp Glu Lys Cys Ser Val Tyr Pro Leu Glu
145     150     155     160
Asp Gly Thr Val Lys Val Ile Phe Asp Val Pro Val Lys Ala Val Thr
165     170     175
Pro Gly Gln Thr Val Ala Phe Tyr Gln Gly Asp Ile Cys Leu Gly Gly
180     185     190
Gly Val Ile Glu Val Pro Met Ile His Gln Leu
195     200

```

(2) INFORMATIONS POUR LA SEQ ID NC: 151:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 431 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(153984..155276)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 151:

```

Ser Trp Ser Ser Cys Thr Ser Gln Tyr Asp Gly Thr Thr Ser Asp Leu
1      5      10      15
Met Arg Leu Glu Ala Glu Ile Glu Lys Thr Lys Gln Ala Lys Glu Gln
20      25      30
Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala Ser Leu Arg Asp Glu
35      40      45
Glu Lys Lys Leu Arg Glu Lys Leu Gly Asn Met Lys Gln Gln Trp Glu
50      55      60
Ser Asn Lys Glu Glu His Gln Val Pro Val Asp Glu Glu Ala Val Ala
65      70      75      80
Gln Val Val Ser Val Gln Thr Gly Ile Pro Ala Ala Arg Leu Thr Glu
85      90      95
Ala Glu Ser Glu Lys Leu Leu Thr Leu Glu Thr Thr Leu Gln Lys Lys
100     105     110
Val Ile Gly Gln Ser Gln Ala Val Ala Ser Ile Cys Arg Ala Ile Arg
115     120     125
Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg Pro Met Gly Ser Phe

```

130		135		140
Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr		Leu Leu Ala Gln Gln		
145		150		155
Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ser		Leu Ile Gln Val Asp		160
	165		170	
Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr		Lys Met Met Gly Ser		175
	180		185	
Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly		His Leu Thr Glu Gln		190
	195		200	
Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe		Asp Glu Ile Glu Lys		205
	210		215	
Ala His Pro Asp Ile Met Asp Leu Met Leu Gln		Ile Leu Glu Gln Gly		220
225		230		235
Arg Leu Thr Asp Ser Phe Gly Arg Lys Ile Asp		Phe Arg Asn Thr Ile		240
	245		250	
Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu		Ile Arg Lys Ser Gly		255
	260		265	
Glu Ile Gly Phe Gly Leu Arg Ser His Met Asp		Tyr Ala Val Ile Lys		270
	275		280	
Glu Lys Ile Asp Ala Ala Val Lys Lys His Leu		Lys Pro Glu Phe Ile		285
	290		295	
Asn Arg Leu Asp Glu Ser Val Ile Phe Lys Pro		Leu Glu Lys Glu Ala		300
305		310		315
Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys		Leu Gly Ser Arg Leu		320
	325		330	
Gln Asn Tyr Gln Met Asp Leu Asn Ile Pro Asp		Ser Val Ile Ser Phe		335
	340		345	
Leu Val Thr Lys Gly His Ser Pro Glu Met Gly		Ala Arg Pro Leu Arg		350
	355		360	
Arg Val Val Glu Gln Tyr Leu Glu Asp Pro Leu		Ala Glu Met Leu Leu		365
	370		375	
Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu		Arg Ala Arg Leu Thr		380
385		390		395
Glu Glu Arg Val Val Phe Glu Arg Glu Glu Glu		Ala Val Ser Ala Leu		400
	405		410	
Ala Ile Glu Gly Asp Gly Ser Glu Pro Ile Thr		Ala Asp Glu Ser		415
	420		425	
				430

(2) INFORMATIONS POUR LA SEQ ID NO: 152:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé -

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(155231..156544)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 152:

Met Phe Glu Lys Phe Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala
1 5 10 15
Lys Lys Glu Ala Gln Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His
20 25 30
Ile Leu Leu Gly Leu Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val
35 40 45

```

Leu Arg Thr Leu Gly Val Asp Phe Asp Thr Ala Lys His Glu Val Glu
 50          55          60
Arg Leu Ile Gly Tyr Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala
65          70          75          80
Leu Thr Gly Arg Val Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala
          85          90          95
Ala Leu Leu Glu His Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly
          100          105          110
Ile Leu Asn Gln Ser Asp Gly Val Ala Leu Gln Val Leu Glu Asn Leu
          115          120          125
His Val Asp Pro Lys Glu Ile Arg Lys Glu Ile Leu Lys Glu Leu Glu
          130          135          140
Thr Phe Asn Leu Gln Leu Pro Pro Ser Ser Ser Ile Thr Pro Arg Asn
145          150          155          160
Thr Asn Ser Ser Ser Ser Ser Ser Lys Ser Ser Ser Pro Leu Gly Gly His
          165          170          175
Thr Leu Gly Gly Asp Lys Pro Glu Lys Leu Ser Ala Leu Lys Ala Tyr
          180          185          190
Gly Tyr Asp Leu Thr Glu Met Phe Lys Glu Ser Arg Leu Asp Pro Val
          195          200          205
Ile Gly Arg Ser Ala Glu Val Glu Arg Leu Ile Leu Ile Leu Cys Arg
          210          215          220
Arg Arg Lys Asn Asn Pro Val Leu Val Gly Glu Ala Gly Val Gly Lys
225          230          235          240
Thr Ala Ile Val Glu Gly Leu Ala Gln Lys Ile Val Ser Gly Glu Val
          245          250          255
Pro Glu Ala Leu Arg Lys Lys Arg Leu Ile Thr Leu Asp Leu Ala Leu
          260          265          270
Met Ile Ala Gly Thr Lys Tyr Arg Gly Gln Phe Glu Glu Arg Ile Lys
          275          280          285
Ala Val Met Asp Glu Val Arg Lys His Gly Asn Ile Leu Leu Phe Ile
          290          295          300
Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ala Glu Gly Ala Ile
305          310          315          320
Asp Ala Ser His Ile Leu Lys Pro Ala Leu Ala Arg Gly Glu Ile Gln
          325          330          335
Cys Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys
          340          345          350
Asp Ala Ala Leu Glu Arg Arg Phe Gln Lys Ile Val Val Gln Pro Pro
          355          360          365
Ser Val Asp Glu Thr Val Glu Ile Leu Arg Gly Leu Lys Lys Lys Tyr
          370          375          380
Glu Glu His His Asn Val Phe Ile Thr Asp Glu Ala Leu Val Ala Ala
385          390          395          400
Ala Lys Leu Ser Asp Gln Tyr Val His Gly Arg Phe Leu Pro Asp Lys
          405          410          415
Ala Ile Asp Leu Leu Asp Glu Ala Gly Ala Arg Val Arg Val Asn Thr
          420          425          430
Met Gly Gln Leu Arg Thr
          435

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 153:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 240 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 156806..157525

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 153:

Ile	Met	Arg	Thr	Arg	Val	Ile	Asp	Ser	Ile	Arg	Gly	Thr	Pro	Lys	Asp
1				5					10					15	
Leu	Met	Gln	Lys	Asp	Arg	Leu	Leu	Leu	Asp	Ser	Leu	Arg	Lys	Gly	Glu
			20					25					30		
Val	Ile	Leu	His	Leu	Tyr	Glu	Trp	Glu	Gly	Ile	Phe	Pro	Leu	Thr	Tyr
		35					40					45			
Gly	Cys	Phe	Ile	Lys	Pro	Glu	Arg	Phe	Leu	Lys	Ala	Asn	Trp	Glu	Ser
	50					55					60				
Leu	Gly	Val	Ser	Ala	Ala	Ser	Arg	Pro	Thr	Gly	Gly	Gly	Val	Thr	Phe
65					70					75					80
His	Asn	Ser	Asp	Tyr	Ala	Phe	Ser	Leu	Leu	Val	Ser	Ser	Glu	His	Pro
				85					90					95	
Leu	Tyr	Gln	Asp	Ser	Ile	Leu	Ala	Asn	Tyr	His	Thr	Val	Asn	Arg	Phe
			100					105					110		
Val	Leu	Lys	Thr	Ile	Asn	Lys	Leu	Phe	Gly	Leu	Glu	Gly	Ser	Leu	Ser
		115					120					125			
Pro	Ile	Glu	Val	Ser	Thr	Asp	Arg	Ala	Glu	Ser	Ser	Asn	Phe	Cys	Val
	130					135						140			
Ala	Lys	Thr	Ser	Lys	Tyr	Asp	Val	Leu	Ile	Gly	Asn	Arg	Lys	Val	Gly
145					150					155					160
Gly	Ala	Ala	Gln	Arg	Ser	Val	Lys	Gln	Gly	Phe	Leu	His	Gln	Gly	Ser
				165					170					175	
Ile	Phe	Leu	Ser	Gly	Asn	Ser	Leu	Asp	Phe	Tyr	Arg	Asn	Ile	Leu	Leu
			180					185					190		
Pro	Asp	Leu	Val	Asp	Lys	Ile	Gly	Pro	Glu	Val	Glu	Lys	Ser	Ala	Phe
		195					200					205			
Phe	Pro	Leu	Gly	Met	Glu	Ala	Ser	Ser	Thr	Val	Leu	Lys	Glu	Val	Arg
	210					215					220				
Lys	Glu	Val	Lys	Asp	Ser	Leu	Met	Arg	Ile	Phe	Met	Gln	Glu	Gly	Ile
225						230				235					240

(2) INFORMATIONS POUR LA SEQ ID NO: 154:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 489 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 157489..158955

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 154:

Arg	Leu	Phe	Asp	Ala	Asp	Leu	Tyr	Ala	Gly	Gly	Asp	Leu	Ile	Arg	Met
1				5					10					15	
Lys	Met	Ala	Phe	Leu	Arg	Lys	Ile	Phe	Val	Phe	Val	Ala	Cys	Val	Val
			20					25					30		
Ser	Leu	Asn	Gly	Phe	Ala	His	Thr	Ile	Ala	Ile	Pro	Asp	Gly	Asp	Lys
		35					40						45		

Lys Ala Lys Val Leu Ile His Asp Asn Gly Tyr Glu Met Tyr Glu His  
 50 55 60  
 Leu Leu Ala Ala Ile Ser Ser Ala Lys Tyr Thr Val Glu Leu Cys Pro  
 65 70 75 80  
 Cys Leu Ala Gly Gly Glu Ile Leu Ser Thr Val Leu Gln Arg Leu Glu  
 85 90 95  
 Gln Arg Met Glu Glu Val Pro Ala Leu Val Ser Tyr Ile Leu Val Gln  
 100 105 110  
 Pro Thr Cys Ile Asp Asp Asn Asp Arg Lys Asn Leu Lys Thr Leu Gln  
 115 120 125  
 Glu Asn Tyr Pro Asp Arg Phe Phe Tyr Leu Phe Ser Asp Trp Pro Pro  
 130 135 140  
 Tyr Cys Asn Val Phe Phe Pro Asn Val Thr Glu Ser His Thr Lys Leu  
 145 150 155 160  
 Ser Ile Val Asp Gly Lys Tyr Ile Phe Ile Gly Gly Ser Asn Leu Glu  
 165 170 175  
 Asp Leu Gln Cys Ser Lys Gly Asp Val Asp Leu Glu Val Ser Asp Ser  
 180 185 190  
 Pro Arg Ala Val Ile Gly Gly Val Leu Arg Pro Ser Ala Met Arg Asp  
 195 200 205  
 Gln Asp Val Thr Ile Val Ser Glu Glu Tyr Gly Ala Leu Leu Arg Lys  
 210 215 220  
 Glu Phe Cys Ala His Tyr Ala Leu Trp Lys Asp Phe Thr Gln Lys Leu  
 225 230 235 240  
 Trp Leu Asn Lys Lys Leu Asp Asp Phe Arg Gly Ile Asp Pro Ile Asn  
 245 250 255  
 Leu Ser Ile Glu Lys Ala Arg Ser Ser Phe Cys Ala Met Ile Glu Thr  
 260 265 270  
 Ser Leu Cys Ala Val Ser Val Pro Leu Asp Lys Met His Phe Ile Phe  
 275 280 285  
 Ser Gly Pro Asp Glu Ser Asn Asn Thr Ile Ala Glu Glu Tyr Val Arg  
 290 295 300  
 Leu Ile Asn Gln Ala Gln His Ser Ile Arg Ile Ala Gln Met Phe Phe  
 305 310 315 320  
 Ile Pro Val Ala Lys Ile Tyr Asp Ser Leu Met Ala Ala Cys Trp Asp  
 325 330 335  
 Arg Gly Val Glu Ile Tyr Leu Val Thr Asn Gly Arg Thr Asp Arg Ser  
 340 345 350  
 Pro Glu Ile Thr Arg Ser Tyr Ala Trp Gly Asn Arg Ile Asn Tyr Phe  
 355 360 365  
 Pro Leu Thr Phe Gly Ser Arg Pro Leu Leu Trp Glu Arg Phe Leu Tyr  
 370 375 380  
 Ser Pro Ser Arg Ala Ser Met Lys Phe Tyr Val Ser Glu Phe Tyr Val  
 385 390 395 400  
 Ala Asn Thr Gln Leu His Lys Lys Cys Met Leu Val Asp Asp His Ile  
 405 410 415  
 Leu Val Ile Gly Ser Tyr Asn Phe Gly Lys Lys Ser Asn Asp Cys Asp  
 420 425 430  
 Tyr Glu Cys Ile Val Val Ile Asp Ser Lys Glu Ala Val Ser Lys Ala  
 435 440 445  
 Gln Val Val Phe Glu Lys Asp Leu Arg Leu Ser Lys Ser Val Thr His  
 450 455 460  
 Asp Asp Ile Ile Asn Trp Tyr Phe Asp Pro Val His Tyr Cys Leu Gly  
 465 470 475 480  
 Tyr Leu Glu Gln Arg Tyr Met Pro Ser  
 485



## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 286 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 159104..159961

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 155:

Phe	Ser	Phe	Phe	Phe	Leu	Lys	Gly	Leu	Phe	Ser	Lys	Lys	Lys	Gly	Leu
1				5					10					15	
Leu	Leu	Ala	Phe	Phe	Asn	Lys	His	Gln	Lys	Lys	Phe	Ile	Gly	Leu	Val
			20					25					30		
Ile	Ala	Gly	Val	Cys	Leu	Ser	Gly	Val	Gly	Val	Ser	Val	Gly	Gln	Thr
		35					40					45			
Val	Lys	Lys	Thr	Asn	Lys	Leu	Gly	Ser	Gly	Lys	Thr	Val	Tyr	Arg	Thr
	50					55					60				
Pro	Ser	Gly	Arg	Lys	Tyr	Ser	Glu	Lys	Glu	Phe	Leu	Leu	Leu	Lys	His
65					70					75					80
Phe	Leu	Ser	Asn	Glu	Ala	Tyr	Pro	Phe	Thr	Gly	Asn	Pro	Arg	Glu	Trp
			85						90					95	
Asn	Phe	Leu	Asn	Glu	Gly	Leu	Leu	Thr	Glu	Arg	Phe	Leu	Thr	Asn	Lys
			100					105					110		
Leu	Gly	Glu	Lys	Leu	Phe	Leu	Ser	Ile	Tyr	Lys	Ser	Gly	Phe	Pro	Ala
		115					120					125			
Phe	Asp	Lys	Glu	Arg	Ser	Tyr	Glu	Gly	Tyr	Arg	Arg	Phe	Asp	Ala	Pro
	130					135					140				
Phe	Ile	Ser	Ser	Glu	Glu	Val	Trp	Lys	Ser	Ser	Ala	Pro	Gln	Leu	Arg
145					150					155					160
Glu	Ala	Phe	His	Ile	Phe	Gln	Gln	Leu	Thr	Asp	Pro	Val	Ser	Pro	Glu
			165						170						175
Gly	Phe	Ala	Val	Arg	Val	Arg	Leu	Phe	Leu	Glu	Glu	Lys	Lys	Phe	Pro
			180					185					190		
His	Tyr	Val	Leu	Arg	Gln	Met	Leu	Glu	Tyr	Arg	Arg	Gln	Met	Phe	Asn
		195					200					205			
Leu	Pro	Val	Asp	Asn	Ser	Leu	Val	Gln	Gly	Arg	Asp	Leu	Arg	Leu	Phe
	210					215					220				
Gly	Tyr	Lys	Asn	Val	Lys	Asp	Trp	Phe	Gly	Asp	Lys	Tyr	Ile	Ser	Ser
225					230					235					240
Val	Thr	Glu	Ala	Met	Leu	Cys	Phe	Ile	Asp	Glu	Gln	Lys	Lys	Lys	Val
			245						250					255	
Gly	Met	Pro	Ser	Leu	Lys	Glu	Ala	Arg	Gln	Asp	Phe	Tyr	Asp	Lys	Ala
			260				265						270		
Gln	Met	His	Leu	Pro	Asp	Leu	Val	Asn	Met	Leu	Ser	Leu	Ile		
		275					280					285			

## (2) INFORMATIONS POUR LA SEQ ID NO: 156:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 435 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 159916..161220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 156:

Ser	Ala	Asp	Ala	Phe	Ala	Arg	Leu	Ser	Lys	His	Ala	Glu	Phe	Asn	Leu	1	5	10	15
Thr	Phe	Glu	Gln	Leu	Val	Ala	Ser	Phe	Tyr	Ala	Phe	Met	Gly	Val	Glu	20	25	30	
Glu	Ser	Asp	Phe	Leu	Gly	Met	Tyr	Arg	Glu	Ile	Leu	Leu	Tyr	Lys	Lys	35	40	45	
Ala	Leu	Leu	Ser	Leu	Glu	Gly	Ala	Val	Ser	Phe	Asp	Tyr	Tyr	Pro	Leu	50	55	60	
Gln	Lys	Phe	Phe	Ser	Met	Gly	Lys	Asp	Ser	Val	Ser	Val	Glu	Leu	Phe	65	70	75	80
His	Leu	Pro	Asp	Ser	Leu	Val	Phe	Lys	Asp	Lys	Glu	Asp	Leu	Glu	Ala	85	90	95	
Phe	Glu	Thr	Tyr	Leu	His	Leu	Thr	Ala	Phe	Pro	Ser	Val	His	Val	Leu	100	105	110	
Asp	Val	Pro	Thr	Lys	Ala	Phe	Pro	Ile	Glu	Arg	Val	Arg	Ser	Lys	Ala	115	120	125	
Glu	Cys	Leu	Val	Gly	Lys	Arg	Phe	Ala	Val	Ser	Tyr	Gln	Ser	Val	Lys	130	135	140	
Leu	Ala	Asp	Leu	Glu	Lys	Tyr	Val	Pro	Met	Ala	Gln	Val	Tyr	Gln	Trp	145	150	155	160
Tyr	Gln	Asn	Pro	Glu	Asn	Phe	Glu	Glu	Ile	Leu	Leu	Glu	Phe	Pro	Glu	165	170	175	
Leu	Glu	Thr	Ser	Ser	Ser	Leu	Arg	Asp	Ile	Leu	Asn	Leu	Lys	Pro	Thr	180	185	190	
Ile	Val	Glu	Lys	Ala	His	Ser	Tyr	Val	Arg	Lys	Ala	Ile	Leu	Arg	Ala	195	200	205	
Asp	Pro	Glu	Arg	Ile	Gln	Ser	Glu	Leu	Ala	Lys	Lys	Glu	Arg	Gln	Glu	210	215	220	
Glu	Glu	Leu	Phe	Leu	Ser	Ile	Gly	Lys	Asp	His	Val	Leu	Pro	Gly	Ile	225	230	235	240
Gln	Asn	Gly	Val	Arg	Leu	Ala	Asn	Val	Leu	Met	Gln	Gln	Asp	Ser	Val	245	250	255	
Asp	Ser	Tyr	Thr	Gln	Asp	Asn	Glu	His	Phe	Tyr	Ser	Ile	Ser	Val	Ile	260	265	270	
Ser	Arg	Ala	Asp	Lys	Asp	Glu	Val	Leu	Pro	Tyr	Lys	Glu	Val	Leu	Arg	275	280	285	
Lys	Gly	Leu	Lys	Lys	Val	Leu	Leu	Glu	Lys	Tyr	Lys	Ala	Glu	Glu	Arg	290	295	300	
Ile	Ser	Arg	Val	Leu	Thr	His	Leu	Gln	Glu	Ser	Phe	Pro	Asn	Ser	Gln	305	310	315	320
Gly	Gln	Asp	Leu	Tyr	Gln	Arg	Arg	Leu	Val	Arg	Phe	Val	Lys	Ala	Phe	325	330	335	
Gln	Thr	Gly	Lys	Leu	Ala	Gln	Gly	Asp	Leu	Phe	Gly	Gly	Leu	Glu	Lys	340	345	350	
Thr	Met	Lys	Thr	Phe	Ser	Arg	Gly	Asp	Gln	Gly	Ala	Pro	Gln	Glu	Phe	355	360	365	
Glu	Asp	Met	Phe	Ala	Leu	Lys	Glu	Gly	Gln	Val	Ser	Asp	Val	Leu	Phe	370	375	380	
Asp	Leu	Asp	Lys	Gly	Pro	Phe	Tyr	Tyr	Thr	Ala	Ile	Ser	Lys	Ser	Cys	385	390	395	400
Cys	Asp	Tyr	Pro	Val	Ser	Leu	Asp	Lys	Leu	Leu	Phe	Ala	Lys	Ser	His	405	410	415	
Leu	Asn	Glu	Glu	Phe	Leu	Arg	Pro	Tyr	Leu	Glu	Glu	Val	Phe	Phe	His				

Asn Pro Ser                    420                    425                    430  
                                  435

(2) INFORMATION POUR LA SEQ ID NO: 157:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 161183..161593

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 157:

Asp	Pro	Ile	Trp	Lys	Lys	Phe	Phe	Phe	Thr	Thr	Leu	Val	Lys	Gly	Leu
1				5					10					15	
Ser	Arg	Thr	Asn	Met	Lys	Gly	Gln	Lys	Tyr	Tyr	Ser	Asp	Tyr	His	Val
			20					25					30		
Trp	Ile	Glu	Pro	Ile	His	Ser	Arg	Ile	Val	Lys	Leu	Gly	Leu	Ser	Ser
		35					40					45			
Gln	Met	Ala	Gly	Xaa	Leu	Gly	Asn	Ile	Leu	His	Ile	Asp	Leu	Pro	Ser
	50					55					60				
Val	Gly	Ser	Phe	Ile	Lys	Glu	Gly	Glu	Glu	Leu	Cys	Ile	Leu	Glu	Ser
65					70				75					80	
Ser	Lys	Ser	Ala	Ile	Glu	Val	Leu	Ser	Pro	Val	Ser	Gly	Glu	Val	Leu
				85					90					95	
Glu	Val	Asn	Thr	Ala	Leu	Glu	Asp	Asp	Ile	Leu	Pro	Val	Asn	Asn	Ala
			100					105					110		
Thr	Glu	Ser	Glu	Gly	Trp	Phe	Val	Val	Leu	Gln	Leu	Thr	Glu	Asp	Phe
		115					120						125		
Arg	Ser	Glu	Ser	Phe	Ser	Leu	Glu	Pro							
		130				135									

(2) INFORMATION POUR LA SEQ ID NO: 158:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 237 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(161623..162333)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 158:

Leu	Leu	Asn	Leu	Leu	Gly	Ile	Phe	Leu	Gln	Ala	Thr	Phe	Ile	Gln	Asn
1				5					10					15	
Ile	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Met	Cys	Ser	Tyr	Leu	Ala	Cys	Ser
			20				25						30		
Ser	Arg	Leu	Ser	Thr	Ala	Asn	Gly	Leu	Gly	Met	Ser	Val	Ala	Leu	Val
		35					40					45			

```

Leu Thr Ile Thr Gly Ser Ile Asn Trp Leu Val His Tyr Phe Ile Thr
 50          55          60
Lys Pro Gly Ala Leu Ala Trp Leu Ser Pro Ala Leu Ala Asn Ile Asp
65          70          75          80
Leu Ser Phe Leu Glu Leu Ile Met Phe Ile Val Val Ile Ala Ala Phe
          85          90          95
Thr Gln Ile Leu Glu Leu Leu Leu Glu Arg Phe Ser Arg Asn Leu Tyr
          100          105          110
Leu Ala Leu Gly Ile Phe Leu Pro Leu Ile Ala Val Asn Cys Ala Ile
          115          120          125
Leu Gly Gly Val Leu Phe Gly Ile Thr Arg Asn Tyr Pro Phe Leu Pro
          130          135          140
Met Val Val Phe Ser Leu Gly Ser Gly Cys Gly Trp Trp Leu Ala Ile
145          150          155          160
Val Leu Phe Ala Thr Ile Arg Glu Lys Leu Ala Tyr Ser Asp Val Pro
          165          170          175
Gln His Leu Arg Gly Thr Gly Ile Ser Phe Ile Thr Thr Gly Leu Met
          180          185          190
Ala Met Ala Phe Met Gly Leu Thr Gly Ile Asp Ile Ser Lys Pro Thr
          195          200          205
Thr Ser Lys Pro Ala Xaa Xaa Met Asn Ile Ala Thr Asp Ser Pro Gln
          210          215          220
Pro Asn Thr His Ser Ser Ser Glu Glu Pro Lys Ala Ser
225          230          235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 159:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 213 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(162363..163001)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 159:

```

Met Thr Thr Asn Lys Ser Tyr Leu Thr Tyr Phe Thr Asp Ala Leu Trp
1          5          10          15
Ile Asn Asn Gln Pro Leu Ile Ala Ile Leu Gly Ile Cys Ser Ala Leu
          20          25          30
Ala Val Thr Thr Thr Val Thr Thr Ala Leu Thr Met Gly Phe Ala Val
          35          40          45
Ser Phe Val Thr Gly Cys Ser Ser Phe Val Val Ser Leu Leu Arg Lys
          50          55          60
Ile Thr Pro Glu Ser Val Arg Met Ile Ala Gln Leu Ile Ile Ile Ser
65          70          75          80
Leu Phe Val Ile Leu Ile Asp Gln Phe Leu Lys Ala Phe Phe Phe Thr
          85          90          95
Ile Ser Lys Thr Leu Ser Val Phe Val Gly Leu Ile Ile Thr Asn Cys
          100          105          110
Ile Val Met Gly Arg Ala Glu Ser Met Ala Arg His Val Ser Pro Ile
          115          120          125
Pro Ala Phe Leu Asp Gly Leu Gly Ser Gly Leu Gly Tyr Gly Trp Val
          130          135          140
Leu Val Cys Ile Ser Ile Ile Arg Glu Leu Phe Gly Phe Gly Thr Ile

```

```

145          150          155          160
Leu Gly Phe Arg Val Ile Pro Glu Ile Leu Tyr Ala Ser Ala Ala His
          165          170          175
Pro Asp Gly Tyr Glu Asn Leu Gly Leu Met Val Leu Ala Pro Ser Ala
          180          185          190
Phe Phe Leu Leu Gly Ile Met Ile Trp Ile Val Asn Ile Ile Arg Ala
          195          200          205
Pro Lys Thr Lys Arg
          210

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 160:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(162994..163785)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 160:

```

Met Leu Met Ala Ala Gln Val Ile Ser Ser Asp Asn Thr Phe Gln Val
1          5          10          15
Tyr Glu Lys Gly Asp Trp His Pro Ala Leu Tyr Asn Thr Lys Lys Gln
          20          25          30
Leu Leu Glu Ile Ser Ser Thr Pro Pro Lys Val Thr Val Thr Thr Leu
          35          40          45
Ser Ser Tyr Phe Gln Asn Phe Val Arg Val Leu Leu Thr Asp Thr Gln
          50          55          60
Gly Asn Leu Ser Ser Phe Glu Asp His Asn Leu Asn Leu Glu Glu Phe
65          70          75          80
Leu Ser Gln Pro Thr Pro Val Ile His Gly Leu Ala Leu Tyr Val Val
          85          90          95
Tyr Ala Ile Leu His Asn Asp Ala Ala Ser Ser Lys Leu Ser Ala Ser
          100          105          110
Gln Val Ala Lys Asn Pro Thr Ala Ile Glu Ser Ile Val Leu Pro Ile
          115          120          125
Glu Gly Phe Gly Leu Trp Gly Pro Ile Tyr Gly Phe Leu Ala Leu Glu
          130          135          140
Lys Asp Gly Asn Thr Val Leu Gly Thr Ser Trp Tyr Gln His Gly Glu
145          150          155          160
Thr Pro Gly Leu Gly Ala Asn Ile Ala Asn Pro Gln Trp Gln Lys Asn
          165          170          175
Phe Arg Gly Lys Lys Val Phe Leu Val Ser Ala Ser Gly Glu Thr Asp
          180          185          190
Phe Ala Lys Thr Thr Leu Gly Leu Glu Val Ile Lys Gly Ser Val Ser
          195          200          205
Ala Ala Leu Gly Asp Ser Pro Lys Ala Ala Ser Ser Ile Asp Gly Ile
          210          215          220
Ser Gly Ala Thr Leu Thr Cys Asn Gly Val Thr Glu Ser Phe Ser His
225          230          235          240
Ser Leu Ala Pro Tyr Arg Ala Leu Leu Thr Phe Phe Ala Asn Ser Lys
          245          250          255
Pro Ser Gly Glu Ser His Asp His
          260

```

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 342 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(164474..165499)

[illegible]

340

(2) INFORMATIONS POUR LA SEQ ID NO: 162:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(166093..166482)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 162:

```

Asp Gln Gln Glu Gly Leu Ala Thr Gln Glu Ser Ser Phe Pro Glu Glu
1      5      10
Pro Glu Thr Thr Leu Gly Glu Gly Val Ser Phe Lys Gly Glu Leu Thr
      20      25      30
Phe Glu Arg Leu Leu Arg Ile Asp Gly Thr Phe Glu Gly Ile Leu Val
      35      40      45
Ser Lys Gly Lys Ile Ile Val Gly Pro Gln Gly Tyr Val Lys Ala Asn
      50      55      60
Ile Glu Leu Glu Glu Ala Val Ile Ala Gly Val Val Glu Gly Asn Ile
65      70      75      80
Thr Val Thr Gly Arg Val Ser Leu Gln Gly Arg Ala Met Val Thr Gly
      85      90      95
Asp Ile Gln Ala Gly Ser Leu Cys Val Asp Glu Gly Val Arg Leu Cys
      100      105      110
Gly Tyr Val Ser Ile Gln Gly Ala Pro Ser Asn Glu Gln Glu Glu Ile
      115      120      125
Asp Ser
      130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 163:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 455 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(166729..168093)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 163:

```

Met Leu Thr Cys Asn Asp Cys Ser Thr Trp Glu Gln Phe Val Asn Tyr
1      5      10      15
Ile Lys Thr Arg Cys Ser Lys Thr Ala Phe Glu Asn Trp Ile Ala Pro
      20      25      30
Ile Gln Val Leu Glu Glu Ser Ser Glu Lys Ile Arg Leu Glu Ile Pro
      35      40      45
Asn Ile Phe Val Gln Ser Tyr Leu Leu Asp Asn Tyr Lys Lys Asp Leu
      50      55      60

```

Cys	Ser	Phe	Val	Pro	Leu	Asp	Ala	Glu	Gly	Asn	Pro	Ala	Leu	Glu	Phe	65	70	75	80
Val	Val	Ala	Glu	Ile	Lys	Arg	Ser	Ser	Pro	Leu	Val	Thr	Pro	Ser	Ile	85	90	95	
Ala	Lys	Pro	Ala	Thr	Glu	Val	Ser	Glu	Glu	Asn	Lys	Asp	Phe	Gln	Leu	100	105	110	
Lys	Leu	Asn	Gly	Ala	Tyr	Arg	Phe	Asp	Asn	Phe	Ile	Glu	Gly	Pro	Ser	115	120	125	
Asn	Gln	Phe	Val	Lys	Ser	Ala	Ala	Leu	Gly	Ile	Ala	Ala	Arg	Pro	Gly	130	135	140	
Arg	Ser	Tyr	Asn	Pro	Leu	Phe	Ile	His	Gly	Gly	Val	Gly	Leu	Gly	Lys	145	150	155	160
Thr	His	Leu	Leu	His	Ala	Val	Gly	His	Tyr	Val	Arg	Glu	His	His	Lys	165	170	175	
Asn	Leu	Arg	Ile	His	Cys	Ile	Thr	Thr	Glu	Ala	Phe	Ile	Asn	Asp	Leu	180	185	190	
Val	His	His	Leu	Arg	Val	Lys	Ser	Ile	Asp	Lys	Met	Lys	Asn	Phe	Tyr	195	200	205	
Arg	Ser	Leu	Asp	Leu	Leu	Leu	Val	Asp	Asp	Ile	Gln	Phe	Leu	Gln	Asn	210	215	220	
Arg	Gln	Asn	Phe	Glu	Glu	Glu	Phe	Cys	Asn	Thr	Phe	Glu	Thr	Leu	Ile	225	230	235	240
His	Leu	Ser	Lys	Gln	Ile	Val	Val	Thr	Ser	Asp	Lys	Pro	Pro	Gly	Gln	245	250	255	
Leu	Lys	Leu	Ser	Glu	Arg	Ile	Ile	Ala	Arg	Met	Glu	Trp	Gly	Leu	Val	260	265	270	
Ala	His	Val	Gly	Val	Pro	Asp	Leu	Glu	Thr	Arg	Val	Ala	Ile	Leu	Gln	275	280	285	
His	Lys	Ala	Glu	Gln	Lys	Gly	Leu	Asn	Ile	Pro	Asn	Glu	Met	Ala	Phe	290	295	300	
Tyr	Ile	Ala	Asp	His	Val	Tyr	Gly	Asn	Val	Arg	Gln	Leu	Glu	Gly	Ala	305	310	315	320
Ile	Asn	Lys	Leu	Thr	Ala	Tyr	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Leu	Thr	325	330	335	
Glu	Thr	Thr	Val	Arg	Asp	Thr	Leu	Lys	Glu	Leu	Phe	Arg	Ala	Pro	Ser	340	345	350	
Lys	Gln	Lys	Val	Ser	Val	Glu	Ser	Ile	Leu	Lys	Ser	Val	Ala	Thr	Val	355	360	365	
Phe	Gln	Val	Lys	Ile	Gln	Asp	Leu	Lys	Gly	Ser	Ser	Arg	Ala	Lys	Asn	370	375	380	
Val	Pro	Leu	Ala	Arg	Gln	Val	Ala	Met	Tyr	Leu	Ala	Lys	Thr	Leu	Ile	385	390	395	400
Thr	Asp	Ser	Leu	Val	Ala	Ile	Gly	Ala	Ala	Phe	Gly	Lys	Thr	His	Ser	405	410	415	
Thr	Val	Leu	Tyr	Ala	Cys	Lys	Thr	Ile	Glu	Gln	Lys	Ile	Glu	Lys	Asp	420	425	430	
Ala	Leu	Leu	Lys	Asn	Gln	Ile	Ser	Leu	Cys	Lys	Asn	Asn	Ile	Ala	Ile	435	440	445	
Asp	Ser	Pro	Gln	His	Phe	Val										450	455		

## (2) INFORMATIONS POUR LA SEQ ID NO: 164:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 134 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire



(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(168848..169249)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 164:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 165:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 169586..170431

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 165:

Leu	Leu	Cys	Arg	Arg	Phe	Pro	Val	Thr	Asp	Ser	Ile	Pro	His	Ile	Pro
1				5					10					15	
Val	Leu	Val	Lys	Glu	Ser	Leu	Ser	Leu	Phe	Arg	Gly	Arg	Asn	Pro	Val
			20					25					30		
Val	Phe	Cys	Asp	Val	Thr	Val	Gly	Ala	Gly	Gly	His	Ala	Glu	Ala	Phe
		35					40				45				
Leu	Thr	Glu	Phe	Pro	Ser	Ile	Glu	Arg	Tyr	Asp	Gly	Ser	Asp	Arg	Asp
	50				55					60					
Leu	Ser	Ala	Leu	Ala	Leu	Ser	Glu	Asn	Arg	Leu	Leu	Pro	Phe	Lys	Asp
65					70				75						80
Arg	Val	Arg	Leu	Arg	His	Ala	Ser	Phe	Glu	Glu	Val	Asp	Thr	Leu	Thr
				85					90					95	
Ser	Asp	Gly	Thr	Tyr	Asp	Gly	Val	Leu	Ala	Asp	Leu	Gly	Val	Ser	Ser
		100					105					110			
Met	Gln	Leu	Asn	Asn	Leu	Glu	Arg	Gly	Phe	Ser	Phe	Gln	Gly	Glu	Asp
		115					120				125				
His	Pro	Leu	Asp	Met	Arg	Met	Asp	Thr	Ser	Arg	Gly	Met	Thr	Ala	Ser
	130					135					140				

Glu Val Leu Asn Ser Leu Arg Glu Glu Glu Ile Gly Glu Ile Phe Arg  
 145 150 155 160  
 Asn Tyr Gly Glu Glu Pro Leu Trp Arg Ser Ala Ala Ala Val Val  
 165 170 175  
 His Phe Arg Lys Lys Lys Lys Ile Leu Thr Val Lys Asp Leu Lys Asp  
 180 185 190  
 Ala Thr Ser Gly Val Phe Pro Ser Tyr Arg Leu Arg Lys Lys Ile His  
 195 200 205  
 Pro Leu Thr Leu Ile Phe Gln Ala Leu Arg Ile Tyr Val Asn Gln Glu  
 210 215 220  
 Gly Ala Gln Leu Lys Val Leu Leu Asp Ser Ala Phe Arg Trp Leu Arg  
 225 230 235 240  
 Pro Gly Gly Arg Leu Ala Val Ile Ser Phe Cys Ser Leu Asp Asp Arg  
 245 250 255  
 Pro Val Lys Trp Ala Phe Arg Glu Ala Glu Ala Arg Gly Leu Gly Lys  
 260 265 270  
 Ile Leu Thr Lys Lys Val Ile Met Pro Ser  
 275 280

(2) INFORMATIONS POUR LA SEQ ID NO: 166:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 185 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 170780..171334

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 166:

Leu Met Asn His Arg Arg Gln Leu Thr Leu Ile Val Val Gly Val Leu  
 1 5 10 15  
 Ser Leu Tyr Ala Leu Leu Ile Val Arg Tyr Tyr Lys Ile Gln Ile Cys  
 20 25 30  
 Asp Gly Glu Arg Trp Ala Val Glu Ala Ala Asn Gln His Glu Phe Arg  
 35 40 45  
 Val Lys Asp Pro Phe Gln Arg Gly Thr Phe Phe Ala Asn Thr Ser Leu  
 50 55 60  
 Arg Lys Gly Glu Lys Glu Gln Phe His Pro Leu Ala Ile Asp Ile Thr  
 65 70 75 80  
 Lys Phe His Leu Cys Leu Asp Ala Val Val Ile Pro Glu Glu Tyr Arg  
 85 90 95  
 Asp Glu Ile Ala Arg Met Val Val Val Met Val Gly Glu Gly Asp Tyr  
 100 105 110  
 Gln Ser Ile Arg Ser Glu Phe Asp Arg Lys Ser Arg Tyr Arg Lys Leu  
 115 120 125  
 Tyr Val Ser Leu Asp Val Ser Ile Arg Asp Arg Ile Leu Ser Trp Trp  
 130 135 140  
 Lys Pro Tyr Ala Val Lys His Lys Ile Pro Ser Asn Ala Leu Phe Phe  
 145 150 155 160  
 Ile Ser Asp Tyr Gln Arg Ser Tyr Pro Phe Gly Lys Leu Leu Gly Gln  
 165 170 175  
 Val Leu His Thr Ser Gly Asp Lys Arg  
 180 185

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 348 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 171333..172376

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 167:

Asp 1	Glu	Lys	Ser	Gly 5	Glu	Ala	Phe	Pro	Thr 10	Gly	Gly	Leu	Glu	Ala 15	Tyr
Phe	Asn	Arg	Leu 20	Leu	Glu	Gly	Glu	Asn 25	Gly	Glu	Arg	Lys 30	Leu	Leu	Arg
Ser	Pro	Leu 35	Asn	Arg	Leu	Asp	Val 40	Asp	Lys	Val	Thr	Lys 45	Ile	Pro	Arg
Asp	Gly 50	Ser	Asp	Ile	Tyr	Leu 55	Thr	Ile	Asp	Ala	Asn 60	Val	Gln	Thr	Ile
Ala 65	Glu	Gln	Glu	Ile	Ala 70	Leu	Gly	Val	Leu	Glu	Ala	Lys	Ala	Arg	Ser 80
Gly	Arg	Ala	Ile 85	Val	Leu	Asn	Ser	His 90	Thr	Gly	Glu	Ile	Leu	Ala 95	Leu
Ala	Gln	Tyr 100	Pro	Phe	Phe	Asn	Pro	Arg 105	Glu	Tyr	Arg	Glu	Tyr	Phe	Asn
Cys	Asn	Asp 115	Arg	Ile	Glu	Asp	Thr 120	Lys	Val	Lys	Ala	Val 125	Ser	Asp	Val
Phe	Glu 130	Pro	Gly	Ser	Ile	Met 135	Lys	Pro	Ile	Thr	Val 140	Ala	Ile	Ala	Leu
Leu 145	Ala	Asn	Glu	Glu	Met 150	Gln	Lys	Arg	Ala	Gly	Glu	Asn	Leu	Phe	Asp 160
Pro	Tyr	Glu 165	Pro	Leu	Asp	Val	Ser	Arg 170	Arg	Val	Phe	Pro	Gly	Arg	Gln
Lys	Met	Pro 180	Leu	Lys	Asp	Ile	Val	Ser 185	Asn	Arg	Tyr	Leu	Asn	Met	Tyr
Met	Ala	Ile 195	Gln	Lys	Ser	Ser	Asn 200	Val	Tyr	Met	Ala	Gln 205	Leu	Ala	Asp
Arg	Ile 210	Val	Gln	Lys	Leu	Gly 215	Ala	Asp	Trp	Tyr	Glu 220	Gln	Arg	Leu	Gln
Asp 225	Phe	Gly	Phe	Gly	Lys 230	Arg	Thr	Gly	Ile	Glu	Leu	Pro	Ala	Glu	Ala 240
Val	Gly	Leu 245	Val	Pro	Ser	Arg	Lys	Arg 250	Phe	His	Lys	Asn	Gly	Ser	Pro
Glu	Trp	Ser 260	Leu	Ser	Thr	Pro	Tyr	Ser 265	Leu	Ala	Met	Gly	Tyr	Asn	Leu
Leu	Ala	Thr 275	Ser	Met	Gln	Met	Val 280	Gln	Ala	Tyr	Ala	Val 285	Phe	Gly	Asn
Gly	Gly 290	Phe	Leu	Ile	Arg	Pro 295	Thr	Leu	Val	Arg	Lys 300	Ile	Val	Ser	Pro
Ser 305	Gly	Glu	Glu	Lys	Ile 310	Leu	Ser	Ser	Asn	Pro	Lys	Lys	Ile	Arg	Val 320
Leu	Ser	Glu 325	Lys	Ile	Val	Ala	Gly	Cys 330	Cys	Ser	Cys	Tyr	Ala	Phe	His
Asn	Met	Phe 340	Arg	Arg	Asp	Gly	Asp	Ser 345	Cys	Cys	Tyr				

(2) INFORMATIONS POUR LA SEQ ID NO: 168:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 172309..172722

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 168:

Leu	Gln	Asp	Val	Val	Arg	Ala	Met	Arg	Phe	Thr	Thr	Cys	Leu	Gly	Gly
1				5					10					15	
Thr	Gly	Ile	Arg	Ala	Ala	Thr	Lys	Gly	Tyr	Ser	Ser	Ala	Gly	Lys	Thr
			20					25					30		
Gly	Thr	Thr	Glu	Lys	Leu	Val	Asp	Gly	Lys	Tyr	Asp	Lys	Lys	Arg	His
		35					40					45			
Ile	Ala	Ser	Phe	Ile	Gly	Leu	Thr	Pro	Ile	Ala	Ala	Leu	Ser	Asp	Thr
	50					55					60				
Ala	Val	Pro	Leu	Val	Ile	Leu	Val	Ser	Ile	Asp	Asp	Pro	Ala	Tyr	Gly
65					70					75					80
Val	Arg	Glu	Asp	Arg	Thr	Lys	Asn	Tyr	Met	Gly	Gly	Arg	Cys	Ala	Ala
				85					90					95	
Pro	Val	Phe	Ser	Arg	Ile	Ala	Ser	Arg	Val	Leu	Pro	Tyr	Leu	Gly	Val
			100					105					110		
Pro	Leu	Asp	Glu	Gln	Leu	His	Thr	Tyr	Arg	Glu	Glu	Val	Ser	Gln	Leu
		115					120					125			
Lys	Leu	Leu	Tyr	Glu	Glu	Trp	Asn	Arg	Lys						
		130					135								

(2) INFORMATIONS POUR LA SEQ ID NO: 169:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 483 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 173048..174496

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 169:

Met	His	Leu	Asp	Gln	Leu	Leu	Arg	Asn	Ile	Pro	Ala	Lys	Ile	Tyr	Gly
1				5					10					15	
Lys	Val	Glu	Ser	Ile	Pro	Val	Arg	Asn	Leu	Thr	Arg	Asp	Ser	Arg	Cys
			20					25					30		
Val	Gly	Val	Gly	Asp	Ile	Phe	Ile	Ala	Arg	Gln	Gly	Gln	Phe	Cys	Asn
		35				40					45				
Gly	Asn	Asp	Tyr	Ser	Ser	Gln	Ala	Val	Ala	Asn	Gly	Ala	Ile	Ala	Val
	50					55					60				
Leu	Ser	Ser	Leu	Tyr	Asn	Pro	Phe	Leu	Ser	Val	Val	Gln	Ile	Ile	Ala

65					70					75				80
Glu	Asp	Pro	Ile	Ala	Leu	Glu	Ala	Ser	Leu	Ala	Ala	Arg	Phe	Tyr Asn
				85					90				95	
Asn	Pro	Ser	Lys	His	Leu	Asp	Val	Ile	Gly	Ile	Thr	Gly	Thr	Asn Gly
			100					105					110	
Lys	Thr	Thr	Val	Ser	Cys	Leu	Val	Arg	Glu	Leu	Met	Glu	Arg	Ser Gly
			115					120				125		
Ile	Arg	Thr	Gly	Leu	Ile	Gly	Thr	Ile	Glu	His	Ile	Leu	Gly	Glu Asn
			130			135					140			
Arg	Ile	Val	Asp	Ser	Phe	Thr	Thr	Pro	Asp	Ala	Ile	Leu	Leu	Gln Lys
145					150				155					160
Tyr	Phe	Ala	Glu	Met	Val	Lys	Gln	Asn	Leu	Ser	Ala	Ala	Val	Met Glu
				165					170					175
Val	Ser	Ser	Ile	Gly	Met	Ala	Leu	Gly	Arg	Val	Arg	Glu	Thr	Glu Phe
			180					185					190	
Leu	Ala	Gly	Val	Leu	Thr	Asn	Ile	Thr	Ser	Asp	His	Leu	Asp	Phe His
			195					200				205		
Gly	Ser	Leu	Glu	Glu	Tyr	Ile	Ala	Ala	Lys	Lys	Gln	Phe	Phe	Ala Ser
			210			215					220			
Leu	Pro	Glu	Lys	Gly	Ile	Ala	Val	Val	Asn	Leu	Asp	Cys	Glu	Tyr Ala
225					230					235				240
Pro	Ser	Phe	Leu	Asn	Gly	Ser	Gln	Ala	Arg	Ala	Val	Ser	Tyr	Ala Ile
				245					250					255
His	Gln	Glu	Ala	Asp	Tyr	Arg	Ala	Asp	Arg	Leu	Lys	Leu	Tyr	Ser Ser
			260					265					270	
Gly	Ser	Ser	Tyr	Asp	Ile	Trp	Tyr	Gln	Gly	Lys	Val	Phe	Pro	Cys Glu
			275				280					285		
Thr	Ser	Leu	Ile	Gly	Glu	His	Asn	Val	Tyr	Asn	Val	Leu	Ala	Ser Leu
			290			295					300			
Ala	Val	Val	His	Gln	Phe	Leu	Gly	Gly	Asp	Phe	Ala	Asp	Leu	Val Arg
305					310				315					320
Asp	Val	Arg	Phe	Leu	Ser	Ala	Pro	Lys	Gly	Arg	Leu	Asp	Pro	Ile Leu
				325					330					335
Leu	Gly	Pro	Phe	Pro	Val	Tyr	Ile	Asp	Tyr	Ala	His	Thr	Pro	Asp Ala
			340					345					350	
Leu	Asp	Asn	Val	Cys	Arg	Ile	Leu	Leu	Gln	Leu	Leu	Pro	Lys	Tyr Gly
			355				360					365		
Arg	Leu	Ile	Ile	Val	Phe	Gly	Cys	Gly	Gly	Asp	Arg	Asp	Arg	Val Lys
					375					380				
Arg	Pro	Leu	Met	Ala	Lys	Val	Ser	Glu	His	Tyr	Gly	Phe	Ser	Phe Val
385					390				395					400
Thr	Ser	Asp	Asn	Pro	Arg	Thr	Glu	Asp	Pro	Asp	Gln	Ile	Ile	Ala Asp
				405					410					415
Ile	Cys	Lys	Gly	Phe	Ser	Thr	Asp	His	Tyr	Val	Val	Glu	Ser	Asp Arg
			420					425					430	
Lys	Leu	Ala	Ile	Glu	Lys	Ala	Ile	Ser	Met	Ala	Ser	Asp	Lys	Asp Ile
			435				440					445		
Val	Leu	Val	Ala	Gly	Lys	Gly	His	Glu	Gly	Tyr	Gln	Ile	Phe	Lys His
			450			455					460			
Gln	Thr	Ile	Val	Phe	Asp	Arg	Glu	Val	Val	Cys	Glu	Ala	Leu	Ala
465					470				475					480
Ala	Leu	Cys												

(2) INFORMATIONS POUR LA SEQ ID NO: 170:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 174399..174968

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 170:

Leu	Arg	Glu	Arg	Asp	Met	Arg	Gly	Ile	Arg	Ser	Ser	Asn	Ile	Arg	Arg	1	5	10	15
Leu	Ser	Leu	Met	Ile	Glu	Arg	Leu	Cys	Val	Lys	Pro	Trp	Gln	Pro	Phe	20	25	30	
Val	Asn	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Thr	Leu	Ser	Ser	Pro	Val		35	40	45	
Ser	Cys	Phe	Ala	Asp	Ala	Ala	Gly	Ile	Pro	Lys	Val	Ser	Arg	Asn	Glu	50	55	60	
Leu	Ile	Val	Ile	Asp	Pro	Gly	His	Gly	Gly	Lys	Asp	Glu	Gly	Thr	Ala	65	70	75	80
Asp	Lys	Glu	Leu	Arg	Tyr	Lys	Glu	Lys	Thr	Leu	Ala	Leu	Ser	Ile	Ala	85	90	95	
Leu	Ser	Val	Gln	Gly	Cys	Leu	Arg	Arg	Met	Gly	Tyr	Lys	Thr	Ile	Met	100	105	110	
Thr	Arg	Ala	Thr	Asp	Val	Tyr	Val	Asp	Leu	Ser	Lys	Arg	Ala	Ala	Ile	115	120	125	
Ala	Asn	Gln	Asn	Lys	Ala	Asp	Val	Phe	Val	Ser	Ile	His	Cys	Asn	His	130	135	140	
Ser	Ser	Asn	Thr	Ser	Ala	Leu	Gly	Thr	Glu	Ile	Tyr	Phe	Tyr	Asn	Asp	145	150	155	160
Lys	Asn	Ile	Leu	Arg	Thr	Arg	Lys	Ser	Glu	Ser	Leu	Gly	Lys	Arg	Ser	165	170	175	
Trp	Leu	Leu	Cys	Lys	Lys	Met	Glu	Leu	Tyr	Ala	Asn	Val	Lys			180	185	190	

(2) INFORMATIONS POUR LA SEQ ID NO: 171:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 100 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 175411..175710

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 171:

Met	Ala	Thr	Met	Thr	Lys	Lys	Lys	Leu	Ile	Ser	Thr	Ile	Ser	Gln	Asp	1	5	10	15
His	Lys	Ile	His	Pro	Asn	His	Val	Arg	Thr	Val	Ile	Gln	Asn	Phe	Leu	20	25	30	
Asp	Lys	Met	Thr	Asp	Ala	Leu	Val	Gln	Gly	Asp	Arg	Leu	Glu	Phe	Arg	35	40	45	
Asp	Phe	Gly	Val	Leu	Gln	Val	Val	Glu	Arg	Lys	Pro	Lys	Val	Gly	Arg	50	55	60	
Asn	Pro	Lys	Asn	Ala	Ala	Val	Pro	Ile	His	Ile	Pro	Ala	Arg	Arg	Ala				

65					70					75				80
Val	Lys	Phe	Thr	Pro	Gly	Lys	Arg	Met	Lys	Arg	Leu	Ile	Glu	Thr
				85					90					95
Thr	Lys	Ser	Ser											
				100										

(2) INFORMATIONS POUR LA SEQ ID NO: 172:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 432 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 175714..177009

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 172:

Ser	Ser	Ser	Leu	Phe	Pro	Ala	Leu	Leu	Ser	Ile	Val	Glu	Ser	Gly	Phe
1				5					10					15	
Ser	Val	Ser	Lys	Leu	Asp	Ser	Lys	Phe	Pro	Gln	Asp	Tyr	Phe	Leu	Pro
			20					25					30		
Leu	Asp	Val	Phe	Leu	Leu	Thr	Met	Leu	Val	Glu	Ser	Gln	Leu	Gly	Leu
		35					40					45			
Glu	Asp	Val	Leu	Glu	Ala	Phe	Ser	Glu	Arg	Asn	Phe	Asp	Ile	Gln	Ser
	50					55					60				
Lys	Ser	Leu	Ile	Glu	Ser	Phe	Gln	Asp	Lys	Lys	Leu	Arg	Arg	Thr	Val
65					70					75					80
Ile	Gln	Arg	Phe	Leu	His	His	Pro	Leu	Leu	His	Ile	His	Asp	Ile	Ala
				85					90					95	
Arg	Ala	Ala	Tyr	Leu	Leu	Ala	Ala	Leu	Glu	Glu	Gly	Val	Asp	Leu	Gly
			100					105					110		
Tyr	Gln	Phe	Leu	Cys	Met	His	Gln	Thr	Gln	Ser	Gly	Ala	Ala	Leu	Leu
		115					120					125			
Phe	Arg	Arg	Ala	Gly	Phe	Leu	Trp	Gly	Gly	Leu	Pro	Tyr	Pro	Gly	Glu
	130					135					140				
His	Ala	Glu	Met	Ala	Met	Leu	Leu	Ser	Arg	Ile	Ala	Glu	Phe	Tyr	Asp
145					150					155					160
Thr	Ser	Tyr	Glu	Gln	Val	Gln	Lys	Met	Ile	Ala	Phe	Gln	His	Ala	Leu
				165					170					175	
Phe	Ser	His	Glu	Arg	Asn	Ile	Phe	Pro	Ala	Leu	Trp	Ser	Gln	Glu	Gly
			180					185					190		
Ser	Arg	Ser	Asn	Gln	Glu	Lys	Thr	Ala	Val	Ser	Lys	Leu	Leu	Phe	Cys
		195				200						205			
Gln	Lys	Glu	Ala	Arg	Ile	Glu	Asp	Gln	Phe	Thr	Leu	Thr	Asp	Met	Ser
	210					215					220				
Leu	Gly	Phe	Trp	Met	Arg	Arg	Thr	Pro	Ser	Phe	Ser	Ala	Tyr	Val	Ser
225					230					235					240
Gly	Ser	Gly	Cys	Lys	Ser	Gly	Val	Gly	Ala	Phe	Leu	Ile	Gly	Asp	Val
				245					250					255	
Gly	Val	Leu	Asn	Tyr	Gly	Pro	Cys	Val	Gly	Asp	Pro	Gly	Glu	Cys	Leu
			260					265					270		
Gly	Phe	Gly	Leu	Cys	Gly	Gln	Val	Lys	Glu	Phe	Ser	Cys	Gln	Glu	Lys
		275				280						285			
Asp	Glu	Glu	Val	Ser	Ile	Ser	Phe	Ala	Gly	Ala	Leu	Ser	Gln	Pro	Ser
	290					295					300				

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Ser Arg Arg Thr Gly Phe Ser Tyr Leu Gln Asp Ala Leu Phe Ser Thr
305                      310                      315                      320
Asn Ser Cys Tyr Arg Ile Asp Ile Thr Glu Gln Lys Cys His Val Ala
                      325                      330                      335
Ser Ser Leu Asp Arg Glu Asn Gln Asp Ala Phe Phe Ala Ile Phe Cys
                      340                      345                      350
Lys Gly Ser Gln Cys Gln Val Cys Asn Gly Pro Lys Leu Arg Thr Gly
                      355                      360                      365
Ser Pro Asp Ser Tyr Lys Gly Pro Ala Tyr Asp Val Leu Ile Lys Gly
370                      375                      380
Glu Lys Glu Thr Val Arg Ile Leu Ser Ser Ser Pro His Met Glu Ile
385                      390                      395                      400
Phe Ser Leu Gln Gly Lys Asp Arg Phe Trp Gly Ser Asn Phe Leu Ile
                      405                      410                      415
Asn Leu Pro Tyr Thr Gln Asn Ser Ile Asn Ile Leu Phe Glu Lys Ala
                      420                      425                      430

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(2) INFORMATIONS POUR LA SEQ ID NO: 173:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 231 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 177423..178115

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 173:

```

Ser Cys Ser Cys Arg Arg Phe Ala Lys Ile Gln Xaa Gln Arg Phe Met
1                      5                      10                      15
Leu Ile Gly Gln Glu Lys Gly Cys Asp Thr Lys Ser Arg Met His Arg
                      20                      25                      30
Asn Phe Gly Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu
                      35                      40                      45
Ala Lys Met Ala Glu Lys Phe Gly Leu Pro Ile Ile Phe Leu Val Asp
50                      55                      60
Thr Pro Gly Ala Phe Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly
65                      70                      75                      80
Trp Ala Ile Ala Thr Asn Leu Phe Glu Leu Ala Arg Leu Ala Thr Pro
                      85                      90                      95
Ile Ile Val Ile Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly
                      100                      105                      110
Met Ala Ile Gly Asp Val Val Ala Met Leu Glu His Ser Tyr Tyr Ser
115                      120                      125
Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys
130                      135                      140
Lys Asn Ser Asp Ala Ala Met Leu Lys Met His Gly Glu Asp Leu
145                      150                      155                      160
Lys Gly Phe Ala Ile Val Asp Ala Val Ile Lys Glu Pro Ile Gly Gly
                      165                      170                      175
Ala His His Asn Pro Ala Ala Thr Tyr Arg Ser Val Gln Glu Tyr Val
                      180                      185                      190
Leu Gln Glu Trp Val Lys Leu Lys Asp Leu Pro Val Glu Glu Leu Leu
195                      200                      205
Glu Lys Arg Tyr Gln Lys Phe Arg Thr Ile Gly Leu Tyr Glu Thr Ser

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210		215		220
Ser Glu Ser Asp Ser Glu Ala				
225		230		

(2) INFORMATIONS POUR LA SEQ ID NO: 174:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 594 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 178240..180021

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 174:

Phe	Gly	Lys	Gln	Glu	Gly	Ala	Ser	Leu	Val	Lys	Arg	Lys	Glu	Leu	Ser
1			5						10					15	
Lys	Asp	Gln	Leu	Leu	Glu	Gln	Trp	Asp	Asn	Ile	Val	Gly	Glu	Gly	Asp
		20						25					30		
Thr	Leu	Ser	Leu	Pro	Gln	Ala	Asn	Ala	Tyr	Ile	Ala	Lys	His	Ser	Gly
		35					40					45			
Gly	Ser	Gln	Ser	Ile	Thr	Lys	Arg	Leu	Ser	Ala	Tyr	Leu	Ser	Gly	Cys
	50					55					60				
Phe	Asp	Phe	Ser	Arg	Leu	Gln	Cys	Leu	Ala	Leu	Phe	Leu	Val	Val	Val
65				70					75						80
Ala	Ile	Leu	Lys	Ser	Thr	Thr	Leu	Phe	Phe	Gln	Arg	Phe	Leu	Ala	Gln
			85					90					95		
Leu	Ile	Ala	Ile	Arg	Val	Ser	Cys	Ser	Leu	Arg	Lys	Asp	Tyr	Phe	Leu
		100						105					110		
Ala	Leu	Gln	Thr	Leu	Pro	Met	Thr	Phe	Phe	His	Ala	His	Asp	Met	Gly
		115					120					125			
Asn	Leu	Ser	Ser	Arg	Val	Ile	Ala	Asp	Ser	Ser	Met	Ile	Ala	Leu	Ala
	130					135					140				
Ile	Asn	Ala	Leu	Met	Val	Asn	Tyr	Ile	Gln	Ala	Pro	Ile	Thr	Met	Thr
145				150					155						160
Leu	Ala	Leu	Val	Val	Cys	Leu	Ser	Ile	Ser	Trp	Lys	Phe	Cys	Ala	Cys
			165					170					175		
Val	Cys	Leu	Ala	Phe	Pro	Ile	Phe	Ile	Leu	Pro	Ile	Val	Ile	Ile	Ala
		180					185					190			
Lys	Lys	Val	Lys	Ala	Leu	Ala	Lys	Arg	Ile	Gln	Lys	Ser	Gln	Asp	His
		195					200					205			
Ser	Ala	Ala	Ala	Leu	Leu	Asp	Phe	Leu	Leu	Gly	Ile	Leu	Thr	Val	Lys
	210					215					220				
Val	Phe	Arg	Thr	Glu	Gln	Phe	Ser	Phe	Ser	Lys	Tyr	Cys	Gln	Lys	Asn
225				230						235					240
Asp	Glu	Ile	Ala	Arg	Leu	Glu	Glu	Arg	Ser	Ala	Val	Tyr	Ser	Leu	Ile
			245					250					255		
Pro	Arg	Pro	Leu	His	Thr	Ile	Ala	Ser	Leu	Phe	Phe	Ala	Leu	Val	
		260					265					270			
Ile	Met	Ile	Gly	Leu	Tyr	His	Phe	His	Ile	Pro	Pro	Glu	Glu	Leu	Val
	275					280						285			
Val	Phe	Cys	Gly	Leu	Leu	Tyr	Leu	Ile	Tyr	Asp	Pro	Ile	Lys	Lys	Phe
	290					295				300					
Ala	Asp	Glu	Asn	Ala	Asn	Ile	Met	Arg	Gly	Cys	Ala	Ala	Ala	Glu	Arg
305					310					315					320

Phe Tyr Glu Val Leu Asp Leu Ala Lys Gln Gln Ser Asn Val Ser Glu  
 325 330 335  
 Lys Leu Asn Glu Phe Gln Gly Leu Gln His Ser Ile Gln Phe Cys Asn  
 340 345 350  
 Val Ser Phe Gly Tyr Val Glu Asp Ser Pro Val Leu Ser Asp Phe Asn  
 355 360 365  
 Leu Val Leu Lys Lys Gly Glu Ala Ile Gly Ile Val Gly Pro Thr Gly  
 370 375 380  
 Ser Gly Lys Ser Thr Ile Ala Lys Leu Leu Pro Arg Leu Tyr Glu Val  
 385 390 395 400  
 Ser His Gly Glu Leu Ile Asp Ser Leu Pro Ile Gln Ser Tyr Cys  
 405 410 415  
 Lys Asn Ser Leu Arg Lys His Ile Gly Cys Val Leu Gln His Pro Phe  
 420 425 430  
 Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys Gly Arg Thr Phe  
 435 440 445  
 Leu Glu Glu Glu Val Phe His Ala Leu Lys Gln Ala His Ala Tyr Glu  
 450 455 460  
 Phe Val Ser Lys Met Pro Gln Gly Val His Ser Leu Leu Glu Glu Ser  
 465 470 475 480  
 Gly Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu Thr Ile Ala Arg  
 485 490 495  
 Ala Leu Leu His Asn Thr Ser Ile Leu Leu Leu Asp Glu Ala Thr Ser  
 500 505 510  
 Ala Leu Asp Ala Ile Ser Glu Asn Tyr Val Lys Glu Ile Val Gly Gln  
 515 520 525  
 Leu Lys Gly Arg Cys Thr Gln Ile Ile Ile Ala His Lys Leu Ser Thr  
 530 535 540  
 Leu Glu Tyr Val Asp Arg Ile Val Tyr Leu Glu Gln Gly Lys Lys Ile  
 545 550 555 560  
 Ala Glu Gly Thr Lys Glu Glu Leu Leu Asp Ser Cys Pro Ala Phe Gln  
 565 570 575  
 Arg Met Trp Val Leu Ser Gly Ala Lys Asp Trp Glu Leu Asn Ala Val  
 580 585 590  
 Val Lys

## (2) INFORMATIONS POUR LA SEQ ID NO: 175:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 219 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: complement(180048..180704)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 175:

Gln Lys Lys Pro Leu Thr Ser Leu Leu Ser Asp Gly Lys Leu Phe Leu  
 1 5 10 15  
 His Tyr Gly Arg Leu Val Val Met Phe Lys Leu Leu Leu Ile Phe Ala  
 20 25 30  
 Asp Pro Ala Glu Ala Ala Arg Thr Leu Ser Leu Phe Pro Phe Ser Leu  
 35 40 45  
 Asn Lys Glu Asn Phe Tyr Thr Tyr His Thr Glu Asn Val Leu Leu Asp

50		55		60	
Val	Met	Val	Leu	Lys	Thr
65					70
Ser	Pro	Pro	Pro	Ser	Gly
					75
					80
					85
Gly	Ala	Ala	Asn	Pro	Asn
					90
					95
					100
Ser	Val	Lys	Glu	Leu	Thr
					105
					110
					115
Val	Thr	Pro	Ile	Pro	Arg
					120
					125
					130
Ser	Pro	Tyr	Arg	Asp	Gly
145					150
					155
Glu	Gly	Phe	Phe	Ile	Ala
					160
					165
Ser	Met	Ile	Lys	Val	Ser
					170
					175
					180
Phe	Leu	Lys	Asn	Asn	Lys
					185
					190
					195
Ile	Phe	Pro	Ile	Tyr	Ser
					200
					205
					210
					215

(2) INFORMATIONS POUR LA SEQ ID NO: 176:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 256 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(180631..181398)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 176:

Met	Thr	Phe	Ser	Ala	Ala	Phe	Ser	Pro	Cys	Pro	Asn	Asp	Ile	Phe	Leu
1				5					10					15	
Phe	Arg	Ser	Phe	Leu	Glu	Lys	His	Lys	Gly	Phe	Pro	Ser	Leu	Arg	Gln
				20				25					30		
Ile	Met	Ile	Ala	Asp	Ile	Ser	Ser	Leu	Asn	Tyr	Tyr	Ala	Leu	Glu	Thr
				35			40					45			
Arg	Phe	Pro	Leu	Ile	Lys	Ile	Ser	Ala	Ser	Leu	Tyr	Pro	Gln	Ile	Ala
				50		55					60				
Asp	Ser	Tyr	Asp	Val	Leu	Asn	Val	Gly	Thr	Thr	Leu	Gly	Tyr	Lys	Ile
65				70					75					80	
Gly	Pro	Leu	Ile	Leu	Ser	Lys	Gln	Leu	Asp	Ser	Pro	Leu	Lys	Ser	Leu
				85					90					95	
Ala	Thr	Pro	Gly	Glu	Thr	Thr	Thr	Ala	His	Ala	Leu	Cys	Arg	Leu	Phe
				100				105					110		
Tyr	Pro	Arg	Ala	Glu	Leu	Val	Pro	Met	Lys	Tyr	His	Glu	Ile	Ile	Pro
				115			120					125			
Ala	Ile	Leu	Ser	Asn	Arg	Val	Asp	Gly	Gly	Ala	Val	Ile	His	Glu	Glu
				130		135					140				
Arg	Phe	Ser	Phe	Pro	Lys	Asp	Leu	Cys	Ile	Val	Glu	Asp	Leu	Gly	Gln
145				150						155					160
Leu	Trp	Glu	Lys	Thr	Trp	His	Leu	Pro	Leu	Pro	Leu	Gly	Cys	Ile	Val
				165					170					175	

Ile Ser Lys Lys Val Ser Asp Asp Asp Ser Tyr Leu Leu Ser His Ala  
                   180                  185                  190  
 Leu Gln Glu Ser Leu Lys Lys Ser Leu Thr Asp Ser Ala Leu Ala Ile  
                   195                  200                  205  
 Gln Lys Ala Ser Glu Tyr Ser Arg Asp Lys Asn Pro Thr Thr Ile Gln  
                   210                  215                  220  
 His Phe Ile Asp Thr Tyr Val Thr Glu Glu Thr Phe Asn Leu Ser Ser  
 225                  230                  235                  240  
 Ile Gly Arg Gln Ala Phe Ser Thr Leu Trp Thr Ala Cys Arg Asn Val  
                   245                  250                  255

(2) INFORMATIONS POUR LA SEQ ID NO: 177:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(181398..182414)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 177:

Phe Pro Tyr Gln Ile Gln Gln Asn Gln Arg Asp Thr Thr Ala Arg Leu  
 1                  5                  10                  15  
 Leu His Leu Val Asn Arg Asp Ile Asp Ile Pro Gly Phe Gly Met Asp  
                   20                  25                  30  
 Glu Glu Gln Asn Ile Ile Phe Tyr Arg Leu Val Ile Pro Cys Leu Lys  
                   35                  40                  45  
 Gly Glu Ile Asn Glu Asp Leu Leu Arg Val Tyr Ile Asp Thr Ile Lys  
                   50                  55                  60  
 Leu Ile Cys Asp Ser Phe Phe His Ala Ile Gly Leu Ile Ser Thr Gly  
 65                  70                  75                  80  
 Asn Met Asp Leu Asp Glu Leu Lys Lys Gln Ala Lys Leu Glu Asn Asn  
                   85                  90                  95  
 Gln Ser Asp Gln Leu Glu Xaa Leu Glu Leu Val Pro Ala Leu Ile  
                   100                  105                  110  
 Phe Tyr Asp Thr Glu Thr Thr Gly Thr Gln Ile Asp Lys Asp Arg Ile  
                   115                  120                  125  
 Val Glu Leu Ala Ala Tyr Asn Gly Thr Thr Ser Glu Ser Phe Gln Thr  
                   130                  135                  140  
 Leu Val Asn Pro Glu Ile Pro Ile Pro Ala Glu Ala Thr Lys Ile His  
 145                  150                  155                  160  
 Gly Ile Thr Thr Ala Glu Val Ala Asp Ala Pro Arg Phe Pro Glu Ala  
                   165                  170                  175  
 Tyr Gln Lys Phe Ile Glu Phe Cys Gly Thr Asp Asn Ile Leu Val Ala  
                   180                  185                  190  
 His Asn Asn Asn Ala Phe Asp Tyr Pro Leu Leu Val Arg Glu Cys Arg  
                   195                  200                  205  
 Arg His Gly Leu Ser Glu Pro Gln Leu Arg Thr Ile Asp Ser Leu Lys  
                   210                  215                  220  
 Trp Ala Lys Lys Tyr Arg Thr Asp Leu Pro Gln His Ser Leu Gln Tyr  
 225                  230                  235                  240  
 Leu Arg Gln Val Tyr Gly Phe Glu Glu Asn Gln Ala His Arg Ala Leu  
                   245                  250                  255  
 Asp Asp Val Ile Thr Leu Tyr Arg Val Phe Ser Ala Leu Val Gly Asp

(2) INFORMATION POUR LA SEQ ID NO: 178:

(A) LONGUEUR: 248 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 182913..183656

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 179:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 374 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 183665..184786

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 179:

Met	Thr	Ile	Tyr	Leu	Asp	Thr	Asn	Ala	Ser	Ala	Leu	Leu	Glu	Pro	Gly	1	5	10	15
Val	Leu	Met	Cys	Leu	His	Ser	Leu	Phe	Ile	Gly	Glu	Gly	Gly	Phe	Gly	20	25	30	
Asn	Pro	Ser	Ser	Val	His	Ser	Phe	Gly	Lys	Lys	Thr	Lys	Lys	Leu	Val	35	40	45	
Lys	Glu	Thr	Ser	Thr	Leu	Ile	Glu	Lys	Ala	Leu	Gly	Phe	Ser	His	Cys	50	55	60	
Arg	Val	Ile	Tyr	Thr	Ser	Gly	Ala	Thr	Glu	Ser	Leu	Asn	Leu	Ala	Ile	65	70	75	80
Gln	Asn	Ile	Pro	Thr	Gly	Ser	His	Val	Ile	Thr	Ser	Ser	Met	Glu	His	85	90	95	
Pro	Ala	Val	Ile	Glu	Pro	Leu	Lys	Gln	Ala	Lys	Leu	Ser	Val	Thr	Tyr	100	105	110	
Leu	Asp	Pro	Ile	Pro	Gly	Glu	Cys	Val	Val	Ser	Leu	Glu	Gln	Ile	Lys	115	120	125	
Glu	Ala	Val	Gln	Ser	Asp	Thr	Ser	Ala	Ile	Val	Leu	Gly	Trp	Val	Asn	130	135	140	
Ser	Glu	Val	Gly	Val	Arg	Ile	Asp	Leu	Glu	Ala	Ile	Ala	Glu	Phe	Ala	145	150	155	160
Lys	Glu	Arg	Gln	Leu	Leu	Ile	Val	Asp	Ala	Thr	Ala	Ile	Val	Gly		165	170	175	
Lys	Glu	Val	Ile	His	Ile	Pro	Glu	Gly	Val	Ser	Met	Val	Ala	Phe	Ser	180	185	190	
Gly	His	Lys	Phe	His	Ala	Leu	Ser	Gly	Ile	Gly	Val	Leu	Leu	Thr	Ser	195	200	205	
Pro	Lys	Ile	Lys	Ile	Ser	Pro	Ile	Ile	Ser	Gly	Gly	Gly	Gln	Gln	Gly	210	215	220	
Gly	Ile	Arg	Ser	Gly	Thr	Glu	His	Ile	His	Gly	Ile	Ala	Ser	Leu	Arg	225	230	235	240
Tyr	Ile	Phe	Ser	Lys	Leu	Leu	Val	Glu	Gln	Pro	Ala	Ile	Ala	Gln	Thr	245	250	255	
Met	Arg	Ser	Tyr	Arg	Asp	Leu	Phe	Glu	Ser	Arg	Ile	Gln	Glu	Ala	Phe	260	265	270	
Pro	Glu	Cys	Ile	Val	His	Cys	Gln	Asp	Lys	Pro	Arg	Val	Ser	Asn	Leu	275	280	285	
Ser	Ala	Ile	Ala	Phe	Pro	Gly	Leu	Glu	Gly	Glu	Val	Met	Gln	Ile	Ala	290	295	300	
Leu	Asp	Leu	Glu	Gly	Val	Ala	Cys	Gly	Tyr	Gly	Ser	Ala	Cys	Ser	Ser	305	310	315	320
Gly	Ala	Thr	Thr	Val	Phe	Lys	Ser	Leu	Thr	Val	Met	Lys	Val	Pro	Gln	325	330	335	
Asp	Leu	Ala	Val	Ala	Thr	Leu	Arg	Phe	Ser	Phe	Ser	Tyr	Leu	Leu	Ser				

		340						345				350		
Glu	Glu	Glu	Ile	Leu	Thr	Ala	Ala	Gln	Arg	Val	Ile	Arg	Val	Lys
		355					360					365		
His	Leu	Gln	Gln	Tyr	Ala									
		370												

(2) INFORMATIONS POUR LA SEQ ID NO: 180:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 389 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(184796..185962)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 180:

Cys	Ile	Phe	Val	Gln	Gly	Phe	Phe	Ser	Met	Met	Glu	Met	Ala	Cys	Val
1				5					10					15	
Ser	Phe	Asn	Arg	Val	Arg	Leu	Gln	Tyr	Tyr	Leu	Thr	Lys	Ser	Asn	Lys
			20					25					30		
Lys	Ala	Ser	Tyr	Ile	Asn	Phe	Leu	Ile	Arg	Arg	Pro	Tyr	Arg	Leu	Phe
		35					40					45			
Gly	Thr	Val	Met	Leu	Gly	Val	Asn	Ile	Ala	Leu	Gln	Ile	Gly	Ser	Glu
	50					55					60				
Ser	Ser	Arg	Thr	Cys	Tyr	Lys	Leu	Leu	Gly	Ile	Ser	Pro	Glu	Tyr	Ala
65					70					75					80
Pro	Ala	Thr	Gln	Ile	Ile	Leu	Val	Val	Ile	Phe	Ala	Glu	Leu	Ile	Pro
			85						90					95	
Leu	Ala	Ile	Ser	Arg	Lys	Ile	Pro	Glu	Lys	Ile	Ala	Leu	Lys	Gly	Ala
			100					105					110		
Pro	Ile	Leu	Tyr	Phe	Ala	His	Tyr	Leu	Phe	Tyr	Pro	Leu	Ile	Gln	Cys
	115						120					125			
Val	Gly	Gly	Ile	Thr	Asn	Met	Ile	Tyr	Phe	Ile	Leu	Asn	Ile	Lys	Glu
	130					135					140				
Glu	Thr	Ile	His	Ser	Thr	Leu	Ser	Arg	Asp	Glu	Leu	Gln	Lys	Thr	Leu
145					150					155					160
Glu	Thr	His	His	Glu	Glu	His	Asp	Phe	Asn	Val	Ile	Ala	Thr	Asn	Ile
			165						170					175	
Phe	Ser	Leu	Ser	Ala	Thr	Ser	Val	Glu	Gln	Val	Cys	Gln	Tyr	Leu	Asp
			180					185					190		
Gln	Ile	Pro	Ile	Leu	Ser	Ala	Thr	Ala	Ser	Val	Arg	Asp	Val	Cys	Gln
	195					200						205			
Leu	Val	Arg	Arg	His	Arg	Leu	Asp	Phe	Val	Pro	Val	Tyr	His	Lys	Val
	210					215					220				
Lys	Lys	Asn	Val	Val	Gly	Ile	Ala	Phe	Pro	Lys	Asn	Leu	Ile	Asn	Arg
225					230					235					240
Asn	Pro	Ser	Asp	Pro	Val	Val	Pro	Tyr	Leu	Ser	Ser	Pro	Trp	Phe	Ile
			245						250					255	
Thr	Ala	Lys	Ser	Lys	Leu	Ile	His	Ala	Ile	Gln	Glu	Phe	Arg	Lys	Asn
			260					265					270		
Ser	Ser	Lys	Ile	Ala	Ile	Val	Leu	Asn	Asn	Asn	Gly	Glu	Pro	Met	Gly
	275						280					285			
Val	Leu	Gly	Leu	His	Thr	Val	Phe	Lys	Thr	Leu	Phe	Asn	Thr	Arg	Asn
	290					295					300				

```

Ile Thr Gln Leu Lys Pro Lys Pro Thr Ser Leu Ile Glu Arg Thr Phe
305                      310                      315                      320
Ser Gly Asn Thr Pro Leu Ser Glu Ile Glu Asn Glu Leu Asp Ile Ile
                      325                      330                      335
Phe Met Asp Asn Asp Cys Thr Thr Ile Glu Gln Leu Met Leu Lys Leu
                      340                      345                      350
Leu Asp Thr Pro Pro Glu Val Gly Ala Ser Ile Ile Ile Asn Asp Leu
                      355                      360                      365
Leu Leu Glu Val Lys Glu Ile Ser Leu Tyr Gly Ile Lys Thr Val Ala
                      370                      375                      380
Ile Lys Asp Thr Leu
385

```

(2) INFORMATIONS POUR LA SEQ ID NO: 181:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 283 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(186000..186848)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 181:

```

Lys Phe Arg Pro Ile Phe Asp Trp Ala Ile Ser Gly Ile Asn Phe Ile
1                      5                      10                      15
Val Gln Lys Met Leu Ala Arg Gln Glu Ser Asp Phe Ile Gln Pro Gln
                      20                      25                      30
Glu Leu Lys Glu Val Leu Arg Ser Cys Lys Asp Phe Gly Val Val Asn
                      35                      40                      45
His Glu Glu Ser Arg Leu Leu Phe Gly Tyr Leu Ser Met Glu Glu Gly
                      50                      55                      60
Ser Ile Lys Glu Arg Met Thr Pro Lys Gln Glu Ile Ile Phe Tyr Asp
65                      70                      75                      80
Val Leu Thr Pro Ile Glu Asn Leu Tyr Lys Leu Phe Ser Gly Pro Lys
                      85                      90                      95
Gln Ser Tyr Ser Lys Val Leu Val Cys Lys Gly Gly Leu Gln Asn Leu
                      100                     105                     110
Leu Gly Val Cys Ser Ala Lys Leu Leu Leu Leu Tyr Lys Glu Lys Leu
                      115                     120                     125
Gln Ser Ala Glu Glu Leu Leu Pro Leu Leu Arg Lys Pro His Tyr Ile
130                     135                     140
Pro Glu Thr Val Ser Ala Lys Thr Ala Leu Tyr His Leu Ala Gly Glu
145                     150                     155                     160
Asp Cys Gly Leu Gly Ile Ile Ile Asp Glu Tyr Gly Ser Ile Glu Gly
                      165                     170                     175
Leu Ile Thr Gln Asn Asp Leu Phe Lys Ile Val Ser Asp Glu Val Ala
                      180                     185                     190
His Asn Arg Pro Ser Phe Lys Gln Phe Ala His Ser Asp Lys Asn Val
                      195                     200                     205
Val Ile Ala Ala Gly Thr Tyr Glu Leu Ser Asp Phe Tyr Asp Leu Phe
210                     215                     220
Gly Val Asp Leu Pro Thr Thr Ala Asn Cys Val Thr Ile Gly Gly Trp
225                     230                     235                     240
Leu Thr Glu Gln Leu Gly Glu Ile Pro Glu Thr Gly Thr Lys Phe Ala

```



				245					250					255					
Trp	Gly	Gln	Phe	Val	Phe	Gln	Ile	Leu	Asp	Ala	Ala	Pro	Asn	Cys	Val				
				260					265					270					
Lys	Arg	Val	Tyr	Ile	Arg	Lys	Thr	His	Gly	Asn									
				275					280										

(2) INFORMATIONS POUR LA SEQ ID NO: 182:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 174 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(186749..187270)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 182:

Ser	Gly	Ser	Ala	His	Asn	Asn	Pro	Asn	Arg	Met	Phe	Ser	Ser	Ala	Ile				
1				5					10					15					
Val	Ile	Leu	Thr	Ala	Ile	Phe	Val	Leu	Cys	Ser	Gly	Phe	Val	Ser	Leu				
			20					25					30						
Ser	His	Ile	Ala	Leu	Phe	Ser	Leu	Pro	Ser	Ser	Leu	Ile	Ala	His	Tyr				
			35				40					45							
Ser	His	Ser	Lys	Asn	Arg	Gln	Leu	Arg	Gln	Ile	Ala	Asn	Leu	Met	Ala				
			50			55					60								
Tyr	Pro	Asn	His	Leu	Leu	Ile	Thr	Leu	Val	Phe	Phe	Asp	Ile	Gly	Ile				
65				70					75					80					
Asn	Ile	Gly	Val	Gln	Asn	Cys	Ile	Ala	Thr	Leu	Val	Gly	Asp	Ser	Ala				
				85				90					95						
Ser	Leu	Leu	Leu	Thr	Val	Gly	Val	Pro	Leu	Ala	Leu	Thr	Leu	Val	Leu				
			100				105						110						
Gly	Glu	Ile	Val	Pro	Lys	Val	Ile	Ala	Ile	Pro	Tyr	Asn	Ala	Arg	Ile				
			115				120					125							
Ala	Lys	Ile	Val	Thr	Pro	Ile	Ile	Phe	Ala	Ser	Thr	Lys	Ser	Ser	Ala				
			130			135					140								
Leu	Tyr	Leu	Ile	Gly	Leu	Ser	Arg	Val	Ser	Ile	Leu	Ser	Phe	Arg	Lys				
145				150					155					160					
Cys	Trp	Pro	Val	Lys	Lys	Val	Ile	Leu	Phe	Asn	Pro	Lys	Asn						
				165					170										

(2) INFORMATIONS POUR LA SEQ ID NO: 183:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 187426..187809

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 183:

```

Ile Met Glu Glu Lys Gly Ile Leu Gln Leu Val Glu Ile Ser Arg Ala
1      5      10      15
Met Ala Leu Gln Gly Val Cys Pro Trp Thr Asn Leu Gln Ser Val Glu
20      25      30
Ser Met Leu Gln Tyr Ile Ala Gly Glu Cys Gln Glu Leu Ala Asp Ala
35      40      45
Val Gln Glu Asn Lys Ala Ser Leu Glu Ile Ala Ser Glu Ala Gly Asp
50      55      60
Val Leu Thr Leu Val Leu Thr Leu Cys Phe Leu Leu Glu Arg Glu Gly
65      70      75      80
Lys Leu Lys Ala Glu Glu Val Phe Val Glu Ala Leu Ala Lys Leu Arg
85      90      95
Arg Arg Ser Pro His Val Phe Asp Pro His Asn Gln Ile Ser Leu Glu
100     105     110
Gln Ala Glu Glu Tyr Trp Ala Arg Ile Lys Gln Gln Glu Lys Ile Ser
115     120     125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 184:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 228 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(188798..189481)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 184:

```

Gly His Lys Ile Glu Ser Ile Phe Ser Leu Ser Cys Val Met Arg Lys
1      5      10      15
Phe Trp Leu Leu Ala Ser Phe Gly Leu Leu Ser Leu Thr Thr Thr Thr
20      25      30
Leu Ser Ser Cys Ala Val Ser Asn Ser Gly Ser Tyr Asn Ala Arg Leu
35      40      45
Tyr Thr Lys Gly Ser Lys Ala Lys Gly Val Val Ala Met Leu Pro Val
50      55      60
Phe Tyr Arg Thr Glu Lys Ser Ala Glu Leu Leu Pro Trp Asn Leu Gln
65      70      75      80
Ala Glu Phe Ser Glu Glu Ile Ser Arg Arg Leu His Ser Ser Asp Lys
85      90      95
Leu Leu Leu Ile Xaa Xaa His Ala Ser Ala Gly Val Ala Ala Gln Phe
100     105     110
Phe Ser Pro Thr Pro Asn Ile Ser Pro Glu Leu Ala Thr Gln Leu Leu
115     120     125
Pro Ala Glu Phe Val Val Ala Ala Glu Ile Leu Glu Gln Lys Thr Thr
130     135     140
Glu Asp Val Leu Asn Pro Ser Ile Ser Ala Ser Val Arg Val Arg Val
145     150     155     160
Phe Asp Ile Arg His Asn Lys Val Ser Met Ile Tyr Gln Glu Ile Leu
165     170     175
Asp Ala Ser Gln Ser Leu Ala Ser Gly Ser Asn Asp Tyr His Arg Tyr
180     185     190
Gly Trp Arg Ser Lys Asn Phe Asp Ser Thr Pro Met Gly Leu Met His
195     200     205
Gln Arg Leu Phe Arg Glu Ile Val Ala Arg Val Glu Gly Tyr Val Cys

```

220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 185:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 190235..190510

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 186:

Thr	Ser	Cys	Ser	Ala	Leu	Arg	Arg	Pro	Trp	Leu	Phe	Ser	Ala	Phe	Leu
1				5					10					15	
Tyr	Ser	Val	Gln	Ala	Leu	Ala	Ile	Val	Val	Leu	Tyr	Arg	Leu	Gly	Ser
			20					25					30		
Gly	Tyr	Ser	Ala	Ala	Gly	Ala	Leu	Ile	Gly	Val	Ala	Val	Ile	Arg	Phe
		35					40					45			
Cys	Ala	Glu	Phe	Phe	Lys	Thr	His	Gln	Gly	Ala	Trp	Leu	Gly	Glu	Glu
	50					55					60				
Asn	Ile	Leu	Thr	Ile	Gly	Gln	Trp	Leu	Ser	Ile	Pro	Met	Val	Phe	Leu
65					70					75					80
Gly	Val	Gly	Ile	Ile	Trp	Ile	Ala	Ser	Lys	Lys	Lys				
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 187:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 334 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 190785..191786

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 187:

Glu	Arg	Gly	Phe	Pro	Pro	His	Arg	Glu	Asn	Pro	Pro	Arg	Met	Arg	Met
1				5					10					15	
Asn	Lys	Arg	Thr	Leu	Leu	Phe	Val	Ser	Leu	Val	Ser	Ala	Ala	Phe	Leu
			20					25					30		
Gly	Cys	Gln	Ile	Phe	Phe	Gly	Tyr	Arg	Asp	Leu	Lys	Ser	Cys	Gln	Asp
		35					40					45			
Leu	Ala	Glu	Lys	Gln	Arg	Ala	Ile	Ser	Glu	Gln	Ile	Leu	Ala	Ser	Thr
	50					55					60				
Glu	Gln	Leu	Ser	Val	Val	Pro	Trp	Thr	Ala	Ser	Leu	Glu	Glu	Ser	Glu
65					70					75					80
Ser	Val	Asn	Gln	Tyr	Ala	Ile	Arg	Leu	Gly	Asn	Arg	Leu	Leu	Leu	Leu
			85						90				95		
Thr	Lys	Gly	Gly	Ser	His	Pro	Glu	Val	Tyr	Ser	Arg	Gly	Thr	Ser	Trp
			100					105					110		
Ser	Leu	Ile	Glu	Gln	Thr	Ser	Thr	Phe	Gly	Gly	Ile	Leu	Val	Ser	Leu
		115					120					125			
Tyr	Gly	Glu	Thr	Gly	Gln	Glu	Val	Leu	Ser	Lys	Gly	Ser	Ser	Val	Tyr
	130					135					140				
Leu	Pro	Asn	Gln	Arg	Asp	Ala	Phe	Pro	Val	Leu	Val	Ala	Glu	Phe	Arg
145					150					155					160
Ser	Asn	Gln	Glu	Pro	Leu	Val	Phe	Leu	Gly	Glu	Tyr	Lys	Asp	Gly	Lys
				165					170				175		
Ile	Ala	Asn	Lys	Ala	Gly	Ala	Ile	Tyr	Gly	Thr	Ser	Leu	Val	Phe	Leu
			180					185				190			
Asn	Thr	Gly	Asn	Glu	Phe	Val	Pro	Leu	Gly	Ile	Tyr	Asn	Ser	Lys	Glu
	195					200						205			
Glu	Cys	Val	Glu	Ser	Leu	Asp	Leu	Pro	Met	Ala	Arg	Ala	Val	Val	Phe

210	215	220
Ala Asp Lys Glu Asn Pro Thr Ala Ser Gly Ser Tyr Tyr Met Leu Ser		
225	230	235
Asn Glu Tyr Met Gln Ile Val Val Ser Gln Glu Ser Gly Ala Ile Glu		240
	245	250
Gly Ile Asn Leu Pro Phe Ala Ser Asp Gln Glu Glu Asn Lys Ser Ile		255
	260	265
Val Asn Glu Ile Gly Phe Asp Arg Glu Leu Ala Ile Asn Ser Pro Ser		270
	275	280
Glu Ala Ser Phe Pro Gly Val Glu Thr Ile Asp Ser Gln Arg Gln Asn		285
	290	295
Ile Ala Asn Val Val Gly Tyr Tyr Pro Leu Leu Arg Arg Gly Thr		300
305	310	315
Leu Ser Asp Val Lys Lys Arg Val Pro Ala Gln Tyr Gln Ala		320
	325	330

(2) INFORMATIONS POUR LA SEQ ID NO: 188:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 225 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 191790..192464

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 188:

Asn Ile Val Ser Gly Arg Glu Leu Ala Ser Pro Val Ala Thr Gly Phe	
1	5 10 15
Arg Val Val Ser Phe Asp Asn Lys Thr Leu Ile Leu Glu Ser Gly Asp	
	20 25 30
Gly Gly Ile Arg Lys Thr Tyr Ser Leu Gly Glu Gln Pro Tyr Ala Phe	
	35 40 45
Glu Leu Glu Ile Gln Thr Thr Gln Gly Arg Glu Asp Leu Trp Ile Thr	
	50 55 60
Ser Gly Val Pro Glu Val Glu Ile Met Ser Asn Ala Phe Val Pro Ala	
65	70 75 80
Val Lys Tyr His Ala Val Lys Lys Asn Lys Ser Asp Leu Phe Asn Val	
	85 90 95
Lys Leu Pro Lys Ala Lys Asp Ser Leu Leu Val Arg Asn Asn Ala Thr	
	100 105 110
Pro Gln Trp Ile Leu Asn Ser Asn Gly Tyr Phe Gly Val Ile Leu Thr	
	115 120 125
Pro Arg Thr Pro Ile Pro Ala Gly Tyr Ala Ser Ser Phe Ile Pro Gly	
	130 135 140
Asn Val Val Pro Thr Arg Leu Ser Gln Leu Pro Pro Lys Asp Gln Ala	
145	150 155 160
Tyr Pro Ala Ser Lys Tyr Pro Gly Tyr Thr Ala Met Leu Pro Leu Pro	
	165 170 175
Lys Glu Ala Gly Arg Tyr Gln Phe Met Val Tyr Ala Gly Pro Leu Ala	
	180 185 190
Asp Pro Thr Leu Lys Thr Leu Asp Arg Leu Thr Arg Ile Leu Lys Glu	
	195 200 205
Lys Leu Leu Ser Ile Leu Met Arg Leu Leu Ser Glu Gly Ser Leu Val	
210	215 220

Leu  
225

(2) INFORMATIONS POUR LA SEQ ID NO: 189:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 192392..193183

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 189:

Thr	Asn	Ala	Asn	Ser	Lys	Gly	Glu	Thr	Pro	Glu	Tyr	Ile	Asp	Ala	Ile
1			5					10					15		
Ala	Phe	Arg	Gly	Phe	Phe	Ser	Phe	Ile	Thr	Glu	Pro	Phe	Ala	Ala	Leu
		20						25				30			
Leu	Phe	Val	Ile	Met	Lys	Phe	Phe	Lys	Phe	Leu	Thr	Gly	Ser	Trp	Gly
		35					40					45			
Ile	Ser	Ile	Ile	Leu	Leu	Thr	Ile	Val	Leu	Lys	Leu	Leu	Leu	Tyr	Pro
	50					55				60					
Leu	Asn	Ala	Trp	Ser	Ile	Arg	Ser	Met	Arg	Arg	Met	Gln	Lys	Leu	Ser
65				70					75					80	
Pro	Tyr	Ile	Gln	Glu	Ile	Gln	Gln	Lys	Tyr	Lys	Arg	Glu	Pro	Lys	Arg
			85					90					95		
Ala	Gln	Met	Glu	Ile	Met	Ala	Leu	Tyr	Lys	Met	Asn	Lys	Val	Asn	Pro
		100						105				110			
Ile	Thr	Gly	Cys	Leu	Pro	Leu	Leu	Ile	Gln	Ile	Pro	Phe	Leu	Ile	Ala
		115					120					125			
Met	Phe	Asp	Leu	Leu	Lys	Ser	Ser	Phe	Leu	Leu	Arg	Gly	Ala	Ser	Phe
	130				135						140				
Ile	Pro	Gly	Trp	Ile	Asp	Asn	Leu	Thr	Ala	Pro	Asp	Val	Leu	Phe	Ser
145				150					155					160	
Trp	Glu	Thr	Pro	Ile	Trp	Phe	Ile	Gly	Lys	Glu	Phe	His	Leu	Leu	Pro
			165					170					175		
Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Ala	Gln	Gln	Lys	Ile	Ser	Ala	Val
		180						185				190			
Lys	Arg	Ser	Gly	Pro	Ala	Ser	Asp	Gln	Gln	Arg	Gln	Gln	Glu	Ala	Met
	195						200				205				
Gly	Thr	Met	Met	Ala	Leu	Leu	Phe	Thr	Phe	Met	Phe	Tyr	Asn	Phe	Pro
	210					215				220					
Ser	Gly	Leu	Asn	Ile	Tyr	Trp	Phe	Ser	Ser	Met	Leu	Leu	Gly	Val	Ile
225				230					235					240	
Gln	Gln	Trp	Val	Thr	Asn	Lys	Ile	Leu	Asp	Glu	Gln	His	Leu	Gln	His
			245					250					255		
Glu	Val	Ile	Ile	Asn	Lys	Lys	Arg								
			260												

(2) INFORMATIONS POUR LA SEQ ID NO: 190:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 459 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 190:

Asp 1	Ser	Phe	Met	Arg 5	Ala	Trp	Glu	Glu	Phe 10	Leu	Leu	Leu	Gln	Glu 15	Lys
Glu	Ile	Gly	Val 20	Asp	Thr	Val	Asn 25	Lys	Trp	Leu	Arg	Ser	Leu 30	Lys	Val
Leu	Cys	Phe 35	Asp	Ala	Cys	Asn 40	Leu	Tyr	Leu	Glu	Ala	Lys 45	Asp	Ser	Phe
Gln	Val 50	Thr	Trp	Phe	Glu	Glu 55	His	Ile	Arg	His 60	Lys	Val	Lys	Ala	Ser
Leu 65	Ile	Asn	Asn	Asn 70	Gly	Lys	Pro	Ile	Arg 75	Val	Arg	Val	Thr	Ser	Leu 80
Asp	Lys	Ser	Thr 85	Pro	Phe	Lys	Asp	Thr	Gln 90	Ile	Gln	Gln	Glu 95	Lys	Thr
Ala	Tyr	Phe 100	Thr	Met	Lys	Tyr	Gly	Asp 105	Ile	Asp	Pro	Asn	Met 110	Ser	Phe
Ala	Asn 115	Phe	Leu	Val	Thr	Pro	Glu 120	Asn	Asp	Leu	Pro	Val 125	Arg	Ile	Leu
Gln	Glu 130	Phe	Ala	Lys	Val	Ser 135	Glu	Gln	Gly	Lys	Gly 140	Phe	Pro	Phe	Asn
Pro 145	Ile	Tyr	Leu	Phe 150	Gly	Pro	Glu	Ser	Ser 155	Gly	Lys	Thr	His	Leu	Met 160
Gln	Ala	Ala	Val 165	Gly	Gly	Leu	Arg	Glu	Ala 170	Gly	Val	Lys	Thr 175	Leu	Tyr
Val	Thr 180	Ser	Glu	Leu	Phe	Thr	Glu 185	His	Leu	Val	Ser	Ala 190	Ile	Arg	Ser
Gly	Glu 195	Met	Gln	Arg	Phe	Arg 200	Ala	Phe	Tyr	Arg	Asn 205	Val	Glu	Ala	Leu
Phe	Ile 210	Glu	Asp	Ile	Glu 215	Val	Leu	Ser	Gly	Lys	Gly 220	Ala	Thr	Gln	Glu
Glu 225	Phe	Phe	His	Thr 230	Phe	Xaa	Ser	Leu	His 235	Thr	Glu	Gly	Lys	Leu	Ile 240
Val	Ile	Ser	Ser 245	Thr	Phe	Ala	Pro	Gly	Asp 250	Leu	Lys	Ala	Met 255	Glu	Glu
Arg	Leu 260	Ile	Ser	Arg	Phe	Glu	Trp 265	Gly	Ile	Ser	Ile 270	Pro	Val	Ser	Pro
Leu	Thr 275	Arg	Glu	Gly	Leu	Lys	Ser 280	Phe	Leu	Glu	Arg 285	Arg	Ile	Glu	Lys
Leu 290	Asn	Ile	Arg	Ile	Glu 295	Glu	Thr	Ala	Leu	Asp 300	Phe	Leu	Ile	Gln	Ala
Leu 305	Ser	Ser	His 310	Val	Lys	Ser	Leu	Leu	His 315	Ala	Leu	Thr	Thr	Leu	Ala 320
Lys	Arg	Val 325	Ala	Tyr	Lys	Lys	Leu	Ser	His 330	Gln	Met	Leu	Tyr 335	Gln	Gly
Asp	Ile 340	Glu	Ala	Leu	Leu	His	Asp 345	Val	Leu	Gln	Ala	Ala 350	Glu	Ser	Ile
Arg	Leu 355	Thr	Pro	Ser	Gly	Ile 360	Val	Arg	Ala	Thr 365	Ala	Gln	Tyr	Tyr	Gly
Val	Ser 370	Pro	Glu	Ser	Val 375	Leu	Gly	Arg	Ser	Gln 380	Ser	Arg	Glu	Tyr	Val
Leu 385	Pro	Arg	Gln	Val 390	Ala	Met	Phe	Leu	Cys 395	Arg	Gln	Lys	Leu	Ser	Leu 400

Ser Tyr Val Lys Ile Gly Glu Val Phe Ser Arg Asp His Ser Thr Val  
                             405                            410                            415  
 Ile Ser Ser Ile Arg Ala Ile Ser Gln Lys Leu Glu Glu Asp Asp Arg  
                             420                            425                            430  
 Glu Cys Asp Val Ser Cys Ala Ile Gln Glu Leu Thr Lys Arg Leu Ser  
                             435                            440                            445  
 Ser Ala Tyr Gln Ser Leu Asp Phe Ile Glu Asp  
                             450                            455

(2) INFORMATIONS POUR LA SEQ ID NO: 191:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(194690..195046)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 191:

Gly Gly Phe Met Gly Ile Lys Pro His Asp Tyr Gly Cys Trp Gly Ser  
 1                            5                            10                            15  
 Arg Gly Asn Val Phe Thr Leu Gln Asp Leu Asn Thr Gln Gln Ala Asn  
                             20                            25                            30  
 Gln Ser Ala Ala Ala Ser Ser Ser Ser Val Leu Lys Ser Glu Cys Ala  
                             35                            40                            45  
 Ala Lys Val Ala Arg Tyr Ala Leu Gly Phe Leu Phe Gly Leu Gly Phe  
                             50                            55                            60  
 Ile Leu Ser Ile Val Thr Phe Ile Ala Ala Ala Thr Leu Pro Leu  
 65                            70                            75                            80  
 Gly Thr Thr Thr Ile Leu Ile Met Val Thr Gln Ile Ala Phe Ala Ala  
                             85                            90                            95  
 Ala Leu Ala Phe Lys Leu Tyr Asp Leu Phe Lys His Asp Val Pro Thr  
                             100                            105                            110  
 Cys Ser Ile Thr Ser Lys Ala  
                             115

(2) INFORMATIONS POUR LA SEQ ID NO: 192:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 616 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 195184..197031

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 192:

Glu Ala Ser Met Tyr Phe Asp Arg Thr Lys Ile Asn Val Glu Ser Met  
 1                            5                            10                            15  
 Lys Gln Ala Ile Leu Glu Arg Val Tyr Cys Gly Val Val Gln Thr Pro



			20					25					30				
Gln	Ser	Ala	Ser	Thr	Arg	Asp	Ile	Phe	Ile	Ala	Val	Ala	Lys	Thr	Val		
		35					40					45					
Leu	Glu	Trp	Met	Ala	Lys	Gly	Trp	Leu	Lys	Thr	Gln	Ser	Ser	Tyr	Tyr		
	50					55					60						
Asp	Asn	Asp	Val	Lys	Arg	Val	Tyr	Tyr	Ile	Ser	Met	Glu	Phe	Leu	Leu		
65				70					75					80			
Gly	Arg	Ser	Leu	Lys	Ser	Asn	Leu	Leu	Asn	Leu	Gly	Leu	Leu	Asp	Leu		
				85				90						95			
Val	Lys	Glu	Ala	Leu	Phe	Asp	Leu	Gly	Tyr	Asp	Phe	Asp	Gln	Leu	Val		
		100					105						110				
Glu	Met	Glu	His	Asp	Ala	Gly	Leu	Gly	Asn	Gly	Gly	Leu	Gly	Arg	Leu		
	115					120					125						
Ala	Ala	Cys	Phe	Leu	Asp	Ser	Met	Ala	Thr	Leu	Glu	Ile	Pro	Ala	Tyr		
	130					135				140							
Gly	Tyr	Gly	Leu	Arg	Tyr	Asp	Tyr	Gly	Ile	Phe	Asp	Gln	Lys	Ile	Glu		
145				150					155					160			
Asn	Gly	Phe	Gln	Val	Glu	Ser	Pro	Ile	Glu	Trp	Leu	Arg	Tyr	Gly	Asn		
			165					170						175			
Pro	Trp	Glu	Ile	Cys	Arg	Gly	Glu	Tyr	Leu	Tyr	Pro	Val	His	Phe	Tyr		
		180					185						190				
Gly	Lys	Val	Lys	His	Ser	Ile	Asp	Ser	Arg	Gly	Arg	Asp	Val	Ala	Glu		
	195					200					205						
Leu	Val	Asp	Ser	Gln	Glu	Val	Leu	Ala	Met	Ala	Tyr	Asp	Val	Pro	Val		
	210				215					220							
Pro	Gly	Phe	Asn	Asn	Asp	Thr	Val	Asn	Ser	Leu	Arg	Leu	Trp	Gln	Ala		
225				230					235					240			
Gln	Ser	Arg	His	Gly	Phe	Glu	Phe	Ser	Tyr	Phe	Asn	His	Gly	Asn	Tyr		
			245					250						255			
Ile	Arg	Ala	Ile	Glu	Asp	Ile	Ala	Leu	Ala	Gly	Asn	Ile	Thr	Arg	Val		
		260					265						270				
Leu	Tyr	Pro	Asn	Asp	Ser	Ile	Ser	Glu	Gly	Gln	Glu	Leu	Arg	Leu	Lys		
	275					280					285						
Gln	Glu	Tyr	Phe	Leu	Val	Ser	Ala	Thr	Ile	Gln	Asp	Ile	Leu	Arg	Arg		
	290				295						300						
Tyr	Thr	Lys	Thr	His	Leu	Ser	Leu	Asp	Lys	Leu	Ser	Glu	Lys	Val	Ser		
305				310					315					320			
Val	Gln	Leu	Asn	Asp	Thr	His	Pro	Ala	Leu	Gly	Ile	Ala	Glu	Met	Met		
			325					330						335			
Arg	Leu	Leu	Val	Asp	Arg	Glu	Glu	Leu	Asp	Trp	Asp	Val	Ala	Trp	Asp		
		340					345						350				
Ala	Thr	Thr	Lys	Ile	Phe	Asn	Tyr	Thr	Asn	His	Thr	Ile	Leu	Pro	Glu		
	355					360					365						
Ala	Leu	Glu	Arg	Trp	Ser	Leu	Asp	Leu	Phe	Ser	Lys	Val	Leu	Pro	Arg		
	370				375												

Tyr	Leu	Thr	Asn	Leu	Thr	His	Leu	His	Lys	Val	Ile	Pro	Leu	Ala	Glu
			500					505					510		
Asp	Ser	Gly	Phe	Arg	Glu	Glu	Trp	Arg	Asn	Ile	Lys	Ile	Gln	Asn	Lys
		515					520					525			
Glu	Glu	Leu	Ala	Ala	Arg	Ile	Tyr	Lys	Glu	Leu	Gly	Val	Thr	Val	Asn
	530					535					540				
Pro	Gln	Ser	Ile	Phe	Asp	Cys	His	Ile	Lys	Arg	Ile	His	Glu	Tyr	Lys
545					550					555					560
Arg	Gln	Leu	Thr	Asn	Ile	Leu	Arg	Val	Ile	Tyr	Phe	Tyr	Asn	Glu	Ile
				565						570				575	
Arg	Asn	Gly	Ser	Gly	Glu	Ile	Val	Pro	Thr	Thr	Val	Ile	Phe	Gly	Gly
			580					585					590		
Lys	Ala	Ala	Pro	Gly	Tyr	Ala	Met	Ala	Lys	Leu	Ile	Ile	Lys	Leu	Ile
		595					600					605			
Asn	Asn	Val	Ala	Ala	Val	Val	Lys								
	610					615									

(2) INFORMATIONS POUR LA SEQ ID NO: 193:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 197018..197635

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 193:

Gln	Leu	Leu	Leu	Asn	Asn	Asp	Pro	Lys	Val	Asn	Asp	Gln	Leu	Lys	Val
1				5					10					15	
Ile	Phe	Trp	Pro	Asn	Tyr	Arg	Val	Ser	Leu	Ala	Glu	Ala	Ile	Ile	Pro
			20					25					30		
Ala	Thr	Asp	Leu	Ser	Glu	Gln	Ile	Ser	Thr	Ala	Gly	Met	Glu	Ala	Ser
		35				40					45				
Gly	Thr	Gly	Asn	Met	Lys	Phe	Ala	Leu	Asn	Gly	Ala	Leu	Thr	Ile	Gly
	50				55					60					
Thr	Met	Asp	Gly	Ala	Asn	Ile	Glu	Met	Ala	Glu	His	Ile	Gly	Lys	Glu
65				70						75				80	
His	Met	Phe	Ile	Phe	Gly	Leu	Leu	Glu	Glu	Glu	Ile	Ser	Glu	Leu	Arg
			85					90					95		
Lys	Glu	Tyr	Tyr	Pro	Gln	Gly	Ile	Cys	Asn	Ala	Asn	Pro	Thr	Ile	Gln
			100					105					110		
Glu	Ile	Leu	Asp	Met	Ile	Ala	Gln	Ala	Lys	Phe	Ser	Gln	Glu	Asp	Lys
		115					120					125			
Asp	Leu	Phe	Lys	Pro	Ile	Val	Asn	Arg	Leu	Leu	Asn	Glu	Gly	Asp	Pro
	130					135					140				
Phe	Phe	Val	Leu	Ala	Asp	Leu	Glu	Ala	Tyr	Ile	Asn	Thr	Gln	Asn	Arg
145					150					155					160
Val	Ala	Ser	Leu	Phe	Lys	Gln	Pro	Glu	Glu	Trp	Thr	Lys	Lys	Ser	Ile
			165					170						175	
Tyr	Asn	Val	Gly	Gly	Ile	Gly	Phe	Phe	Ser	Ser	Asp	Arg	Ser	Ile	Ala
		180					185						190		
Glu	Tyr	Ala	Ser	Asn	Ile	Trp	Xaa	Val	Ser	Arg	Pro	Thr	Ser		
		195					200						205		

(2) INFORMATIONS POUR LA SEQ ID NO: 194:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 149 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 197762...198208

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 194:

Asp	Asn	Val	Asn	Ile	Gln	Val	Glu	Pro	Thr	Ala	Ser	Ser	Pro	Phe	Lys
1				5					10					15	
Thr	Thr	Gly	Cys	Ser	Ser	Thr	Leu	Pro	Thr	Ala	Arg	Ile	Ala	Ala	Cys
			20					25					30		
Gly	Gly	Phe	Lys	Ile	Ala	Val	Lys	Ser	Glu	Ile	Pro	Val	Ile	Pro	Arg
		35					40					45			
Leu	Asp	Thr	Gln	Lys	Glu	Pro	Pro	Leu	Tyr	Ser	Ser	Ser	Ala	Arg	Asp
	50					55					60				
Cys	Cys	Leu	Ala	Leu	Val	Ala	Ser	Pro	Leu	Ile	Ser	Ala	Glu	Ile	Ile
65					70					75				80	
Pro	Ile	Phe	Phe	Leu	Ser	Ala	Gln	Arg	Thr	Ile	Gly	Val	Ile	Thr	Pro
				85					90					95	
Ser	Gly	Ile	Ala	Thr	Ala	Ile	Glu	Ile	Ser	Ile	Val	Glu	Asn	Arg	Ile
			100					105					110		
Ile	Leu	Leu	Ser	Thr	Leu	Leu	Asn	Pro	Glu	Leu	Ile	Ser	Gly	Asn	Ser
		115					120					125			
Phe	Arg	Ala	Lys	Ala	Gln	Ala	Arg	Thr	Ile	Gln	Ser	Leu	Ile	Glu	Ser
	130					135					140				
Leu	Ile	Phe	Cys	Ser											
145															

(2) INFORMATIONS POUR LA SEQ ID NO: 195:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 432 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(197668...198963)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 195:

Gly	Asn	Val	Val	Val	Ser	Leu	Leu	Lys	Met	Pro	Lys	Leu	Ser	Pro	Thr
1				5					10					15	
Met	Glu	Ile	Gly	Ile	Leu	Val	Lys	Trp	His	Lys	Lys	Ala	Gly	Asp	Glu
			20					25					30		
Ile	His	Phe	Gly	Asp	Val	Leu	Leu	Glu	Ile	Ser	Thr	Asp	Lys	Ala	Val
		35					40					45			
Leu	Glu	His	Thr	Ala	Ser	Glu	Asp	Gly	Trp	Leu	Leu	Glu	Ile	Leu	Val
	50					55					60				

Lys	Glu	Gly	Thr	Lys	Thr	Pro	Ile	Gly	Thr	Pro	Ile	Ala	Val	Phe	Ser	65	70	75	80
Thr	Glu	Gln	Asn	Ala	Gln	Tyr	Asp	Leu	Lys	Gln	Leu	Leu	Pro	Leu	Glu	85	90	95	
Glu	Thr	Val	Val	Thr	Asp	Ala	Ala	Thr	Glu	Ala	Ser	Pro	Lys	Asp	Ser	100	105	110	
Ala	Gln	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Gly	Pro	Ser	Ile	Thr	Met	Met	115	120	125	
Gly	Phe	Arg	Pro	Glu	Pro	Pro	Leu	Ala	Thr	Pro	Leu	Thr	Ile	Lys	His	130	135	140	
Ser	Asn	Asp	Pro	Val	Leu	Ala	Ser	Pro	Leu	Ala	Lys	Lys	Leu	Ala	Lys	145	150	155	160
Glu	Gln	Asn	Leu	Asp	Leu	Ser	Gly	Val	Thr	Gly	Ser	Gly	Pro	Gly	Gly	165	170	175	
Arg	Ile	Ile	Lys	Lys	Asp	Leu	Glu	Lys	Ala	Pro	Pro	Leu	Arg	Ile	Ala	180	185	190	
Gly	Phe	Gly	Tyr	Pro	Glu	Ala	Pro	Asn	Val	Asn	Pro	Gly	Ser	Tyr	Ile	195	200	205	
Glu	Glu	Pro	Leu	Ser	Pro	Val	Arg	Glu	Val	Ile	Ser	Lys	Arg	Leu	Gln	210	215	220	
Ala	Ala	Lys	Thr	Phe	Ile	Pro	His	Phe	Tyr	Val	Arg	Gln	Arg	Ile	Tyr	225	230	235	240
Ala	Ser	Pro	Leu	Leu	Ala	Leu	Leu	Lys	Glu	Leu	Gln	Glu	Gln	Asn	Ile	245	250	255	
Lys	Leu	Ser	Ile	Asn	Asp	Cys	Ile	Val	Arg	Ala	Cys	Ala	Leu	Ala	Leu	260	265	270	
Lys	Glu	Phe	Pro	Glu	Ile	Asn	Ser	Gly	Phe	Asn	Ser	Val	Asp	Asn	Lys	275	280	285	
Ile	Ile	Arg	Phe	Ser	Thr	Ile	Asp	Ile	Ser	Ile	Ala	Val	Ala	Ile	Pro	290	295	300	
Asp	Gly	Val	Ile	Thr	Pro	Ile	Val	Arg	Cys	Ala	Asp	Arg	Lys	Asn	Ile	305	310	315	320
Gly	Met	Ile	Ser	Ala	Glu	Ile	Lys	Gly	Leu	Ala	Thr	Lys	Ala	Lys	Gln	325	330	335	
Gln	Ser	Leu	Ala	Glu	Glu	Glu	Tyr	Lys	Gly	Gly	Ser	Phe	Cys	Val	Ser	340	345	350	
Asn	Leu	Gly	Met	Thr	Gly	Ile	Ser	Asp	Phe	Thr	Ala	Ile	Leu	Asn	Pro	355	360	365	
Pro	Gln	Ala	Ala	Ile	Leu	Ala	Val	Gly	Ser	Val	Glu	Glu	Gln	Pro	Val	370	375	380	
Val	Leu	Asn	Gly	Glu	Leu	Ala	Val	Gly	Ser	Thr	Cys	Met	Leu	Thr	Leu	385	390	395	400
Ser	Val	Asp	His	Arg	Val	Ile	Asp	Gly	Tyr	Pro	Ala	Ala	Met	Phe	Met	405	410	415	
Lys	Arg	Leu	Gln	Arg	Leu	Leu	Glu	Ala	Pro	Ser	Val	Leu	Leu	Leu	Asn	420	425	430	

(2) INFORMATIONS POUR LA SEQ ID NO: 196:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 332 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(198962..199957)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 196:

Lys	Arg	Gly	Ser	Met	Pro	Asn	Phe	Val	Thr	Leu	Glu	Ile	Arg	Glu	Ala	1	5	10	15
Ile	Arg	Gln	Ala	Ile	Asp	Glu	Glu	Met	Thr	Arg	Asp	Pro	Asn	Val	Cys	20	25	30	
Ile	Leu	Gly	Glu	Glu	Val	Ala	Glu	Tyr	Asn	Gly	Ala	Tyr	Lys	Val	Thr	35	40	45	
Lys	Asn	Leu	Leu	Asp	Lys	Trp	Gly	Pro	Thr	Arg	Val	Ile	Asp	Thr	Pro	50	55	60	
Ile	Ser	Glu	Ala	Ala	Phe	Ser	Gly	Ile	Gly	Ile	Gly	Ala	Ala	Leu	Thr	65	70	75	80
Gly	Leu	Arg	Pro	Ile	Ile	Glu	Phe	Met	Ser	Trp	Asn	Phe	Ser	Leu	Val	85	90	95	
Ala	Ala	Asp	Gln	Ile	Ile	Ser	His	Ala	Ala	Lys	Met	Tyr	Tyr	Met	Thr	100	105	110	
Gly	Gly	Lys	Phe	Ala	Val	Pro	Ile	Val	Phe	Arg	Gly	Ala	Asn	Gly	Ala	115	120	125	
Ala	Ala	Gln	Val	Ser	Cys	Gln	His	Ser	His	Cys	Val	Glu	Ala	Leu	Tyr	130	135	140	
Ala	Asn	Ile	Pro	Gly	Leu	Ile	Val	Ile	Ala	Pro	Ser	Thr	Pro	Ala	Asp	145	150	155	160
Ala	Lys	Gly	Leu	Leu	Lys	Ser	Ala	Ile	Arg	Asp	Asn	Asn	Pro	Val	Leu	165	170	175	
Phe	Leu	Glu	Asn	Glu	Leu	Asp	Tyr	Asn	Leu	Lys	Gly	Glu	Val	Pro	Ser	180	185	190	
Glu	Glu	Tyr	Leu	Ile	Pro	Ile	Gly	Lys	Ala	Arg	Ile	Val	Gln	Glu	Gly	195	200	205	
Lys	Asp	Leu	Thr	Ile	Ile	Ser	His	Ser	Arg	Met	Val	Ser	Ile	Val	Glu	210	215	220	
Gln	Ala	Ala	Lys	Thr	Ala	Lys	Gln	Arg	Trp	Gly	Leu	Ser	Ile	Glu	Thr	225	230	235	240
Ile	Asp	Leu	Arg	Thr	Ile	Lys	Pro	Leu	Asp	Val	Ala	Thr	Leu	Leu	Thr	245	250	255	
Ser	Val	Lys	Lys	Thr	Gly	Asn	Cys	Leu	Val	Val	Glu	Glu	Gly	His	Tyr	260	265	270	
Phe	Cys	Gly	Ile	Ser	Ala	Glu	Val	Ile	Thr	Thr	Ile	Thr	Glu	His	Ile	275	280	285	
Phe	Asp	Tyr	Leu	Asp	His	Pro	Pro	Leu	Arg	Val	Cys	Gln	Lys	Glu	Thr	290	295	300	
Pro	Met	Pro	Tyr	Asn	Lys	Thr	Leu	Glu	Met	Ala	Thr	Leu	Pro	Asn	Ile	305	310	315	320
Asn	Arg	Ile	Leu	Asp	Ala	Ile	Glu	Lys	Ile	Met	Arg					325	330		

## (2) INFORMATIONS POUR LA SEQ ID NO: 197:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(199941..200327)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 197:

Gln	Asn	Pro	Lys	Arg	Phe	Leu	Met	Val	Phe	Leu	Ser	Ile	Thr	Leu	Asn
1				5					10					15	
Gly	Phe	Asp	Leu	Phe	Asn	Ser	Leu	Ile	Gly	Phe	Arg	Glu	Ala	Tyr	His
			20					25					30		
His	Met	Gln	Gln	Thr	Gly	Ser	Pro	Ile	Ile	Val	Glu	Ala	Leu	Cys	Ser
		35					40					45			
Arg	Phe	Arg	Gly	His	Ser	Ile	Ser	Asp	Pro	Asn	Leu	Tyr	Arg	Ser	Lys
	50					55					60				
Glu	Glu	Met	Gln	Cys	Leu	Leu	Lys	Arg	Asp	Pro	Ile	Leu	Phe	Ala	Lys
65					70					75					80
Glu	Trp	Leu	Ile	Arg	Ala	Asn	Val	Leu	Ser	Glu	Asp	Asp	Phe	Lys	Asp
				85					90					95	
Leu	Arg	Gln	Thr	Ser	Lys	Thr	Ala	Val	Leu	Glu	Ala	Val	Ala	Gln	Ala
			100					105					110		
Arg	Leu	Asp	Pro	Glu	Pro	Ala	Val	Ala	Thr	Leu	Glu	Glu	Gly	Val	Tyr
		115					120					125			
Ala															

## (2) INFORMATIONS POUR LA SEQ ID NO: 198:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(200266..200685)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 198:

Leu	Cys	Cys	Trp	Asn	Ile	Pro	Leu	Arg	Gln	Leu	Ala	Ala	Glu	Leu	Leu
1				5					10					15	
Gly	Lys	Glu	Thr	Gly	Cys	Ala	Leu	Gly	Arg	Gly	Gly	Ser	Met	His	Met
			20					25					30		
Cys	Gly	Asp	Arg	Leu	Pro	Gly	Gly	Phe	Gly	Ile	Val	Gly	Gly	Gln	Ile
		35					40					45			
Pro	Leu	Ala	Ala	Gly	Ala	Ala	Phe	Ser	Met	Lys	Tyr	Gln	Asn	Ser	Ser
	50					55					60				
Ser	Ile	Ser	Met	Cys	Phe	Ile	Gly	Asp	Gly	Ala	Val	Ala	Gln	Gly	Val
65				70						75					80
Phe	His	Glu	Thr	Leu	Asn	Phe	Val	Ala	Leu	His	Ser	Leu	Pro	Leu	Met
				85					90					95	
Leu	Ile	Ile	Glu	Asn	Asn	Gly	Trp	Ser	Met	Gly	Thr	Ala	Leu	His	Arg
			100					105					110		
Ala	Ile	Ala	Lys	Gln	Pro	Ile	Ala	Glu	Ser	Gln	Ala	Ile	Ser	Tyr	Gly
		115					120					125			
Leu	Ser	Phe	Asp	His	Phe	Glu	Trp	Ile	Arg	Phe	Ile				
	130						135				140				

## (2) INFORMATIONS POUR LA SEQ ID NO: 199:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 104 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(200585..200896)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 199:

Glu	Asn	Phe	Gly	Asn	Ala	Phe	Cys	Ile	Asp	Leu	Leu	Lys	Lys	Met	Leu
1			5						10					15	
Leu	Ile	Arg	Glu	Phe	Glu	Ile	Arg	Gly	Glu	Glu	Ala	Tyr	Leu	Glu	Gly
		20						25					30		
Leu	Val	Gly	Gly	Phe	Tyr	His	Ser	Tyr	Ile	Gly	Gln	Glu	Ala	Val	Ala
		35						40				45			
Thr	Ala	Ala	Ile	Ala	Cys	Thr	Gly	Lys	Asp	His	Trp	Phe	Phe	Ser	Ser
	50					55					60				
Tyr	Arg	Cys	His	Gly	Val	Ala	Leu	Leu	Leu	Glu	Tyr	Pro	Phe	Thr	Thr
65					70					75					80
Thr	Gly	Ser	Arg	Thr	Ser	Arg	Glu	Arg	Asn	Arg	Val	Cys	Phe	Arg	Thr
			85					90						95	
Arg	Arg	Ile	Tyr	Ala	Tyr	Val	Trp								
						100									

(2) INFORMATIONS POUR LA SEQ ID NO: 200:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 403 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 201169..202377

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 200:

Ser	Trp	Phe	Glu	Val	Leu	Lys	Phe	His	Phe	Pro	Cys	Ser	Glu	Gly	Leu
1				5					10					15	
Ile	Arg	Gly	Phe	Ser	Ile	Glu	Phe	Leu	Cys	Cys	Ile	Leu	Thr	Asp	Lys
		20						25					30		
Lys	Ile	Gln	Tyr	Pro	Leu	Lys	Asn	Phe	Ile	Cys	Val	Glu	Phe	Ile	Val
		35					40					45			
Asn	Ser	Phe	Phe	Gly	Ile	Leu	Pro	Arg	Gly	Ile	Pro	Asn	Val	Gly	Gly
	50					55					60				
Leu	Ser	Glu	Val	Ala	Gly	Glu	Asn	Lys	Gln	Ser	Leu	Glu	Glu	Arg	Glu
65					70					75					80
Gln	Asp	Lys	Glu	Leu	Lys	Leu	Glu	Lys	Lys	Leu	Leu	Ala	Ile	Arg	Lys
			85					90						95	
Arg	Ile	Lys	Cys	Phe	Cys	Pro	Gln	Gln	Pro	Glu	Ile	Ser	Val	Gln	Ala
			100					105					110		
Ala	Pro	Leu	Lys	His	Thr	Gly	Thr	Phe	Pro	Cys	Ser	Glu	Glu	Glu	Leu
		115				120						125			
Arg	Asp	Ile	Ser	Asp	Leu	Phe	Ser	Ser	Leu	Lys	Ser	Phe	Arg	Gln	Gln
	130					135					140				

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Leu Ala Gln Leu Phe Phe Tyr Thr Pro Pro Leu Asn Leu Glu Trp Glu
145          150          155          160
Asp Phe Leu Lys Phe Phe Phe Ala Phe Glu Lys Arg Glu Leu Gly Gly
          165          170          175
Ile Leu Phe Ser Ala Gly Pro Phe Glu Ser Phe Asp Arg Tyr Leu Tyr
          180          185          190
Gln Val Asn Lys Ala Arg Pro Val Pro Val Leu Ile Ala Thr Thr Val
          195          200          205
Ser Tyr Ala Leu Gln Ala Tyr Cys Ser Tyr Ile Asn Arg Ala Pro Phe
          210          215          220
Gln Glu Lys Glu Asn Phe Phe Gln Leu Gly Glu Ala Val Gly Ile Phe
225          230          235          240
Leu Lys Glu Arg Lys Val Ser Ile Ala Leu Met Tyr Lys Glu Ile Leu
          245          250          255
Asp Leu Asp Asn Lys Gln Tyr Ser Glu Leu Cys Arg Gly Leu Gln Lys
          260          265          270
Ser Gln Ile Val Gln Gly Glu Val Phe His Ser Ser Thr Gln Glu Arg
          275          280          285
Asp Gly Leu Asn Pro Ile Ser Val Asn Tyr Asp Leu Met Gly Thr Ile
          290          295          300
Ala Ala Leu Ser Val Asn Ile Asp Arg Ser Cys Leu Arg Phe Ser Gly
305          310          315          320
Ser His Ile Phe His Asp Asp Glu Met Ala Ile Glu Thr Leu His Lys
          325          330          335
Gly Gly Asp Val Phe Thr Phe Ser Ser Leu Ala Glu Phe Gln Phe Ser
          340          345          350
Glu Lys Arg Leu Leu His Leu Val Ser Thr Gly Arg Val Cys Pro Glu
          355          360          365
Ile Ile Arg Lys Lys Leu Ile Lys Val Leu Leu Leu Lys Lys Arg Ala
          370          375          380
Leu Cys Lys Pro Phe Cys Arg His Ile Gln Ile Thr Ser Glu Thr Ala
385          390          395          400
Gln Leu Asn

```

(2) INFORMATIONS POUR LA SEQ ID NO: 201:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 354 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui\_

(viii) POSITION DANS LE GENOME: complement(202380..203441)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 201:

```

Met Ser Gln Ser Thr Tyr Ser Leu Glu Gln Leu Ala Asp Phe Leu Lys
1          5          10          15
Val Glu Phe Gln Gly Asn Gly Ala Thr Leu Leu Ser Gly Val Glu Glu
          20          25          30
Ile Glu Glu Ala Lys Thr Ala His Ile Thr Phe Leu Asp Asn Glu Lys
          35          40          45
Tyr Ala Lys His Leu Lys Ser Ser Glu Ala Gly Ala Ile Ile Ile Ser
          50          55          60
Arg Thr Gln Phe Gln Lys Tyr Arg Asp Leu Asn Lys Asn Phe Leu Ile

```



65					70					75				80
Thr	Ser	Glu	Ser	Pro	Ser	Leu	Val	Phe	Gln	Lys	Cys	Leu	Glu	Leu
				85					90				95	
Ile	Thr	Pro	Val	Asp	Ser	Gly	Phe	Pro	Gly	Ile	His	Pro	Thr	Ala
			100					105					110	
Ile	His	Pro	Thr	Ala	Ile	Ile	Glu	Asp	His	Val	Cys	Ile	Glu	Pro
		115					120					125		
Ala	Val	Val	Cys	Gln	His	Ala	His	Val	Gly	Ser	Ala	Cys	His	Ile
		130				135					140			
Ser	Gly	Ser	Val	Ile	Gly	Ala	Tyr	Ser	Thr	Val	Gly	Gln	His	Ser
145					150					155				160
Ile	His	Pro	Arg	Val	Val	Ile	Arg	Glu	Arg	Val	Ser	Ile	Gly	Lys
			165					170					175	
Val	Ile	Ile	Gln	Pro	Gly	Ala	Val	Ile	Gly	Ser	Cys	Gly	Phe	Gly
		180						185					190	
Val	Thr	Ser	Ala	Phe	Gly	Gln	His	Lys	His	Leu	Lys	His	Leu	Gly
		195				200						205		
Val	Ile	Ile	Glu	Asp	Asp	Val	Glu	Ile	Gly	Ala	Asn	Thr	Thr	Ile
	210					215					220			
Arg	Gly	Arg	Phe	Lys	His	Ser	Val	Val	Arg	Glu	Gly	Ser	Lys	Ile
225					230					235				240
Asn	Leu	Val	Gln	Ile	Ala	His	Gln	Val	Glu	Val	Gly	Gln	His	Ser
			245						250				255	
Ile	Val	Ala	Gln	Ala	Gly	Ile	Ala	Gly	Ser	Thr	Lys	Ile	Gly	Asn
		260					265						270	
Val	Ile	Ile	Gly	Gly	Gln	Ala	Gly	Ile	Thr	Gly	His	Ile	Cys	Ile
		275					280					285		
Asp	His	Val	Ile	Met	Met	Ala	Gln	Thr	Gly	Val	Thr	Lys	Ser	Ile
	290					295					300			
Ser	Pro	Gly	Ile	Tyr	Gly	Gly	Ala	Pro	Ala	Arg	Pro	Tyr	Gln	Glu
305					310					315				320
His	Arg	Gln	Val	Ala	Lys	Val	Arg	Asn	Leu	Pro	Arg	Leu	Glu	Glu
			325					330					335	
Ile	Ala	Ala	Leu	Glu	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala	Leu	Ser
			340					345				350		
Gln	His													

(2) INFORMATIONS POUR LA SEQ ID NO: 202:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé -

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(203471..203998)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 202:

Glu	Arg	Ile	Met	Lys	Lys	Phe	Leu	Leu	Leu	Ser	Leu	Met	Ser	Leu	Ser
1			5					10				15			
Ser	Leu	Pro	Thr	Phe	Ala	Ala	Asn	Ser	Thr	Gly	Thr	Ile	Gly	Ile	Val
		20					25					30			
Asn	Leu	Arg	Arg	Cys	Leu	Glu	Glu	Ser	Ala	Leu	Gly	Lys	Lys	Glu	Ser
		35					40					45			

Ala	Glu	Phe	Glu	Lys	Met	Lys	Asn	Gln	Phe	Ser	Asn	Ser	Met	Gly	Lys
50						55					60				
Met	Glu	Glu	Glu	Leu	Ser	Ser	Ile	Tyr	Ser	Lys	Leu	Gln	Asp	Asp	Asp
65					70					75					80
Tyr	Met	Glu	Gly	Leu	Ser	Glu	Thr	Ala	Ala	Ala	Glu	Leu	Arg	Lys	Lys
				85					90					95	
Phe	Glu	Asp	Leu	Ser	Ala	Glu	Tyr	Asn	Thr	Ala	Gln	Gly	Gln	Tyr	Tyr
			100					105					110		
Gln	Ile	Leu	Asn	Gln	Ser	Asn	Leu	Lys	Arg	Met	Gln	Lys	Ile	Met	Glu
		115					120				125				
Glu	Val	Lys	Lys	Ala	Ser	Glu	Thr	Val	Arg	Ile	Gln	Glu	Gly	Leu	Ser
130						135					140				
Val	Leu	Leu	Asn	Glu	Asp	Ile	Val	Leu	Ser	Ile	Asp	Ser	Ser	Ala	Asp
145					150					155					160
Lys	Thr	Asp	Ala	Val	Ile	Lys	Val	Leu	Asp	Asp	Ser	Phe	Gln	Asn	Asn
				165					170					175	

(2) INFORMATIONS POUR LA SEQ ID NO: 203:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 781 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(204059..206401)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 203:

Leu	Ala	Val	Leu	Leu	Leu	Leu	Thr	Phe	Ser	Gln	Ser	Ser	Phe	Cys	Ser
1			5						10					15	
Thr	Ser	Glu	Gly	Arg	Met	Val	Val	Glu	Ser	Ile	Thr	Ile	Thr	Thr	Gln
		20						25				30			
Gly	Glu	Asn	Thr	Gln	Asn	Lys	Arg	Ala	Ile	Pro	Lys	Ile	Lys	Thr	Lys
		35				40					45				
Gln	Gly	Thr	Leu	Phe	Ser	Gln	Ala	Asp	Phe	Asp	Glu	Asp	Leu	Arg	Thr
50						55					60				
Leu	Ser	Lys	Asn	Phe	Asp	Arg	Val	Glu	Pro	Ile	Val	Glu	Phe	Arg	Asn
65					70					75					80
Gly	Gln	Ala	Val	Ile	Ser	Leu	Ile	Leu	Thr	Ala	Lys	Ser	Val	Ile	Arg
			85					90					95		
Glu	Ile	Asn	Ile	Ser	Gly	Asn	Glu	Ala	Ile	Pro	Thr	His	Lys	Ile	Leu
		100						105				110			
Lys	Thr	Leu	Glu	Leu	Tyr	Lys	Asn	Asp	Leu	Phe	Asp	Arg	Glu	Leu	Phe
		115					120				125				
Phe	Lys	Asn	Phe	Asp	Ala	Leu	Arg	Thr	Leu	Tyr	Leu	Lys	Arg	Gly	Tyr
130						135					140				
Tyr	Asp	Ser	Gln	Leu	Ser	Tyr	Ser	His	Asn	His	Asn	Glu	Lys	Glu	Gly
145					150					155					160
Phe	Ile	Asp	Ile	Ser	Ile	Glu	Ile	Lys	Glu	Gly	Arg	His	Gly	Arg	Ile
			165					170					175		
Lys	Lys	Leu	Thr	Ile	Ser	Gly	Ile	Thr	Arg	Thr	Glu	Ala	Ser	Asp	Leu
		180						185				190			
Gly	Asp	Ile	Val	Leu	Thr	Lys	Gln	Tyr	Ser	Thr	Thr	Thr	Ser	Trp	Phe
		195					200				205				
Thr	Gly	Ala	Gly	Val	Tyr	His	Pro	Asp	Met	Val	Glu	Gln	Asp	Leu	Phe

210		215		220
Ala Ile Thr Asn Tyr	Phe Gln Asn Lys Gly Tyr	Ala Asp Ala Lys Val		
225	230	235		240
Ser Lys Glu Val Ser	Thr Asp Ala Lys Gly Asn	Ile Thr Leu Leu Ile		
	245	250		255
Val Val Asp Lys Gly	Pro Leu Tyr Thr	Leu Gly His Val His	Ile Glu	
	260	265		270
Gly Phe Thr Ala Leu	Ser Lys Arg Leu Leu	Asp Lys Gln Leu Leu	Val	
	275	280		285
Gly Pro Asn Ser Leu	Tyr Cys Pro Asp Lys	Ile Trp Thr Gly Ala	Gln	
	290	295		300
Lys Ile Arg Ser Ala	Tyr Ala Arg Tyr Gly	Tyr Val Asn Thr Asn	Val	
305	310	315		320
Asp Val Ser Phe Ser	Ala His Pro Thr Leu	Pro Val Tyr Asp Val	Thr	
	325	330		335
Tyr Arg Val Ser Glu	Gly Ser Pro Tyr Lys	Ile Gly Leu Ile Lys	Ile	
	340	345		350
Lys Gly Asn Thr His	Thr Lys His Asp Val	Ile Leu His Glu Thr	Ser	
	355	360		365
Leu Phe Pro Gly Asp	Thr Phe Tyr Arg Leu	Lys Leu Glu Asp Thr	Glu	
	370	375		380
Thr Arg Leu Arg Asn	Thr Gly Tyr Phe Lys	Ser Val Ser Val Tyr	Thr	
385	390	395		400
Val Arg Ser Gln Leu	Asp Pro Leu Asp Ser	Asn Asp Leu Tyr Arg	Asp	
	405	410		415
Val Phe Ile Glu Val	Lys Glu Thr Glu Thr	Gly Asn Leu Gly Leu	Phe	
	420	425		430
Leu Gly Phe Ser Ser	Ile Asp His Leu Phe	Gly Gly Ala Glu Ile	Ala	
	435	440		445
Glu Ser Asn Phe Asp	Leu Phe Gly Ala Arg	Asn Phe Leu Lys Lys	Gly	
	450	455		460
Phe Lys Ser Leu Arg	Gly Gly Glu Tyr Leu	Phe Leu Lys Ala Asn		
465	470	475		480
Leu Gly Asp Lys Val	Thr Asp Tyr Thr Val	Lys Trp Thr Lys Pro	His	
	485	490		495
Phe Leu Asn Thr Pro	Trp Ile Leu Gly Val	Glu Leu Asp Lys Ser	Ile	
	500	505		510
Asn Lys Ala Leu Ser	Lys Asp Tyr Ser Val	Asp Thr Tyr Gly Gly	Asn	
	515	520		525
Ile Ser Thr Thr Tyr	Ile Leu Asn Asp Lys	Leu Lys Tyr Gly Met	Tyr	
	530	535		540
Tyr Arg Gly Ser Gln	Thr Ser Leu Ser Leu	Arg Lys Lys Thr Ser	Ser	
545	550	555		560
Ser Asn Arg Leu Gly	Pro Asp Leu Asp Ser	Asn Lys Gly Phe Val	Ser	
	565	570		575
Ala Ala Gly Leu Asn	Val Leu Tyr Asp Ser	Ile Asp Asn Pro Arg	Lys	
	580	585		590
Pro Thr Met Gly Ile	Arg Ser Phe Leu Asn	Xaa Glu Leu Ser Gly	Leu	
	595	600		605
Gly Gly Thr Tyr Gln	Phe Thr Lys Leu Thr	Ala Ser Gly Ser Ile	Tyr	
	610	615		620
Arg Leu Leu Thr Lys	Lys Gly Val Leu Lys	Xaa Arg Ala Glu Ala	Xaa	
625	630	635		640
Phe Ile Lys Pro Phe	Gly Thr Thr Thr Ala	Gln Gly Ile Pro Val	Ser	
	645	650		655
Glu Arg Phe Phe Leu	Gly Gly Glu Thr Thr	Val Arg Gly Tyr Lys	Pro	
	660	665		670
Phe Ile Ile Gly Pro	Lys Phe Ser Pro Thr	Glu Pro Gln Gly Gly	Leu	
	675	680		685

Ser	Ser	Leu	Leu	Leu	Thr	Glu	Glu	Phe	Gln	Tyr	Pro	Leu	Ile	Ser	Gln
690						695					700				
Pro	Cys	Ile	Asn	Ala	Phe	Val	Phe	Leu	Asp	Ser	Gly	Phe	Ile	Gly	Ile
705					710					715					720
Glu	Glu	His	Thr	Ile	Arg	Leu	Lys	Asp	Leu	Cys	Ser	Ser	Ala	Gly	Phe
				725					730					735	
Gly	Leu	Arg	Phe	Asp	Met	Met	Asn	Asn	Val	Pro	Ile	Met	Leu	Gly	Trp
			740						745				750		
Gly	Trp	Pro	Phe	Arg	Pro	Thr	Glu	Ile	Leu	Asn	Asn	Glu	Lys	Ile	Asp
		755					760					765			
Val	Ser	Gln	Arg	Phe	Phe	Phe	Ala	Leu	Gly	Gly	Val	Phe			
	770					775					780				

(2) INFORMATIONS POUR LA SEQ ID NO: 204:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 205 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(206811..207425)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 204:

Ile	Gly	Leu	Lys	Asp	Met	Leu	Lys	Tyr	Pro	Asp	Tyr	Ile	Ser	Lys	Leu
1			5					10						15	
Ile	Ser	Phe	Leu	Lys	Lys	Leu	Pro	Gly	Ile	Gly	Phe	Lys	Ser	Ala	Glu
		20						25					30		
Lys	Ile	Ala	Phe	Glu	Leu	Leu	Glu	Trp	Asp	Pro	Ser	Gln	Ile	Glu	Ala
		35					40					45			
Met	Ala	Leu	Ala	Leu	Gln	Glu	Phe	Ser	Thr	Ser	His	Ala	Thr	Cys	Ser
	50					55				60					
Asn	Cys	Phe	Cys	Leu	Lys	Ile	Ser	Gln	Thr	Ser	Pro	Cys	Asn	Phe	Cys
65				70					75					80	
Ser	Glu	Ser	Arg	Asp	Ser	Ser	Ser	Leu	Cys	Ile	Val	Ala	Thr	Pro	Lys
			85					90					95		
Asp	Val	Phe	Ala	Leu	Glu	Lys	Ser	Lys	Ile	Phe	Lys	Gly	His	Tyr	Phe
		100						105					110		
Val	Leu	Gly	Asn	Leu	Leu	Ser	Pro	Ile	Thr	Gly	Lys	His	Leu	Ser	Leu
		115					120					125			
Glu	Lys	Leu	Ala	Ile	Leu	Lys	Gln	Arg	Ile	Glu	Ala	Cys	Ser	Pro	Lys
	130					135					140				
Glu	Met	Ile	Ile	Ala	Leu	Asp	Ala	Thr	Leu	Glu	Gly	Asp	Ala	Thr	Ala
145				150					155					160	
Leu	Phe	Leu	Lys	Gln	Glu	Phe	Ser	Tyr	Leu	Pro	Ile	Lys	Ile	Ser	Arg
			165					170					175		
Leu	Ala	Leu	Gly	Met	Pro	Val	Gly	Leu	Ser	Phe	Asp	Phe	Val	Asp	Ala
		180					185						190		
Asn	Thr	Leu	Ala	Arg	Ala	Phe	Ser	Gly	Arg	Asn	Cys	Phe			
	195						200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 205:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 327 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 207548..208528

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 205:

Val	Arg	Ala	Ser	Ile	Trp	Gly	Thr	Gly	Ser	Tyr	Leu	Pro	Lys	Lys	Ile
1				5					10					15	
Leu	Thr	Asn	Ala	Asp	Leu	Glu	Lys	Ile	Val	Glu	Thr	Ser	Asp	Glu	Trp
			20					25					30		
Ile	Ser	Thr	Arg	Thr	Gly	Ile	Lys	Glu	Arg	Arg	Ile	Ala	Ser	Ala	Glu
		35					40					45			
Glu	Phe	Ser	Ser	Phe	Met	Gly	Ala	Lys	Ala	Ala	Glu	Lys	Ala	Ile	Glu
	50					55					60				
Ala	Ala	Lys	Ile	Ser	Lys	Ser	Gln	Val	Asp	Cys	Ile	Val	Phe	Ser	Thr
65					70					75					80
Ala	Ala	Pro	Asp	Tyr	Ile	Phe	Pro	Ser	Ser	Ala	Ala	Leu	Ala	Gln	Ala
				85					90					95	
Tyr	Leu	Gly	Ile	Lys	Glu	Ile	Pro	Ala	Phe	Asp	Cys	Leu	Ala	Ala	Cys
			100					105					110		
Thr	Gly	Phe	Leu	Tyr	Gly	Leu	Ser	Ile	Ala	Lys	Ala	Tyr	Val	Glu	Ser
		115					120					125			
Gly	Met	Tyr	Gln	Cys	Val	Leu	Val	Ile	Ala	Ala	Asp	Lys	Leu	Ser	Ser
	130					135					140				
Phe	Val	Asn	Tyr	Gln	Asp	Arg	Asn	Thr	Cys	Val	Leu	Phe	Gly	Asp	Gly
145					150					155					160
Gly	Ser	Ala	Cys	Ile	Val	Gly	His	Ser	Arg	Pro	Gly	Ala	Leu	Glu	Ile
				165					170					175	
Ser	Lys	Val	Asn	Leu	Gly	Ala	Asp	Gly	Lys	Gln	Gly	Asp	Leu	Leu	Arg
			180					185					190		
Leu	Pro	Ala	Gly	Gly	Ser	Arg	Cys	Pro	Ala	Ser	Gln	Asp	Thr	Val	Gln
		195					200					205			
Asn	His	Gln	His	Phe	Ile	Thr	Met	Glu	Gly	Lys	Glu	Val	Phe	Lys	His
	210					215					220				
Ala	Val	Arg	Arg	Met	Glu	Phe	Ala	Ala	Lys	Thr	Cys	Ile	Thr	Glu	Ala
225					230					235					240
Gly	Leu	Gln	Glu	Lys	Asp	Ile	Asp	Trp	Leu	Val	Pro	His	Gln	Ala	Asn
				245					250					255	
Glu	Arg	Ile	Ile	Asp	Ala	Ile	Ala	Lys	Arg	Phe	Ala	Val	Lys	Asp	Ser
			260					265					270		
Arg	Val	Phe	Lys	Thr	Leu	Ala	Lys	Tyr	Gly	Asn	Thr	Ala	Ala	Ser	Ser
		275					280					285			
Val	Gly	Ile	Ala	Leu	Asp	Glu	Leu	Leu	Arg	Thr	His	Asp	Ile	His	Val
	290					295					300				
Ala	Glu	Arg	Leu	Leu	Leu	Val	Ala	Phe	Gly	Gly	Gly	Leu	Ser	Trp	Gly
305					310					315					320
Ala	Val	Ile	Leu	Gln	Gln	Val									
					325										

(2) INFORMATIONS POUR LA SEQ ID NO: 206:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 308 acides aminés

(B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 208548..209471

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 206:

Met	Asp	Arg	Val	Gly	Leu	Leu	Phe	Pro	Gly	Gln	Gly	Ser	Gln	Phe	Val
1				5					10					15	
Gly	Met	Gly	Arg	Asp	Leu	Tyr	Gln	Gln	Ser	Ser	Glu	Val	Ala	Arg	Leu
			20					25					30		
Phe	Ser	Gln	Ala	Asp	Glu	Phe	Leu	Gly	Phe	Ser	Leu	Ser	Ser	Ile	Met
		35				40					45				
Phe	Glu	Gly	Pro	Glu	Glu	Val	Leu	Leu	Lys	Thr	Ser	Asn	Ser	Gln	Leu
	50					55					60				
Ala	Ile	Tyr	Leu	His	Ser	Leu	Ala	Val	Leu	Glu	Val	Leu	Ser	Thr	His
65				70						75				80	
Cys	Pro	Phe	Glu	Pro	Ile	Leu	Val	Ser	Gly	Leu	Ser	Leu	Gly	Glu	Tyr
				85					90					95	
Thr	Ala	Leu	Thr	Ala	Ser	Lys	Arg	Ile	Ser	Leu	Glu	Asp	Gly	Leu	Arg
			100					105					110		
Ile	Val	Gln	Lys	Arg	Ala	Glu	Leu	Met	Asn	Ala	Ala	Cys	Glu	Glu	Ser
		115				120						125			
Ser	Gly	Ala	Met	Ala	Ala	Val	Leu	Gly	Leu	Thr	Ala	Asp	Val	Val	Leu
	130					135					140				
Pro	Ala	Leu	Glu	Ser	Leu	Gly	Glu	Gly	Ile	Trp	Val	Ala	Asn	Tyr	Asn
145					150					155					160
Ala	Pro	Lys	Gln	Ile	Val	Ile	Ala	Gly	Ile	Arg	Asn	Lys	Val	Glu	Glu
				165					170					175	
Ala	Ser	Val	Ile	Leu	Arg	Glu	Leu	Gly	Ala	Lys	Lys	Val	Val	Met	Leu
			180					185					190		
Lys	Val	Ala	Gly	Ala	Phe	His	Thr	Pro	Leu	Met	Gln	Thr	Ala	Gln	Asp
		195					200					205			
Glu	Leu	Ala	Pro	Tyr	Leu	Tyr	Gln	Leu	Ala	Ile	Lys	Asp	Ser	Asn	Val
	210					215					220				
Ala	Phe	Ala	Ser	Asn	Val	Ile	Gly	Glu	Leu	Val	Tyr	Glu	Ser	Glu	Ala
225					230					235					240
Ile	Arg	Ser	Leu	Xaa	Val	Arg	Gln	Met	Thr	Ser	Pro	Thr	Leu	Trp	Tyr
				245					250					255	
Gln	Thr	Cys	Phe	Gln	Ile	Asp	Pro	Lys	Val	Asp	Leu	Phe	Leu	Glu	Leu
			260					265					270		
Gly	Pro	Gly	Asn	Val	Leu	Thr	Gly	Leu	Ser	Arg	Ser	Ile	Gly	Leu	Ser
		275					280					285			
Ser	Pro	Cys	Lys	His	Leu	Gly	Ser	Met	Glu	Asp	Ile	Glu	Asn	Phe	Cys
	290					295					300				
Arg	Xaa	Cys	Glu												
305															

(2) INFORMATIONS POUR LA SEQ ID NO: 207:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 248 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 209471..210214

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 207:

```

Met Xaa Gly Leu Leu Val Asn Lys Thr Ala Ile Val Thr Gly Gly Ser
1          5          10          15
Arg Gly Ile Gly Phe Ser Ile Ala Lys Leu Phe Ala Glu Gln Gly Ala
          20          25          30
Asn Val Gln Ile Trp Gly Ile Asn Gly Glu Ala Gly Gln Ala Ala Ala
          35          40          45
Gln Thr Leu Ser Glu Gln Thr Gly Arg Gln Val Ser Phe Ala Leu Val
          50          55          60
Asp Val Ser Lys Asn Asp Met Val Ser Ala Gln Val Gln Asn Phe Leu
65          70          75          80
Ser Glu Tyr Asn Thr Ile Asp Val Ile Val Asn Asn Ala Gly Ile Thr
          85          90          95
Arg Asp Ala Leu Leu Met Arg Met Ser Glu Glu Glu Trp Ser Ser Val
          100          105          110
Ile Asn Thr Asn Leu Gly Ser Ile Tyr Asn Val Cys Ser Ala Val Ile
          115          120          125
Arg Pro Met Ile Lys Ala Arg Ser Gly Ala Ile Ile Asn Ile Ser Ser
          130          135          140
Ile Val Gly Leu Arg Gly Ser Pro Gly Gln Thr Asn Tyr Ala Ala Ala
145          150          155          160
Lys Ala Gly Ile Ile Gly Phe Ser Lys Ala Leu Ser Lys Glu Val Gly
          165          170          175
Ser Lys Asn Ile Arg Val Asn Cys Ile Ala Pro Gly Phe Ile Asp Thr
          180          185          190
Asp Met Thr Lys Ser Leu Asn Asp Asn Leu Lys Asn Glu Trp Leu Lys
          195          200          205
Gly Val Pro Leu Gly Arg Val Gly Met Pro Glu Glu Ile Ala Lys Ala
210          215          220
Ala Leu Phe Leu Xaa Ser Asp Gly Ser Ser Tyr Ile Thr Gly Gln Val
225          230          235          240
Leu Ser Val Asp Gly Gly Met Ala
          245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 208:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 77 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 210586..210816

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 208:

```

Met Ser Leu Glu Asp Asp Val Lys Ala Ile Ile Val Asp Gln Leu Gly
1          5          10          15
Val Ser Pro Glu Asp Val Lys Val Asp Ser Ser Phe Ile Glu Asp Leu
          20          25          30

```

Asn	Ala	Asp	Ser	Leu	Asp	Leu	Thr	Glu	Leu	Ile	Met	Thr	Leu	Glu	Glu
		35					40				45				
Lys	Phe	Ala	Phe	Glu	Ile	Ser	Glu	Asp	Asp	Ala	Glu	Gln	Leu	Arg	Thr
	50					55				60					
Val	Gly	Asp	Val	Ile	Lys	Tyr	Ile	Gln	Glu	His	Gln	Asn			
65					70					75					

(2) INFORMATIONS POUR LA SEQ ID NO: 209:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(210883..211332)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 209:

Leu	Val	Pro	Ser	Phe	Lys	Ser	Leu	Val	Gly	Gly	Thr	Ser	Leu	Asn	Leu
1				5					10					15	
Ile	Asp	Lys	Ala	Phe	Leu	Leu	Lys	Lys	Thr	Xaa	Leu	Phe	Ala	Ser	Leu
		20					25					30			
Asp	Met	Asp	Val	Leu	Leu	Ser	Ile	Ala	Asp	Lys	Ser	Glu	Val	Met	Leu
		35				40					45				
Phe	Lys	Ala	Gly	Ser	Glu	Ile	Phe	Ser	Glu	Gly	Gln	Pro	Ser	Phe	Ser
	50					55					60				
Leu	Tyr	Val	Ile	Ala	Glu	Gly	Cys	Val	Arg	Ile	Phe	Ala	Lys	Glu	Pro
65				70					75					80	
Thr	Ile	Asn	Val	Arg	Leu	Lys	Pro	Leu	Asp	Cys	Phe	Gly	Glu	Glu	Ser
			85				90						95		
Phe	Phe	Asn	Asn	Lys	Val	Arg	Glu	Tyr	Ser	Ala	Glu	Ala	Ile	Thr	Leu
		100					105						110		
Val	Lys	Thr	Leu	Ile	Leu	Asn	Lys	Gly	Gln	Phe	Leu	Ser	Ile	Ile	Glu
		115				120						125			
Glu	Cys	Pro	Ser	Val	Ser	Leu	Val	Leu	Leu	Glu	Phe	Tyr	Ser	Lys	Gln
	130					135					140				
Ile	Val	Phe	Arg	Asp	Gln										
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 210:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 535 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(211374..212978)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 210:

Asn Leu Leu Leu Ser Cys Gly Asp Val His Leu Arg Thr Thr Met Phe



1		5		10		15
Ile	His	Pro	Ala	Pro	Ile	Arg
		20				
Tyr	Ser	Phe	Ser	Asn	Ile	Xaa
		35				
Arg	Asn	Leu	Ser	Leu	Glu	Ser
		50				
Trp	Phe	Ala	Asp	Met	Asn	Asp
65						
Ser	Val	Thr	His	Leu	Lys	Asn
Phe	Gln	His	Leu	Leu	Asn	Leu
Leu	Leu	His	Met	Asn	Lys	Leu
Asn	Met	Leu	Lys	Asn	Ser	Val
Leu	Leu	Lys	Arg	Trp	Ser	Ser
145						
Ala	Leu	His	Leu	Tyr	Phe	Val
Ile	Ala	Asp	Asp	Leu	Tyr	Asp
Val	Leu	Ile	Val	Arg	Lys	His
Ala	Glu	Lys	His	Leu	Ser	Glu
Ile	Ile	Lys	Gly	Leu	Ser	Ile
225						
Phe	Pro	Ile	Ile	Leu	Pro	Phe
Leu	Gln	Ala	Cys	Leu	Ser	Leu
Gln	Tyr	Gly	Arg	Thr	Val	Leu
Gln	Ala	Ala	Gln	Ala	Leu	Leu
Ser	Leu	Val	Tyr	Glu	Phe	Val
305						
Leu	Arg	Lys	Leu	Ala	Glu	Thr
Ile	Pro	Ile	Leu	Ile	Glu	Met
Cys	Arg	Ile	Met	Ala	Ala	Lys
Leu	Lys	Arg	Leu	Ala	Leu	Lys
Leu	Phe	Tyr	Asp	Tyr	His	Lys
385						
Tyr	Asp	Leu	His	Leu	Leu	Ile
Glu	Val	Asn	Phe	Met	Leu	Ala
Tyr	Ala	Asp	Val	Leu	Ile	Arg
Arg	Ala	Gln	Ala	Leu	Glu	Ser
Phe	Thr	Leu	Val	Thr	Pro	Phe
465						

Glu Lys Tyr Tyr Met Lys Lys Gly Val Glu Pro Leu Ala Ile Glu Glu  
 485 490 495  
 Leu Leu Asn Arg Leu Glu Gln Thr Pro Phe Leu Phe Ser Lys Leu Ile  
 500 505 510  
 Ala Gln Gln Leu Lys Glu Gly Ala Phe Ser Leu Arg Cys Arg Val Leu  
 515 520 525  
 Phe Cys Ser Thr Lys Leu Cys  
 530 535

(2) INFORMATIONS POUR LA SEQ ID NO: 211:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 402 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(212875..214080)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 211:

Ser Leu Arg Ala Leu Arg Phe Leu Leu Ser Leu Arg Arg Gly Glu Glu  
 1 5 10 15  
 Lys Arg Ala Leu Leu Phe Leu Leu Leu Gly Leu Ile Trp Ser Val Ala  
 20 25 30  
 Cys Tyr Gly Ser Leu Ala Leu Gly Glu Ser Xaa Phe Leu Glu Glu Ile  
 35 40 45  
 Gly Ala Glu Lys Leu Pro Phe Ala Tyr Leu Gly Ala Ser Phe Phe Leu  
 50 55 60  
 Cys Phe Ile Ser Cys Leu Ile Leu Tyr Asn Leu Ser Arg Lys Arg Val  
 65 70 75 80  
 Ser Pro Lys Ala Leu Phe Leu Ser Phe Ile Ser Cys Val Leu Ile Cys  
 85 90 95  
 Asn Leu Tyr Leu Phe Trp His Leu Ala Ile His Lys Gly Val Ser Gly  
 100 105 110  
 Thr Pro Thr Phe Leu Tyr Arg Ile Leu Ile Trp Gly Leu Thr Ile Leu  
 115 120 125  
 Cys Tyr Ala Asn Phe Trp Gly Phe Ile Asp Gln Phe Phe Asn Ile Gln  
 130 135 140  
 Asp Ala Lys Arg His Phe Cys Ile Phe Asn Ala Ile Thr Phe Cys Gly  
 145 150 155 160  
 Asp Phe Leu Gly Ala Arg Ile Val Asn Gln Ile Gln Tyr Leu Gly Ala  
 165 170 175  
 Glu Leu Ile Leu Leu Ala Phe Ile Val Val Ile Thr Phe Ile Phe Pro  
 180 185 190  
 Leu Val His Tyr Ile Ser Ser Ser Leu Lys Glu Leu Ser Glu Asp His  
 195 200 205  
 Asp Leu Phe Leu Asp Thr Gly Tyr Pro Pro Ser Thr Lys Gln Thr Leu  
 210 215 220  
 Lys Leu Cys Leu Lys Asp Lys Tyr Thr Phe Tyr Leu Val Ser Phe Tyr  
 225 230 235 240  
 Phe Leu Met Gln Leu Leu Val Val Phe Thr Glu Phe Asn Tyr Leu Lys  
 245 250 255  
 Ile Phe Asp Ala Gln Phe Gly Asn Ala Glu Thr Cys Glu Leu Thr Glu  
 260 265 270  
 Asn Phe Thr Lys Tyr Ser Ser Trp Ile Ser Leu Gly Asn Met Phe Phe

(2) INFORMATION POUR LA SEQ ID NO: 212:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(214168..214710)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 212:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 213:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(214754..215143)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 213:

Phe	Thr	Glu	Gly	Asn	Met	Val	His	Ser	Val	Tyr	Asn	Ser	Leu	Ala	Pro
1				5					10					15	
Glu	Gly	Phe	Ser	Gln	Val	Ser	Ile	Gln	Pro	Ser	Gln	Ile	Pro	Thr	Ser
			20					25					30		
Lys	Lys	Val	Met	Ile	Ala	Ile	Met	Thr	Leu	Phe	Ala	Leu	Thr	Ala	Ile
		35					40					45			
Ala	Ala	Ile	Val	Leu	Ser	Ile	Val	Thr	Val	Cys	Gly	Phe	Pro	Phe	
	50					55				60					
Leu	Leu	Ala	Ala	Leu	Asn	Thr	Val	Thr	Ile	Gly	Ala	Cys	Val	Ser	Leu
65				70					75						80
Pro	Ile	Phe	Thr	Cys	Ile	Ala	Thr	Thr	Leu	Leu	Leu	Leu	Cys	Leu	Arg
				85				90					95		
Asn	Ile	Glu	Leu	Leu	Gly	Gln	Thr	Ala	Ser	Ile	Asp	Pro	Leu	His	Ser
		100					105					110			
Ile	Gln	Pro	Asn	Lys	Thr	Ser	Arg	Asn	Arg	Val	Val	Ala	Gln	Gln	Lys
		115					120					125			
Met	Ser														
	130														

(2) INFORMATIONS POUR LA SEQ ID NO: 214:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 490 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(215236..216705)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 214:

Met	Asn	Lys	Lys	Asn	Thr	Val	Phe	Ser	Ser	Arg	Leu	Gly	Phe	Ile	Leu
1				5					10					15	
Ser	Met	Met	Gly	Val	Ala	Ile	Gly	Ala	Gly	Asn	Ile	Trp	Arg	Phe	Pro
		20					25					30			
Arg	Met	Val	Ala	Gln	Asn	Gly	Gly	Gly	Thr	Phe	Ile	Leu	Leu	Trp	Leu
		35				40					45				
Leu	Phe	Leu	Ile	Ile	Trp	Ser	Ile	Pro	Leu	Ile	Ile	Val	Glu	Leu	Ser
	50				55				60						
Ile	Gly	Lys	Leu	Thr	Arg	Lys	Ala	Pro	Ile	Gly	Ala	Leu	Ile	Arg	Thr
65				70					75					80	
Ala	Gly	Pro	Lys	Ser	Ala	Trp	Leu	Gly	Gly	Phe	Ile	Val	Leu	Val	Ala

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 342 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(216892..217917)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 215:

Lys	Ser	Met	Val	Ser	Val	Val	Arg	Ser	Ser	Leu	Tyr	Tyr	Thr	Leu	Leu	1	5	10	15
Thr	Thr	Leu	Ile	Ser	Ala	Ala	Ile	Ala	Leu	Val	Leu	Phe	Ile	Phe	Ile	20	25	30	
Lys	Pro	Ser	Val	Pro	Leu	Ser	Gly	Phe	Asn	Ala	Ala	Thr	Glu	Thr	Asn	35	40	45	
Ala	Thr	Gly	Tyr	Leu	Ser	Val	Leu	Ser	Lys	Thr	Ile	Pro	Gly	Asn	Ile	50	55	60	
Leu	Glu	Pro	Phe	Leu	Glu	Ser	Asn	Val	Ile	Ala	Ala	Ala	Phe	Leu	Ser	65	70	75	80
Ala	Leu	Leu	Ala	Thr	Phe	Ser	Leu	Ser	Leu	Pro	Glu	Asn	Glu	Arg	Leu	85	90	95	
Phe	Val	Arg	Asn	Ala	Phe	Asn	Thr	Leu	Phe	Ser	Leu	Leu	Leu	Ser	Ile	100	105	110	
Ser	Lys	Gly	Ile	Leu	Lys	Met	Leu	Pro	Leu	Ala	Thr	Phe	Ala	Phe	Ser	115	120	125	
Leu	Leu	Phe	Val	Arg	Glu	Met	Arg	Thr	Gly	Asn	Leu	Glu	Leu	Ser	Ser	130	135	140	
Phe	Gly	Glu	Tyr	Leu	Phe	Cys	Ile	Val	Thr	Ala	Asn	Cys	Leu	Gln	Gly	145	150	155	160
Phe	Leu	Val	Leu	Pro	Leu	Leu	Leu	Lys	Met	Lys	Gly	Ile	Ser	Pro	Leu	165	170	175	
Arg	Thr	Phe	Lys	Leu	Met	Ser	Arg	Pro	Leu	Ala	Thr	Ala	Phe	Phe	Ser	180	185	190	
Lys	Ser	Ser	Ala	Val	Thr	Leu	Pro	Leu	Thr	Met	Glu	Val	Ala	Glu	Glu	195	200	205	
Asn	Leu	His	Ile	Arg	Pro	Thr	Ile	Ser	Arg	Phe	Val	Phe	Pro	Leu	Cys	210	215	220	
Ser	Val	Ile	Asn	Met	Asn	Ala	Cys	Ala	Ala	Phe	Ile	Leu	Thr	Thr	Val	225	230	235	240
Leu	Phe	Val	Gly	Val	Ser	Asn	Gly	Ile	Val	Phe	Ser	Pro	Leu	Ser	Leu	245	250	255	
Ile	Ser	Trp	Val	Phe	Ile	Ala	Thr	Leu	Ala	Ala	Val	Gly	Asn	Ala	Gly	260	265	270	
Val	Pro	Met	Gly	Cys	Tyr	Phe	Leu	Thr	Ser	Ser	Leu	Leu	Ala	Ser	Met	275	280	285	
Asn	Val	Pro	Leu	Gly	Leu	Leu	Gly	Leu	Ile	Leu	Pro	Ala	Tyr	Ala	Leu	290	295	300	
Leu	Asp	Met	Leu	Glu	Thr	Leu	Ile	Asn	Val	Trp	Ser	Asp	Cys	Cys	Ile	305	310	315	320
Val	Ser	Val	Ile	Asn	Lys	Lys	Phe	Ser	Glu	Thr	Glu	Asp	Leu	Pro	Pro	325	330	335	
Cys	Ser	Tyr	Thr	Asn	Glu											340			

(2) INFORMATIONS POUR LA SEQ ID NO: 216:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 216:

(2) INFORMATION POUR LA SEQ ID NO: 217:

(A) LONGUEUR: 113 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 218364..218702 .

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 217:

[illegible]

## (2) INFORMATIONS POUR LA SEQ ID NO: 218:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 105 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 218695..219009

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 218:

Arg	Ser	Phe	Glu	Glu	Glu	Tyr	Lys	Ala	Leu	Ser	Glu	Val	Tyr	Arg	Ala
1			5						10					15	
Asn	Leu	Glu	Ala	Arg	Arg	Ala	Val	Ser	Lys	Tyr	Cys	Gln	Glu	Leu	Glu
		20						25					30		
Glu	Lys	Ile	Leu	Asp	Leu	Cys	Lys	Arg	His	Ala	Ala	Thr	Ile	Cys	Ser
		35					40						45		
Ile	Glu	Glu	Asp	Ala	Lys	Gln	Glu	Ile	Arg	His	Gln	Thr	Glu	Arg	Phe
	50					55					60				
Lys	Gln	Arg	Leu	Gln	Gln	Asn	Gln	Asn	Thr	Cys	Ser	Gln	Ile	Thr	Ala
65				70						75					80
Glu	Leu	Cys	Lys	Leu	Arg	Ser	Glu	Asn	Lys	Ala	Leu	Ser	Glu	Arg	Leu
			85						90					95	
Gln	Val	Gln	Ala	Ser	Arg	Arg	Lys	Lys							
			100					105							

## (2) INFORMATIONS POUR LA SEQ ID NO: 219:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 190 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 219179..219748

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 219:

Arg	Arg	Arg	Phe	Phe	Phe	Thr	Val	Ala	Asn	Ser	Phe	Leu	Arg	Arg	Asp
1			5						10					15	
Lys	Ile	Tyr	Phe	Val	Phe	Asn	Lys	Arg	Glu	Tyr	Leu	Phe	Gln	Asn	Phe
		20						25					30		
Gly	Tyr	Ser	Phe	Ser	Tyr	Arg	Arg	Arg	Phe	Ser	Cys	Cys	Arg	Trp	Gly
		35					40					45			
Ile	Ser	Phe	Gly	Phe	Val	Arg	Tyr	Asn	Val	Ile	Phe	Thr	Val	Ile	Gly
	50					55					60				
Ile	Pro	Ala	Leu	Ile	Ile	Gly	Ser	Ala	Cys	Val	Gly	Ala	Gly	Ile	Ser
65				70					75						80
Arg	Leu	Met	Tyr	Arg	Ser	Ser	Tyr	Ala	Ser	Leu	Glu	Ala	Lys	Asn	Val
			85						90					95	
Leu	Ala	Glu	Gln	Arg	Leu	Arg	Asn	Leu	Ser	Glu	Glu	Lys	Asp	Ala	Leu
			100					105					110		
Ala	Ser	Val	Ser	Phe	Ile	Asn	Lys	Met	Phe	Leu	Arg	Gly	Leu	Thr	Asp



(2) INFORMATION POUR LA SEQ ID NO: 220:

(A) LONGUEUR: 180 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 219891..220430

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 220:

(2) INFORMATION POUR LA SEQ ID NO: 221:

(A) LONGUEUR: 192 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 220499..221074

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 221:

Leu	Pro	Leu	Lys	Tyr	Ile	Lys	Ile	Phe	Thr	Leu	Ile	Ser	Phe	Pro	Val
1				5					10					15	
Ala	Cys	Arg	Pro	Phe	Leu	Arg	Asn	Arg	Gly	Ala	Met	Phe	Asn	Ile	Ser
			20					25					30		
Phe	Cys	Cys	Asn	Ser	Ser	Lys	Pro	Leu	Arg	Ala	Asp	His	Thr	Glu	Thr
		35					40					45			
Ile	Gly	Ala	Gln	Thr	Thr	Thr	Ser	Arg	Lys	Glu	Gln	Leu	Leu	Ala	Ile
	50					55					60				
Gly	Ala	Leu	Val	Leu	Gly	Val	Leu	Ala	Val	Leu	Gly	Gly	Ala	Leu	Leu
65					70					75					80
Leu	Leu	Phe	Ser	Gly	Ser	Val	Leu	Ser	Leu	Phe	Ala	Pro	Ile	Leu	Ser
				85					90					95	
Leu	Leu	Ala	Met	Thr	Leu	Gly	Ser	Ala	Cys	Ile	Gly	Gly	Ser	Leu	Val
		100						105					110		
Tyr	Met	Tyr	Gly	Phe	Ser	Leu	Lys	Pro	Thr	Arg	Leu	Pro	Ser	Glu	Ser
		115					120					125			
Ser	Gly	Leu	Ala	Pro	Glu	Ala	Val	Thr	Pro	Gly	Leu	Val	Leu	Ser	Tyr
	130					135					140				
Gln	Glu	Leu	Leu	Tyr	Glu	Ala	Glu	Glu	Asp	Leu	Lys	Glu	Val	Glu	Gly
145					150					155					160
Leu	Leu	Ala	Gln	Lys	Ser	Lys	Asp	Leu	Glu	Leu	Ala	Gln	Lys	Lys	Ile
				165					170					175	
Glu	Gln	Leu	Gln	Ser	Gly	Leu	Lys	Cys	Val	Leu	Glu	Glu	Ser	Leu	Arg
		180						185					190		

(2) INFORMATIONS POUR LA SEQ ID NO: 222:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 135 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 221137..221541

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 222:

Gly	Ile	Val	Val	Gln	Gln	Lys	Leu	Arg	Tyr	Ser	Glu	Asn	Val	Ala	Asn
1				5					10					15	
Asn	Ser	Phe	Ile	His	Arg	Ser	Lys	Arg	Tyr	Gln	Leu	Phe	Val	Val	Val
		20						25					30		
Leu	Thr	Ser	Leu	Leu	Ala	Ala	Leu	Gly	Gly	Val	Phe	Leu	Cys	Leu	Gly
		35					40					45			
Gly	Val	Tyr	Ser	Ser	Leu	Val	Leu	Gly	Val	Val	Gly	Gly	Ala	Ala	Ile
	50					55					60				
Ile	Gly	Ser	Cys	Ile	Gly	Ala	Phe	Gly	Leu	Val	Ser	Tyr	Leu	Leu	Ser
65					70					75					80
Val	Ile	Arg	Asn	Ser	Asp	Gln	Leu	Leu	Gln	Glu	Ala	Lys	Glu	Ser	Asp
				85					90					95	
Arg	Lys	Ile	Ser	Ser	His	Tyr	Arg	Val	Leu	Glu	Thr	Gln	Lys	Asn	Arg

		100				105			110
Glu	Ile	Gly	Leu	Leu	Glu	Glu	Arg	Val	Asn
		115				120			125
Ala	Lys	Phe	His	Gly	Trp	Asp			
		130				135			

(2) INFORMATIONS POUR LA SEQ ID NO: 223:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 164 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 221601..222092

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 223:

Arg	Lys	Ala	Ser	Leu	Leu	Ile	Thr	Asp	Leu	Phe	Tyr	Leu	Lys	Trp	Asp
1				5					10					15	
Ala	Met	Ser	Phe	Val	Gly	Asp	Ser	Val	Pro	Leu	Arg	Ser	Tyr	Met	Pro
			20					25					30		
Glu	Ala	Pro	Leu	Val	Asp	Ser	Ala	Ser	Lys	Ala	Arg	Val	Ser	Cys	Cys
		35					40					45			
Ser	Glu	Arg	Ile	Ala	Val	Leu	Ala	Leu	Gly	Ile	Leu	Ser	Ile	Leu	Phe
	50					55					60				
Ile	Val	Thr	Gly	Ala	Ala	Leu	Phe	Ile	Gly	Ala	Gly	Trp	Thr	Thr	Leu
65				70					75						80
Pro	Met	Ile	Asn	Val	Val	Val	Thr	Leu	Val	Val	Phe	Gly	Ser	Val	Met
			85					90						95	
Leu	Gly	Ala	Val	Leu	Thr	Arg	Ile	Ser	Gly	Tyr	Gly	Gly	Glu	Pro	Lys
			100					105					110		
Lys	Val	Ser	Leu	Asp	Arg	Phe	Val	Leu	Glu	Asn	Glu	Arg	Gln	Gly	Phe
		115				120						125			
Leu	Asp	Lys	Gln	Arg	Leu	Ala	Asp	Ile	Ser	Lys	Glu	Glu	Ile	Ala	Leu
	130					135					140				
Ala	Lys	Gln	Gln	Ile	Glu	Glu	Glu	Lys	Glu	Ala	Ile	Leu	His	Ser	Ile
145				150						155					160
Phe	Pro	Asn	Asp												

(2) INFORMATIONS POUR LA SEQ ID NO: 224:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 273 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 222472..223290

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 224:

```

Arg Lys Gly Gly Lys Met Val Ser Leu Ala Leu Gly Thr Ser Asn Arg
1      5      10      15
Val Glu Ala Asn Asn Gly Ile Asn Asp Leu Ser Pro Ala Pro Glu Ala
20      25      30
Lys Lys Thr Gly Phe Gly Leu Cys Tyr Lys Ile Ser Ala Val Ala Ala
35      40      45
Leu Val Leu Gly Leu Leu Ala Ala Ala Gly Gly Ala Val Val Leu Ala
50      55      60
Leu Phe Cys Thr Phe Thr Pro Pro Leu Phe Phe Tyr Ala Gly Val Ala
65      70      75      80
Leu Val Ala Leu Gly Ala Val Ile Leu Gly Val Gly Val Ser Asn Thr
85      90      95
Cys Ser Cys Cys Leu Arg Ser Lys Arg Ile Glu Ala Arg Glu Gln Leu
100     105     110
Leu Leu Gln Gln Lys Glu Glu Ile Ser Gln Leu Glu Gln Gln Leu Ala
115     120     125
Lys Ala Leu Gly Glu Leu Asp Thr Lys Cys Ala Ser Leu Leu Glu Arg
130     135     140
Arg Asp Leu Arg Glu Asn Leu Lys Ala Trp Gln Ala Tyr Cys Leu Asn
145     150     155     160
Leu Glu Glu Asp Val Arg Asp Leu Leu Lys Lys Leu Glu Gly Tyr Gln
165     170     175
Glu Arg Leu Lys Val Leu Pro Ala Lys Glu Lys Gln Ile Glu Glu Leu
180     185     190
Lys Ala Met Leu Glu His Tyr Ser Arg Ile Cys Tyr Glu Arg Gly Asp
195     200     205
Leu Ile Arg Met Leu Lys Thr Ala Asn Lys Lys Leu Ser Lys Glu Cys
210     215     220
Glu Lys Leu Leu Leu Asn Tyr Lys Ala His Leu Asp Val Cys Leu Gly
225     230     235     240
Glu Lys Val Leu Ala Lys Ser Val Asn Leu Ile Asp Leu Asp Leu Lys
245     250     255
Ser Asp Ser Ser Asp Gly Asp Asp Tyr Asp Phe Asn Tyr Gly Ser Arg
260     265     270
Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 225:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 223435..223818

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 225:

```

Met Arg Cys Cys Cys Val Arg Thr Asn Cys Glu Glu Val Arg Ser Ser
1      5      10      15
Ser Thr Gly Asp Gln Val Val Ser Ala Val Lys Glu Arg Lys Cys Asp
20      25      30
Ser Ser Leu Arg Arg Lys Ile Ala Ser Val Ala Phe Thr Leu Ile Gly
35      40      45
Ala Leu Leu Leu Gly Ile Gly Met Val Leu Ser Phe Ala Leu Leu Gly

```

50		55		60											
Ser	Ser	Ala	Gly	Leu	Ile	Gly	Val	Gly	Val	Leu	Ser	Ala	Leu	Gly	Ala
65				70				75							80
Val	Cys	Leu	Ser	Leu	Gly	Leu	Tyr	Lys	Leu	Phe	Leu	Arg	Met	Lys	Arg
			85					90						95	
Val	Ser	Leu	Asp	Lys	Ala	Glu	Gln	Lys	Met	Leu	Glu	Asp	Gln	Val	Glu
		100						105					110		
Leu	Leu	Arg	Gln	Glu	Asn	Gln	Glu	Leu	Lys	Ala	Ile	Ser	Val	Phe	His
		115					120						125		

(2) INFORMATIONS POUR LA SEQ ID NO: 226:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 224278..225171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 226:

Met	Ala	His	Thr	Ile	Arg	Phe	Thr	Lys	Phe	Ser	Phe	Pro	Leu	Tyr	Phe
1				5					10					15	
Ser	Lys	Thr	Leu	Ser	Trp	Phe	Ile	Ile	Gly	Gly	Phe	Leu	Ala	Ala	Cys
			20					25					30		
Val	Val	His	Met	Ile	Leu	Ala	Pro	Asn	Asp	Leu	Ile	Asp	Gly	Gly	Ile
		35					40					45			
Val	Gly	Leu	Ser	Met	Ile	Ala	Ala	His	Ser	Phe	Gly	His	Gln	Phe	Leu
	50					55					60				
Pro	Val	Phe	Leu	Val	Leu	Phe	Asn	Leu	Pro	Phe	Ile	Ile	Leu	Ala	Tyr
65					70					75					80
Lys	Arg	Ile	Gly	Lys	Tyr	Phe	Val	Val	Gln	Met	Ile	Thr	Ala	Val	Ile
				85					90					95	
Ile	Phe	Ser	Cys	Trp	Leu	Trp	Leu	Ile	Glu	Val	Leu	Pro	Glu	Trp	Leu
			100					105					110		
Gly	Ile	Gln	Pro	Phe	Ile	Phe	Asp	Gly	Ser	Glu	Ile	Glu	Thr	Ile	Val
		115					120					125			
Leu	Gly	Gly	Val	Val	Leu	Gly	Ala	Gly	Gly	Gly	Leu	Ile	Ile	Arg	His
	130					135					140				
Gly	Gly	Ala	Thr	Asp	Gly	Thr	Glu	Ile	Leu	Gly	Ile	Ile	Val	Asn	Lys
145					150					155					160
Lys	Arg	Gly	Tyr	Thr	Val	Gly	Gln	Val	Ile	Leu	Phe	Val	Asn	Phe	Phe
				165					170					175	
Ile	Phe	Ser	Leu	Gly	Gly	Ile	Val	Tyr	Arg	Asn	Trp	His	Thr	Ala	Phe
			180					185					190		
Met	Ser	Leu	Leu	Thr	Tyr	Ala	Val	Ala	Ile	Lys	Val	Met	Asp	Met	Val
		195					200					205			
Ile	Leu	Gly	Phe	Glu	Asp	Thr	Lys	Ser	Val	Thr	Ile	Ile	Thr	Ser	Ser
	210					215					220				
Pro	Arg	Lys	Leu	Gly	Asn	Ile	Leu	Met	Glu	Thr	Leu	Gly	Val	Gly	Leu
225					230					235					240
Thr	Tyr	Leu	His	Ala	Glu	Gly	Gly	Phe	Ser	Gly	Glu	Pro	Arg	Asn	Leu
				245					250					255	
Leu	Tyr	Ile	Val	Val	Glu	Arg	Leu	Gln	Leu	Ser	Gln	Leu	Lys	Glu	Ile
			260					265					270		

Val His Arg Glu Asp Pro Ser Ala Phe Ile Ala Ile Glu Asn Leu His  
           275                                  280                                  285  
 Glu Val Ile Asn Glu Lys Arg Thr Ser His  
           290                                  295

(2) INFORMATIONS POUR LA SEQ ID NO: 227:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 185 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(225174..225728)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 227:

Ile Ser Gly Ala Ser Gly Ile Xaa Leu Ala Val Thr Leu Val Ser Glu  
 1                  5                  10                  15  
 Leu Ala Arg Leu Gly His His Ile Asp Val Ile Ile Ser Pro Ser Ala  
                   20                  25                  30  
 Gln Lys Thr Leu Tyr Tyr Glu Leu Asp Thr Lys Ser Phe Leu Ser Thr  
                   35                  40                  45  
 Ile Pro Gln Asn Phe His Asn Gln Ile Val Leu His His Ile Ser Ser  
                   50                  55                  60  
 Ile Glu Ser Ser Val Ser Ser Gly Ser Asn Thr Val Asp Ala Thr Ile  
 65                  70                  75                  80  
 Ile Val Pro Cys Ser Val Ala Thr Val Ala Ala Ile Ser Cys Gly Leu  
                   85                  90                  95  
 Ala Asp Asn Leu Leu Arg Arg Val Ala Asp Val Ala Leu Lys Glu Lys  
                   100                  105                  110  
 Arg Pro Leu Ile Leu Val Pro Arg Glu Ala Pro Leu Ser Ala Ile His  
                   115                  120                  125  
 Leu Glu Asn Leu Leu Lys Leu Ala Gln Asn Gly Ala Val Ile Leu Pro  
                   130                  135                  140  
 Pro Met Pro Ile Trp Tyr Phe Lys Pro Gln Thr Ala Glu Asp Ile Ser  
 145                  150                  155                  160  
 Asn Asp Ile Val Gly Lys Ile Leu Ala Ile Leu Gln Leu Asp Ser Pro  
                   165                  170                  175  
 Leu Ile Lys Arg Trp Glu Asn Pro Arg  
                   180                  185

(2) INFORMATIONS POUR LA SEQ ID NO: 228:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 72 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 225334..225549

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 228:

```

Lys Phe Ser Lys Cys Ile Ala Asp Arg Gly Ala Ser Arg Gly Thr Arg
1          5          10          15
Ile Arg Gly Leu Phe Ser Phe Arg Ala Thr Ser Ala Thr Leu Leu Lys
          20          25          30
Arg Leu Ser Ala Lys Pro His Glu Ile Ala Ala Thr Val Ala Thr Leu
          35          40          45
Gln Gly Thr Ile Ile Val Ala Ser Thr Val Phe Glu Pro Asp Asp Thr
          50          55          60
Glu Leu Ser Ile Glu Asp Ile Trp
65          70

```

(2) INFORMATIONS POUR LA SEQ ID NO: 229:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 288 acides aminés.

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(225749..226612)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 229:

```

Tyr Ala Leu Phe Ala Ala Leu Phe Leu Ala Ser Ser Thr Leu Phe Cys
1          5          10          15
Phe Ser Leu Pro Cys Thr Pro Phe Ser Leu Phe Ser Leu Gly Ser Ile
          20          25          30
Lys Thr Ile Ser Leu Gly Gly Ser Ala Phe Phe Ile Ala Arg Ala Leu
          35          40          45
Gly Met Ile Val Asn Gln Val Val Asp Cys Ala Ile Asp Lys Arg Asn
          50          55          60
Pro Arg Thr Gln Ser Arg Val Leu Pro Ala Glu Leu Leu Ser Ile Lys
65          70          75          80
His Ser Met Leu Leu Leu Thr Leu Cys Leu Ile Leu Phe Leu Ser Thr
          85          90          95
Cys Trp Leu Phe Asn Pro Leu Cys Phe Ser Leu Ala Val Leu Ser Thr
          100          105          110
Leu Ile Met Ile Ile Tyr Pro Tyr Thr Lys Arg Phe Thr Phe Leu Cys
          115          120          125
His Trp Ile Leu Gly Leu Val Tyr Tyr Leu Ala Ile Leu Met Asn Phe
          130          135          140
Phe Ala Ile Ile Glu Thr Pro Ser Phe Ser Leu Phe Cys Met Ser Ser
145          150          155          160
Leu Leu Gly Ile Ser Phe Gly Met Ile Ile Ala Ala Asn Asp Ile Ile
          165          170          175
Tyr Ala Leu Gln Asp Val Glu Phe Asp Gln Lys Glu Gly Leu Phe Ser
          180          185          190
Ile Pro Ala Arg Phe Gly Thr Lys Gln Ala Ile Thr Ile Ala Ser Ala
          195          200          205
Asn Leu Ile Xaa Ser Ala Ile Ala Tyr Leu Leu Ile Gly Tyr Phe Val
210          215          220
Pro Asn Lys Thr Ile Phe Tyr Leu Cys Ser Leu Val Pro Leu Thr Gly
225          230          235          240
Ile Leu Arg Thr Ile Lys His Tyr Ser Leu Ile Asp Pro Arg Ala Lys
          245          250          255

```

Ser Thr Leu Gln Gln Asn Phe Phe Leu Gly Asn Leu Ser Leu Gly Ile  
                   260                  265                  270  
 Ala Phe Phe Ala Asn Met Ile Gly Leu Phe Leu Leu Arg Gly Ile Leu  
                   275                  280                  285

(2) INFORMATIONS POUR LA SEQ ID NO: 230:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(226769..227299)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 230:

Trp Glu Lys Phe Arg Thr Leu Pro Leu Leu Cys His Cys Arg Ser  
 1                  5                  10                  15  
 Tyr Lys Arg Ser Glu Ser Pro Trp Asn Ser Cys Asp Ser Leu Ser Gln  
                   20                  25                  30  
 Ser Glu Asn Ile Ala Phe Phe Gln Glu Ala His Met Ala Ser Leu Ile  
                   35                  40                  45  
 Arg Ser Leu Cys Glu Phe Thr Val Ala Tyr Lys His Thr Asp Pro Leu  
                   50                  55                  60  
 Gly Leu Asn Val Asn Phe Pro Ala Ser Ala Asp Ser Pro Trp Lys  
 65                  70                  75                  80  
 Gly Ile Arg Phe Thr Leu Ser Gly Asn Glu Phe Leu Phe Gly Ile Pro  
                   85                  90                  95  
 Arg Leu Val Arg Thr Glu Gly Asn Arg Arg Tyr Tyr Thr Leu Tyr Asp  
                   100                  105                  110  
 Met Arg Asp Lys Val Ser Glu Glu Phe Ser Glu Glu Tyr Leu Ala Leu  
                   115                  120                  125  
 Ala Asn Asn Tyr Ile Ser Ala Ala Pro Leu Val Ser Lys Asn Thr Pro  
                   130                  135                  140  
 Arg Ala Thr Leu Ser Glu Glu Glu Leu Ala Phe Leu Lys Asp Ser Phe  
 145                  150                  155                  160  
 Glu Gln Ser Val Leu Trp Lys Ala Ser Leu Asn Leu Glu Glu Asp Leu  
                   165                  170                  175  
 Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 231:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 152 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(227161..227616)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 231:



```

Met Thr Glu Thr Arg Arg Leu Arg Ile Leu Ile Thr Asn Asp Asp Gly
1          5          10          15
Ile Lys Ala Lys Gly Ile Ser Leu Leu Ile Ser Leu Leu Arg Glu Ala
20          25          30
Asp Phe Ala Asp Leu Tyr Val Val Ala Pro Leu Glu Glu Gln Ser Gly
35          40          45
Arg Ser Met Ala Phe Ser Leu Val Glu Pro Thr Ala Leu Glu Pro Phe
50          55          60
Asp Tyr Pro Gln Arg Val Gln Glu Ala Trp Ala Val Thr Gly Thr Pro
65          70          75          80
Val Asp Cys Val Lys Leu Ala Ile Gly Glu Leu Phe Lys Glu Asn Ala
85          90          95
Leu Asp Leu Ile Leu Ser Gly Ile Asn Asn Gly Lys Asn Ser Gly Arg
100          105          110
Cys Leu Tyr Tyr Ser Ala Thr Val Gly Ala Ile Arg Glu Ala Asn Leu
115          120          125
His Gly Ile Pro Ala Ile Val Phe Leu Lys Val Arg Ile Ser Leu Phe
130          135          140
Ser Lys Lys Leu Ile Trp Pro Pro
145          150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 232:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(227750..228457)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 232:

```

Lys Phe Ser Ala Gln Ser Val Tyr Thr His Ala Met Leu Gln Lys His
1          5          10          15
Thr Arg Ile Ala Val Ala Leu Ser Gly Gly Lys Asp Ser Leu Ser Leu
20          25          30
Leu Leu Met Leu Lys Ala Ile Ser Gly Arg Gly Phe Pro Glu Leu Thr
35          40          45
Ile His Ala Ile His Ile Gly Gly Lys Tyr Ser Cys Gly Ala Ala Val
50          55          60
Ser Gly Asn Tyr Leu Ser Ser Ile Cys Asp Lys Ile Gln Val Pro Leu
65          70          75          80
Ile Ser Ile Pro Ser Pro Tyr Glu Thr Glu Asn Pro Glu Cys Tyr Thr
85          90          95
Cys Ser Arg Ile Arg Arg Arg Leu Leu Phe Asp Thr Ala Lys Ala Val
100          105          110
Gly Ala Thr Ala Val Ala Phe Gly His His Arg Asp Asp Val Val Gln
115          120          125
Thr Thr Leu Met Asn Leu Leu His Lys Ala Glu Phe Ala Gly Met Leu
130          135          140
Pro Val Val Asp Met Val Asn Phe Gly Ile Thr Ile Leu Arg Pro Leu
145          150          155          160
Ile Phe Ile Pro Glu Asp Leu Ile Arg Lys Phe Ala Lys Glu Ser Gly
165          170          175

```

Phe	Ala	Arg	Ile	Thr	Cys	Arg	Cys	Pro	Val	Ile	Ser	Leu	Arg	Thr	Lys
			180					185				190			
Thr	Glu	Glu	Ala	Leu	Lys	Thr	Leu	Glu	Thr	Ile	Phe	Pro	Gln	Ala	Arg
		195					200					205			
His	Asn	Ile	Ala	Leu	Ala	Val	Arg	Glu	Thr	Gly	Leu	Ser	Lys	Ala	Asn
	210					215					220				
Arg	Val	Glu	Gln	Tyr	Asp	Ser	Leu	Leu	Thr	Glu	Thr				
225					230					235					

(2) INFORMATIONS POUR LA SEQ ID NO: 233:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 465 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(228607..230001)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 233:

Ala	Ser	Ser	Gln	Ile	Phe	Tyr	Pro	Ile	Gly	Tyr	Phe	Tyr	Cys	Arg	Asp
1				5					10					15	
Val	Ile	Pro	Cys	Ser	Ser	Tyr	Gln	Phe	Thr	Lys	Pro	Ser	Phe	Asn	Ser
			20					25					30		
Lys	Thr	Trp	Leu	Ile	Tyr	Ser	Ile	Leu	Leu	Ser	Val	Ala	Val	Ala	Cys
		35					40					45			
Phe	Met	Ile	Pro	Tyr	Ala	Leu	Ile	Ala	Ala	Glu	Leu	Ala	Ser	Phe	Lys
	50					55					60				
Pro	Gln	Gly	Ile	Tyr	Val	Trp	Thr	Arg	Asp	Ala	Leu	Gly	Lys	Arg	Trp
65					70				75						80
Gly	Phe	Phe	Ala	Ile	Trp	Met	Gln	Trp	Phe	His	Asn	Met	Thr	Trp	Tyr
				85					90					95	
Pro	Ala	Met	Leu	Ala	Phe	Ile	Ala	Ser	Thr	Leu	Val	Tyr	Gln	Ile	Ser
			100					105					110		
Pro	Asp	Leu	Ala	Asn	Asn	Arg	Leu	Tyr	Leu	Ser	Ser	Val	Ile	Leu	Leu
		115					120					125			
Gly	Phe	Trp	Gly	Leu	Thr	Phe	Phe	Asn	Phe	Leu	Gly	Ile	Gly	Thr	Ser
	130					135					140				
Ala	Leu	Phe	Ser	Ser	Ile	Cys	Val	Ile	Val	Gly	Thr	Leu	Ile	Pro	Gly
145					150					155					160
Ala	Ile	Leu	Val	Ala	Phe	Ala	Ala	Tyr	Trp	Ile	Gln	Gly	Gly	Asn	Pro
				165					170					175	
Ile	Ala	Ile	Asn	Phe	Ser	Trp	Ser	Glu	Leu	Leu	Pro	Asp	Phe	Ser	Ser
			180					185					190		
Pro	Ser	Ser	Phe	Val	Leu	Leu	Ser	Gly	Met	Leu	Leu	Ala	Leu	Cys	Gly
		195					200					205			
Leu	Glu	Ala	Asn	Ala	Asn	Leu	Ala	Ser	Asp	Met	Glu	Asp	Pro	Lys	Arg
	210					215					220				
Asn	Tyr	Pro	Lys	Ala	Val	Phe	Ile	Gly	Ala	Val	Ser	Thr	Leu	Ala	Ile
225					230					235					240
Leu	Val	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ile	Val	Ile	Pro	Lys	Glu	Glu
				245					250					255	
Ile	Ser	Leu	Val	Ser	Gly	Leu	Ile	Arg	Ala	Phe	Ser	Leu	Phe	Phe	Glu
			260					265					270		
Lys	Tyr	Asn	Leu	Ser	Trp	Met	Thr	Gly	Ile	Ile	Val	Ala	Met	Thr	Ile

Ala	Gly	275	Leu	Gly	Glu	Leu	280	Asn	Ala	Trp	Met	Phe	285	Ala	Gly	Thr	Lys
290						295						300					
Gly	Leu	Phe	Ile	Ser	Thr	Gln	Asn	Asp	Cys	Leu	Pro	Lys	Ile	Phe	Lys		
305					310					315					320		
Lys	Thr	Asn	Ser	Arg	Asp	Val	Pro	Thr	Asn	Leu	Met	Leu	Phe	Gln	Ala		
				325					330					335			
Ile	Val	Val	Thr	Leu	Phe	Thr	Phe	Ile	Phe	Val	Tyr	Val	Asp	Ser	Ala		
			340				345						350				
Asp	Leu	Ala	Tyr	Trp	Ile	Leu	Ser	Ala	Leu	Ser	Leu	Gln	Met	Tyr	Leu		
		355					360					365					
Val	Met	Tyr	Ile	Cys	Leu	Phe	Ile	Val	Gly	Pro	Val	Leu	Arg	Ile	Lys		
370						375					380						
Glu	Pro	Lys	Ala	Gln	Arg	Leu	Tyr	Ser	Val	Pro	Gly	Lys	Leu	Val	Gly		
385					390					395					400		
Met	Cys	Val	Leu	Ser	Thr	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Phe	Ala	Leu		
				405					410					415			
Gly	Ile	Ser	Phe	Leu	Pro	Pro	Gln	Glu	Val	Val	Ser	Phe	Ser	Thr	Met		
			420					425					430				
Gly	Gly	Asn	Phe	Gly	Tyr	Thr	Ala	Leu	Leu	Leu	Leu	Ala	Phe	Val	Ile		
		435					440					445					
Asn	Cys	Cys	Ile	Pro	Phe	Gly	Met	Tyr	Tyr	Ser	His	Lys	Lys	Leu	Ile		
450						455					460						
Lys																	
465																	

(2) INFORMATIONS POUR LA SEQ ID NO: 234:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 308 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(230151..231074)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 234:

Glu	His	Leu	Arg	Met	Thr	Thr	Ile	Phe	Asp	Leu	Leu	Gly	Lys	Asp	Ala
1				5					10					15	
Asp	Tyr	Leu	Leu	Asn	His	Lys	Cys	Val	Ile	Lys	Lys	Glu	Ala	Leu	Thr
		20					25						30		
Leu	Pro	Ser	Gly	Asp	Phe	Val	Ser	Arg	Val	Phe	Ala	Glu	Ser	Asp	Arg
		35					40					45			
Asn	Asn	Arg	Val	Leu	Arg	Ser	Leu	Gln	Gln	Met	Phe	Ser	Tyr	Gly	Arg
	50					55					60				
Leu	Gly	Gly	Thr	Gly	Tyr	Leu	Ser	Ile	Leu	Pro	Val	Asp	Gln	Gly	Val
65					70				75					80	
Glu	His	Thr	Ala	Gly	Ala	Ser	Phe	Ala	Lys	Asn	Pro	Met	Tyr	Phe	Asp
			85					90					95		
Pro	Glu	Asn	Ile	Val	Arg	Leu	Ala	Met	Glu	Ala	Gly	Cys	Ser	Ala	Val
		100					105					110			
Ala	Ser	Ser	Tyr	Gly	Val	Leu	Ser	Ile	Leu	Ala	Arg	Arg	Tyr	Ala	His
		115					120					125			
Lys	Ile	Pro	Phe	Leu	Leu	Lys	Leu	Asn	His	Asn	Glu	Leu	Leu	Ser	Tyr
130						135					140				

Pro	Thr	Thr	Tyr	His	Gln	Ile	Phe	Phe	Ser	Gln	Val	Glu	Asp	Ala	Tyr
145					150					155					160
Asn	Met	Gly	Ala	Val	Ala	Val	Gly	Ala	Thr	Ile	Tyr	Phe	Gly	Ser	Glu
				165					170					175	
Ser	Ser	Ser	Glu	Glu	Ile	Val	Ala	Val	Ala	Glu	Ala	Phe	Ala	Arg	Ala
			180					185					190		
Arg	Glu	Leu	Gly	Leu	Ala	Thr	Val	Leu	Trp	Cys	Tyr	Leu	Arg	Asn	Pro
	195						200					205			
His	Phe	Val	Val	Asn	Asn	Val	Asp	Tyr	His	Thr	Ala	Ala	Asp	Leu	Thr
	210					215					220				
Gly	Gln	Ala	Asp	His	Leu	Gly	Ala	Thr	Leu	Gly	Ala	Asp	Ile	Val	Lys
225					230					235					240
Gln	Lys	Leu	Pro	Thr	Leu	Gln	Gly	Gly	Phe	Lys	Thr	Ile	Asn	Phe	Ser
				245					250					255	
Lys	Thr	Asp	Asp	Leu	Val	Tyr	Ser	Glu	Leu	Ser	Ser	Asn	His	Pro	Ile
			260					265					270		
Asp	Leu	Cys	Arg	Tyr	Gln	Val	Leu	Asn	Ser	Tyr	Cys	Gly	Lys	Val	Gly
		275					280					285			
Leu	Ile	Asn	Ser	Gly	Ala	Leu	Leu	Gly	Lys	Met	Thr	Leu	Leu	Lys	Gln
	290					295					300				
Leu	Lys	Gln	Gln												
305															

## (2) INFORMATIONS POUR LA SEQ ID NO: 235:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 553 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 231348..233006

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 235:

Lys	Glu	Lys	Ile	Val	Phe	Met	Arg	Thr	Asp	Ser	Pro	Leu	Asn	Pro	Pro
1			5						10					15	
Asp	Ser	Thr	Arg	Gly	Val	Phe	Gln	Phe	Leu	Glu	Thr	Gln	Cys	Asp	Arg
			20					25					30		
Ala	Met	Ala	Arg	Ser	Arg	Gln	Ser	Gln	Phe	Ile	Gly	Leu	Val	Ser	Ala
		35				40						45			
Val	Ala	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Val	Val	Ala	Leu	Ser	Val	
	50				55					60					
Pro	Gly	Phe	Pro	Val	Ala	Ala	Ser	Ile	Val	Val	Gly	Val	Leu	Phe	Ala
65				70						75				80	
Leu	Ser	Ile	Val	Ala	Leu	Thr	Ala	Ser	Phe	Leu	Val	Tyr	Ile	Ala	Asn
			85					90					95		
Ala	Lys	Leu	Val	Ala	Ile	Arg	Ile	Lys	Phe	Leu	Ser	Ser	Gly	Leu	Gln
			100					105					110		
Asp	His	Phe	Ser	Glu	Ser	Pro	Ile	Leu	Gly	Thr	Leu	Arg	Lys	Gly	Arg
		115					120					125			
Gly	Ala	Ser	Ile	Pro	Leu	Ile	Ser	Gly	Gln	Ala	Asp	Asp	Ser	Leu	Pro
	130				135						140				
Asn	Arg	Ile	Gly	Ile	Lys	Lys	Ser	Ala	Glu	Met	Arg	Val	Leu	Gln	Lys
145				150						155					160
Gly	Ile	Gly	Thr	Asp	Tyr	Lys	Lys	Tyr	Lys	Gln	His	Leu	Asp	Arg	Val

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 233134..233829

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 236:

```

Ser Asp Lys Phe Phe Pro Ile Lys Gln Lys Leu Ala Leu Glu Ala Val
1      5      10      15
Ala Leu Val Glu Pro Gly Met Cys Val Gly Leu Gly Ser Gly Ser Thr
20      25      30
Ala Arg Glu Phe Ile Leu Ala Leu Gly Asp Arg Val Arg Thr Glu Arg
35      40      45
Leu Val Ile Thr Ala Val Ala Ser Ser Arg Ile Ser Gln Leu Leu Ala
50      55      60
Glu Ala Val Gly Ile Pro Leu Leu Asp His Ser Leu Leu Gln Asp Val
65      70      75      80
Asp Leu Val Val Asp Gly Ala Asp Glu Val Asp Pro Cys Leu Arg Met
85      90      95
Ile Lys Gly Gly Gly Gly Ala Leu Phe Arg Glu Lys Ile Leu Leu Gln
100     105     110
Ser Gly Lys Arg Asn Val Ile Leu Val Asp Glu Arg Lys Leu Val Pro
115     120     125
Thr Leu Gly Lys Phe Ser Leu Pro Ile Glu Ile Ala Pro Phe Gly Cys
130     135     140
Ser Ser Val Gln Arg Ile Leu Asn Lys Gln Gly Tyr Phe Gly Glu Trp
145     150     155     160
Arg Glu Thr Ser Ala Gly Glu Arg Phe Ile Thr Asp Asn Gly Asn Tyr
165     170     175
Ile Tyr Asp Val Arg Thr Pro Asp Ser Tyr Ala Asn Pro Glu Glu Asp
180     185     190
Met Ile Arg Leu Leu Gln Ile Arg Gly Ile Ile Asp Val Gly Phe Val
195     200     205
Ile Ala Lys Ala Glu Val Trp Val Gly Tyr Ala Asp Gly Ser Ile Val
210     215     220
Arg Lys Lys Glu His Asn Glu Tyr
225     230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 237:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 233855..234265

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 237:

```

Ser Leu Ile Leu Ile Asn Phe Tyr Lys Leu Val Ser Phe Arg Asn Tyr
1      5      10      15
Ala Gly Ile Ile Leu Gly Thr Asp Glu Lys Gln Phe Ala Ile Tyr Gly
20      25      30
His Ala Ser Met Asp Thr Ala Phe Lys Lys Arg Glu Asp Leu Ala Ala
35      40      45
Glu Glu Glu Arg Ser Arg Pro Ser Thr His Asp Val Leu Asn Phe Val

```

50		55		60
Leu Thr Ser Phe Asp	Leu Ser Val Val Arg	Val Val Ile Thr Glu Tyr		
65	70	75		80
Lys Asp Asn Val Phe Tyr Ser Arg Leu Phe Leu Glu Gln Lys Arg Gly				
	85	90		95
Asp Arg Leu Tyr Ile Ala Asp Ile Asp Ala Arg Pro Ser Asp Ser Ile				
	100	105		110
Pro Leu Ala Ile Lys Tyr Gln Val Pro Ile Leu Cys Val Lys Ser Ile				
	115	120		125
Phe Asp Glu Ala Ile Pro Tyr Glu Asp				
130		135		

(2) INFORMATIONS POUR LA SEQ ID NO: 238:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 191 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 234282..234854

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 238:

Asp Val Met Thr Lys Leu Pro Tyr Ala Leu Leu Asp Lys Gly Ser Leu				
1	5	10		15
Leu Val Ala Ser Pro Asp Val Asn Gly Gly Ile Phe Ser Arg Ser Val				
	20	25		30
Val Leu Leu Cys Glu His Ser Pro Asn Gly Ser Phe Gly Leu Ile Leu				
	35	40		45
Asn Lys Ile Leu Glu Ile Asp Ser Pro Glu Glu Ile Phe Pro Leu Asp				
	50	55		60
His Phe Asp Glu Ser Lys Val Arg Phe Cys Met Gly Gly Pro Leu Gln				
65	70	75		80
Ala Asn Gln Ile Met Leu Leu His Thr Ser Pro Asp Ser Ala Asn Ser				
	85	90		95
Ser Ile Glu Ile Cys Pro Ser Val Phe Leu Gly Gly Asp Phe Ser Phe				
	100	105		110
Ala Gly Glu Lys Glu Gly Arg Thr Arg Asp Asp Lys Met Leu Leu Cys				
	115	120		125
Phe Gly Tyr Ser Gly Trp Gln Gly Gly Gln Leu Glu Lys Glu Phe Leu				
	130	135		140
Glu Gly Leu Trp Phe Leu Ala Pro Ser Ser Gln Glu Ile Ile Phe Thr				
145	150	155		160
Asp Ala Pro Glu Arg Met Trp Ser Asp Val Leu Gln His Leu Gly Gly				
	165	170		175
Arg Phe Ala Ser Leu Ser Thr Ile Pro Glu Asn Leu Leu Leu Asn				
	180	185		190

(2) INFORMATIONS POUR LA SEQ ID NO: 239:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 297 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(235227..236117)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 239:

Met	Ser	His	Leu	Phe	Ser	Lys	Ala	Cys	Gln	Tyr	Phe	Pro	Gly	Gly	Val
1				5					10					15	
Asn	Ser	Pro	Val	Arg	Ala	Cys	Arg	Ala	Val	Asn	Ile	Thr	Pro	Pro	Ile
			20					25					30		
Val	Ala	Arg	Ala	Ser	Lys	Glu	Val	Phe	Ile	Asp	Ser	Leu	Asp	Lys	Thr
		35					40					45			
Phe	Ile	Asp	Phe	Cys	Gly	Ser	Trp	Gly	Ser	Leu	Ile	His	Gly	His	Ser
	50				55					60					
His	Pro	Lys	Ile	Cys	Ala	Ala	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Gly	Ser
65				70					75						80
Ser	Tyr	Gly	Leu	Thr	Ser	Glu	Gln	Glu	Ile	Leu	Phe	Ala	Glu	Glu	Ile
			85					90					95		
Phe	Ser	Tyr	Leu	Gly	Leu	Glu	Thr	Asn	Tyr	Lys	Ile	Arg	Phe	Met	Ser
		100						105					110		
Thr	Gly	Ser	Glu	Ala	Thr	Met	Thr	Ala	Val	Arg	Leu	Ala	Arg	Gly	Ile
		115					120					125			
Thr	Gly	Arg	Pro	Ile	Ile	Ile	Lys	Phe	Leu	Gly	Cys	Tyr	His	Gly	His
	130					135					140				
Ala	Asp	Thr	Phe	Leu	Gln	Glu	Lys	Pro	Phe	Ser	His	Thr	Ser	Leu	Asp
145				150					155						160
Thr	Leu	Asp	Leu	Ala	His	Pro	Leu	Thr	Leu	Ser	Leu	Pro	Phe	Asn	Asp
			165					170					175		
Phe	Pro	Leu	Phe	Gln	Thr	Val	Met	Asn	Ser	Leu	Gly	His	Lys	Val	Ala
		180						185					190		
Gly	Val	Ile	Phe	Glu	Pro	Val	Cys	Ala	Asn	Met	Gly	Val	Ile	Leu	Pro
	195						200					205			
Val	Pro	Asp	Phe	Ile	Glu	Gly	Val	Ile	Gln	Thr	Cys	Gln	Gln	Thr	Gly
	210				215						220				
Ser	Phe	Ser	Ile	Met	Asp	Glu	Val	Val	Thr	Gly	Phe	Arg	Val	Ala	Gln
225				230					235						240
Gly	Gly	Ala	Ala	Ala	Leu	Tyr	His	Val	Lys	Pro	Asp	Ile	Leu	Val	Phe
			245					250					255		
Gly	Lys	Ile	Leu	Gly	Gly	Gly	Leu	Pro	Ala	Ser	Ala	Val	Val	Ala	Pro
		260					265					270			
Lys	Asp	Ile	Met	Asp	His	Leu	Ala	Pro	Glu	Glu	Lys	Ser	Ser	Lys	Leu
	275					280						285			
Glu	His	Phe	Gln	Glu	Ile	Leu	Trp	Leu							
	290					295									

(2) INFORMATIONS POUR LA SEQ ID NO: 240:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 632 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 236314..238209



(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 240:

Met	Arg	Tyr	Asp	Pro	Gly	Leu	Ile	Glu	Glu	Lys	Trp	Gln	Lys	Phe	Trp	1	5	10	15
Lys	Asn	Glu	Gln	Val	Phe	Lys	Ala	Glu	Glu	Asp	Glu	Thr	Lys	Thr	Lys	20	25	30	
Tyr	Tyr	Val	Leu	Asp	Met	Phe	Pro	Tyr	Pro	Ser	Gly	Ala	Gly	Leu	His	35	40	45	
Val	Gly	His	Leu	Ile	Gly	Tyr	Thr	Ala	Thr	Asp	Ile	Val	Ala	Arg	Cys	50	55	60	
Lys	Arg	Ala	Gln	Gly	Phe	Ser	Val	Leu	His	Pro	Met	Gly	Trp	Asp	Ser	65	70	75	80
Phe	Gly	Leu	Pro	Ala	Glu	Gln	Tyr	Ala	Ile	Arg	Thr	Gly	Thr	His	Pro	85	90	95	
Arg	Glu	Thr	Thr	Glu	Lys	Asn	Ile	Ala	Asn	Phe	Lys	Lys	Gln	Leu	Thr	100	105	110	
Ala	Met	Gly	Phe	Ser	Tyr	Asp	Glu	Ser	Arg	Glu	Phe	Ala	Thr	Ser	Asp	115	120	125	
Pro	Glu	Tyr	Tyr	Lys	Trp	Thr	Gln	Lys	Leu	Phe	Leu	Ile	Leu	Tyr	Glu	130	135	140	
Lys	Gly	Leu	Ala	Tyr	Met	Ala	Asp	Met	Ala	Val	Asn	Tyr	Cys	Pro	Glu	145	150	155	160
Leu	Gly	Thr	Val	Leu	Ser	Asn	Glu	Glu	Ile	Glu	Asn	Gly	Phe	Ser	Val	165	170	175	
Asp	Gly	Gly	Tyr	Pro	Val	Glu	Arg	Arg	Met	Leu	Arg	Gln	Trp	Val	Leu	180	185	190	
Arg	Ile	Thr	Ala	Phe	Ala	Asp	Gln	Leu	Leu	Glu	Gly	Leu	Asp	Glu	Leu	195	200	205	
Asp	Trp	Pro	Glu	Ser	Val	Lys	Gln	Leu	Gln	Lys	Asn	Trp	Ile	Gly	Lys	210	215	220	
Ser	Ser	Gly	Ala	Ser	Val	Asn	Phe	Ala	Thr	Glu	His	Gly	Ala	Ile	Glu	225	230	235	240
Val	Phe	Thr	Thr	Arg	Pro	Asp	Thr	Leu	Ile	Gly	Val	Ser	Phe	Leu	Ala	245	250	255	
Leu	Ala	Pro	Glu	His	Pro	Leu	Val	Asp	Leu	Leu	Thr	Ser	Asp	Glu	Gln	260	265	270	
Lys	Ala	Val	Val	Ala	Gln	Tyr	Ile	Lys	Glu	Thr	Gln	Ser	Lys	Ser	Glu	275	280	285	
Arg	Asp	Arg	Ile	Ser	Glu	Met	Lys	Thr	Lys	Ser	Gly	Val	Phe	Thr	Gly	290	295	300	
Ser	Tyr	Ala	Lys	His	Pro	Val	Thr	His	Glu	Leu	Ile	Pro	Ile	Trp	Ile	305	310	315	320
Ala	Asp	Tyr	Val	Leu	Met	Gly	Phe	Gly	Ser	Gly	Ala	Val	Met	Gly	Val	325	330	335	
Pro	Ala	His	Asp	Glu	Arg	Asp	Leu	Leu	Phe	Ala	Glu	Gln	Phe	Asn	Leu	340	345	350	
Pro	Val	Val	Ser	Val	Leu	Asn	Glu	Gly	Val	Cys	Ile	Asn	Ser	Cys		355	360	365	
Cys	Glu	Gly	Phe	His	Leu	Asp	Gly	Leu	Ser	Gly	Glu	Glu	Ala	Lys	Gln	370	375	380	
Tyr	Val	Ile	Asn	Phe	Leu	Glu	Glu	Asn	His	Leu	Gly	Ala	Ala	Lys	Ile	385	390	395	400
Ala	Tyr	Lys	Leu	Arg	Asp	Trp	Leu	Phe	Ser	Arg	Gln	Arg	Tyr	Trp	Gly	405	410	415	
Glu	Pro	Ile	Pro	Ile	Ile	His	Phe	Glu	Asp	Gly	Ser	Cys	Arg	Pro	Leu	420	425	430	
Arg	Asp	Asp	Glu	Leu	Pro	Leu	Leu	Pro	Pro	Glu	Ile	Gln	Asp	Tyr	Arg	435	440	445	

```

Pro Glu Gly Val Gly Gln Gly Pro Leu Ala Lys Val Arg Glu Trp Val
  450                      455                      460
Gln Val Phe Asp Thr Glu Thr Gln Arg Ala Gly Lys Arg Glu Thr His
465                      470                      475                      480
Thr Met Pro Gln Trp Ala Gly Ser Cys Trp Tyr Tyr Leu Arg Phe Cys
                      485                      490                      495
Asp Ala His Asn Ser Ala Ala Pro Trp Ala Lys Glu Lys Glu Gln Tyr
                      500                      505                      510
Trp Met Pro Val Asp Leu Tyr Ile Gly Gly Ala Glu His Ala Val Leu
                      515                      520                      525
His Leu Leu Tyr Ala Arg Phe Trp His Gln Val Phe Tyr Glu Ala Gly
                      530                      535                      540
Ile Val Ser Thr Pro Glu Pro Phe Lys Lys Leu Val Asn Gln Gly Leu
545                      550                      555                      560
Val Leu Ala Thr Ser Tyr Arg Ile Pro Gly Lys Gly Tyr Ile Tyr Pro
                      565                      570                      575
Glu Thr Ala Lys Glu Glu Asn Gly Lys Trp Val Ala Pro Ser Gly Glu
                      580                      585                      590
Glu Leu Asp Val Arg Gln Glu Lys Met Ser Lys Ser Lys Leu Asn Gly
                      595                      600                      605
Val Asp Pro Gln Ile Leu Ile Asp Glu Phe Gly Leu Thr Leu Phe Gly
                      610                      615                      620
Cys Thr Gln Cys Phe Gln Gly Leu
625                      630

```

(2) INFORMATIONS POUR LA SEQ ID NO: 241:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 202 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 238164..238769

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 241:

```

Ile Trp Thr Asp Ala Val Arg Met Tyr Ala Met Phe Ser Gly Pro Leu
1                      5                      10                      15
Asp Lys Asn Lys Leu Trp Ser Asn Gln Gly Val Ala Gly Cys Arg Arg
                      20                      25                      30
Phe Leu Asn Arg Phe Tyr Glu Met Val Ser Ser Asp Arg Val Lys Glu
                      35                      40                      45
Asp Asn Asn Phe Glu Gly Leu Ser Leu Ala His Lys Leu Val Gln Arg
50                      55                      60
Val Thr Asp Ala Ile Glu Lys Leu Ser Leu Asn Thr Ile Pro Ser Ser
65                      70                      75                      80
Phe Met Glu Phe Ile Asn Asp Phe Val Lys Leu Ala Val Tyr Pro Lys
                      85                      90                      95
Ser Ala Val Glu Met Ala Val Arg Ala Leu Ala Pro Ile Ala Pro His
100                      105                      110
Ile Ser Glu Glu Leu Trp Val Leu Leu Gly Asn Ser Pro Gly Val Gln
115                      120                      125
Lys Ser Gly Trp Pro Ser Val Leu Pro Glu Tyr Leu Glu Glu Gln Thr
130                      135                      140
Val Thr Ile Val Val Gln Val Asn Gly Lys Leu Arg Ala Arg Leu Asp

```

145		150		155		160
Ile Met Lys Asp Ala Ser Lys Glu Glu Val Leu Ala Leu Ala Arg Glu						
	165		170		175	
Ser Ala Ser Lys Tyr Leu Glu Gly Cys Glu Val Lys Lys Ala Ile Phe						
	180		185		190	
Val Pro Ala Arg Leu Val Asn Phe Val Val						
	195		200			

(2) INFORMATIONS POUR LA SEQ ID NO: 242:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 431 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 238769..240061

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 242:

Met	Ile	Arg	Arg	Trp	Leu	Thr	Ser	Arg	Leu	Tyr	Asp	Ala	Phe	Leu	Val
1				5					10					15	
Cys	Ala	Phe	Phe	Val	Ser	Ala	Pro	Arg	Ile	Phe	Tyr	Lys	Val	Phe	Phe
			20					25					30		
His	Gly	Lys	Tyr	Ile	Asp	Ser	Trp	Lys	Ile	Arg	Phe	Gly	Val	Gln	Lys
		35					40					45			
Pro	Phe	Val	Lys	Gly	Glu	Gly	Pro	Leu	Val	Trp	Phe	His	Gly	Ala	Ser
	50					55					60				
Val	Gly	Glu	Val	Ser	Leu	Leu	Ala	Pro	Leu	Leu	Asn	Arg	Trp	Arg	Glu
65					70					75					80
Glu	Phe	Pro	Glu	Trp	Arg	Phe	Val	Val	Thr	Thr	Cys	Ser	Glu	Ala	Gly
				85					90					95	
Val	His	Thr	Ala	Arg	Arg	Leu	Tyr	Glu	Ser	Leu	Gly	Ala	Thr	Val	Phe
			100					105					110		
Val	Leu	Pro	Leu	Asp	Leu	Ser	Cys	Ile	Ile	Lys	Ser	Val	Val	Arg	Lys
		115					120					125			
Leu	Ala	Pro	Asp	Ile	Val	Ile	Phe	Ser	Glu	Gly	Asp	Cys	Trp	Leu	His
	130					135					140				
Phe	Leu	Thr	Glu	Ser	Lys	Arg	Leu	Gly	Ala	Lys	Ala	Phe	Leu	Ile	Asn
145					150				155						160
Gly	Lys	Leu	Ser	Glu	His	Ser	Cys	Lys	Arg	Phe	Ser	Phe	Leu	Lys	Arg
			165					170						175	
Leu	Gly	Arg	Asn	Tyr	Phe	Ala	Pro	Leu	Asp	Leu	Leu	Ile	Leu	Gln	Asp
			180					185					190		
Glu	Leu	Tyr	Lys	Gln	Arg	Phe	Met	Gln	Ile	Gly	Ile	Ser	Ser	Asp	Lys
		195					200					205			
Ile	His	Val	Thr	Gly	Asn	Met	Lys	Thr	Phe	Ile	Glu	Ser	Ser	Leu	Ala
	210					215					220				
Thr	Asn	Arg	Arg	Asp	Phe	Trp	Arg	Ala	Lys	Leu	Gln	Ile	Ser	Ser	Gln
225					230					235					240
Asp	Arg	Leu	Ile	Val	Leu	Gly	Ser	Met	His	Pro	Lys	Asp	Val	Glu	Val
			245					250						255	
Trp	Ala	Glu	Val	Val	Ser	His	Phe	His	Asn	Ser	Ser	Thr	Lys	Ile	Leu
			260				265						270		
Trp	Val	Pro	Arg	His	Leu	Glu	Lys	Leu	Lys	Glu	His	Ala	Lys	Leu	Leu
		275					280					285			

Glu	Lys	Ala	Gly	Ile	Leu	Phe	Gly	Leu	Trp	Ser	Gln	Gly	Ala	Ser	Phe
290						295					300				
Arg	Gln	Tyr	Asn	Ser	Leu	Ile	Met	Asp	Ala	Met	Gly	Val	Leu	Lys	Asp
305					310					315					320
Ile	Tyr	Ser	Ala	Ala	Asp	Ile	Ala	Phe	Val	Gly	Gly	Thr	Phe	Asp	Pro
				325					330					335	
Ser	Val	Gly	Gly	His	Asn	Leu	Leu	Glu	Pro	Leu	Gln	Lys	Glu	Ala	Pro
			340					345					350		
Leu	Met	Phe	Gly	Pro	Tyr	Ile	Tyr	Ser	Gln	Ser	Val	Leu	Ala	Glu	Arg
		355					360					365			
Leu	Arg	Glu	Lys	Glu	Ala	Gly	Leu	Ser	Val	Asn	Lys	Glu	Thr	Leu	Leu
		370				375					380				
Asp	Val	Val	Thr	Asp	Leu	Leu	Gln	Asn	Glu	Lys	Asn	Arg	Gln	Ala	Tyr
385					390					395					400
Ile	Glu	Lys	Gly	Lys	Ser	Phe	Leu	Lys	Gln	Glu	Glu	Asn	Ser	Phe	Gln
				405					410					415	
Gln	Thr	Trp	Glu	Ile	Leu	Lys	Ser	Gln	Ile	Thr	Cys	Met	Lys	Ile	
			420					425					430		

(2) INFORMATIONS POUR LA SEQ ID NO: 243:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 556 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(240313..241980)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 243:

Lys	Thr	Ser	Ile	Ile	Gly	His	Thr	Met	Glu	Leu	Leu	Ser	Val	Asn	Lys
1			5					10						15	
Ser	Tyr	Phe	Glu	Leu	Gln	Arg	Leu	His	Tyr	Arg	Pro	Asp	Thr	Leu	Ser
			20					25					30		
Leu	Leu	Asn	Ser	Leu	Cys	Ser	Met	His	Ile	Gln	Glu	Lys	Pro	Ser	Ser
		35					40					45			
Glu	Pro	Ala	Ser	Asp	Leu	Leu	Ala	Lys	His	Ile	Pro	His	Leu	Cys	Ala
		50					55				60				
Leu	Pro	Asp	Leu	Thr	Leu	Gln	Lys	Asp	Ala	Pro	Ser	Ser	Ser	Glu	Pro
65				70						75					80
Leu	Arg	Ile	Gly	Val	Leu	Leu	Ser	Gly	Gly	Gln	Ala	Pro	Gly	Gly	His
			85					90						95	
Asn	Val	Val	Ile	Gly	Leu	Phe	Glu	Gly	Leu	Arg	Ala	Phe	Asn	Lys	Glu
			100					105					110		
Thr	Lys	Leu	Phe	Gly	Phe	Ile	Lys	Gly	Pro	Leu	Gly	Leu	Ile	Arg	Gly
			115				120						125		
Leu	Tyr	Lys	Asp	Leu	Asp	Ile	Ser	Val	Ile	Tyr	Asp	Tyr	Tyr	Asn	Ala
		130				135					140				
Gly	Gly	Phe	Asp	Met	Leu	Ser	Ser	Ser	Arg	Glu	Lys	Ile	Lys	Thr	Lys
145				150						155					160
Glu	Gln	Lys	Ser	Ala	Ile	Leu	Ala	Thr	Val	Lys	Lys	Met	Lys	Leu	His
			165						170					175	
Gly	Leu	Leu	Ile	Val	Gly	Gly	Asp	Asn	Ser	Asn	Thr	Asp	Thr	Ala	Met
			180					185					190		
Leu	Ala	Glu	Tyr	Phe	Ile	Glu	His	Asn	Cys	Pro	Thr	Ala	Val	Ile	Gly

(viii) POSITION DANS LE GENOME: complement(241941..242846)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 244:

```

Met Ala Lys Thr Leu Phe Tyr Leu Phe Arg Asn Pro Arg Ser Gly Leu
1      5      10      15
Leu Thr Ile Ser Met Asp Ile Thr Lys Glu Leu Pro Phe Ile Met Met
      20      25      30
Gln Gln Pro His Tyr Phe Xaa His Ser Lys Lys Ile Phe Glu Ile Pro
      35      40      45
Leu Leu Asp Asn Val Thr Ser Leu Gly Val Leu His Ile Pro His Ser
      50      55      60
Gln Glu Lys Thr Phe Pro Leu Val Ile Val Leu His Gly Leu Ala Ser
65      70      75      80
Ser Lys Ile Gly Thr Lys Arg Ser Tyr Leu His Leu Ala Asn Gln Leu
      85      90      95
Val Gln Glu Gly Ile Gly Val Leu Arg Val Asp Leu Pro Gly His Gly
      100     105     110
Asp Ser Glu Gly Phe Ile His Glu Phe Ser Leu Thr Asp Tyr Ile Gln
      115     120     125
Ala Ser Gln Lys Ile Ile Gln Phe Gly Leu Ser Leu Pro Gln Ala Asn
      130     135     140
His Ser Val Ala Leu Phe Gly Ser Ser Leu Gly Gly Ser Leu Ser Leu
145      150     155     160
Leu Asn Leu Pro Tyr Phe Pro Glu Ile Gln His Ala Ala Ile Trp Thr
      165     170     175
Pro Thr Ile Gln Gly Ala Leu Trp Leu Glu Asp Thr Met Gln Ser Met
      180     185     190
Ser Pro Ser Leu Gln Leu Pro Pro Asp Asn Phe Ser Tyr Gln Gly Ile
      195     200     205
Pro Leu Gly Lys Lys Phe Cys Ser Gln Phe Ile Glu Leu Asp Thr Val
      210     215     220
Asp Ala Leu Ser Lys Ile Thr Gln Glu Val Ser Ile Leu Tyr Leu Gln
225      230     235     240
Gly Glu Asp Asp Ala Val Val Ser Leu Arg His Gln Ala Leu Phe Ala
      245     250     255
Lys Thr Phe Thr Gly Lys Ala Ser Tyr Arg Thr Tyr Pro Lys Met Thr
      260     265     270
His Gln Leu Cys Ile Tyr Ser Glu Ala Phe Gln Asp Leu Val Asp Trp
      275     280     285
Leu Lys His Gln Leu Leu Gly Thr Pro Trp Ser Tyr Ser Leu
      290     295     300

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 245:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 561 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(242798..244480)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 245:

```

Ala Asn Val Phe Glu Gln Lys Leu Met Ser Ser Asn Lys His Ala Ser
1      5      10      15
Leu Cys Gln Lys Thr Pro Ser Leu Cys Arg Glu Leu Gln Lys Ala Pro

```

						20											25																30
Ala	Leu	Leu	Leu	Thr	Glu	Asp	Ile	Arg	Phe	Lys	Ala	Leu	Leu	Asn	Glu																		
		35					40					45																					
Arg	Ile	Asp	Ser	Val	Ala	Glu	Leu	Phe	Pro	Cys	Thr	Tyr	Asn	Ser	Pro																		
	50					55					60																						
Tyr	Tyr	Lys	Phe	Ile	Ser	Lys	Ser	Asp	Leu	Ser	Ala	Glu	Thr	Phe	Pro																		
65					70					75																							
Leu	Lys	Val	Gly	Val	Met	Leu	Ser	Gly	Gly	Pro	Ala	Pro	Gly	Gly	His																		
				85				90																									
Asn	Val	Ile	Leu	Gly	Leu	Leu	His	Ser	Ile	Lys	Lys	Leu	His	Pro	Asp																		
		100						105																									
Ser	Gln	Leu	Leu	Gly	Phe	Ile	Arg	Asn	Gly	Glu	Gly	Leu	Leu	Asn	Asn																		
	115						120					125																					
Asn	Thr	Val	Glu	Ile	Thr	Asp	Glu	Phe	Ile	Glu	Glu	Phe	Arg	Asn	Ser																		
	130					135					140																						
Gly	Gly	Phe	Asn	Cys	Ile	Gly	Thr	Gly	Arg	Thr	Asn	Ile	Ile	Thr	Glu																		
145					150					155																							
Glu	Asn	Lys	Ala	Arg	Cys	Leu	Gln	Thr	Ala	Asn	Glu	Leu	Asp	Leu	Asp																		
				165					170																								
Gly	Leu	Val	Ile	Ile	Gly	Gly	Asp	Gly	Ser	Asn	Thr	Ala	Thr	Ala	Ile																		
			180					185																									
Leu	Ala	Glu	Tyr	Phe	Ala	Lys	His	Gln	Ala	Lys	Thr	Val	Leu	Val	Gly																		
		195					200					205																					
Val	Pro	Lys	Thr	Ile	Asp	Gly	Asp	Leu	Gln	His	Leu	Phe	Leu	Asp	Leu																		
	210					215					220																						
Thr	Phe	Gly	Phe	Asp	Thr	Ala	Thr	Lys	Phe	Tyr	Ser	Ser	Ile	Ile	Ser																		

```

Pro Val Phe Asn Lys Phe Ser Leu Tyr Arg Lys Ile Trp Ala Leu Glu
      500      505      510
Asp Ser Tyr Arg Phe Val Gly Pro Leu Gln Ile His Ser Pro Glu Asp
      515      520      525
Ala His Ser Asp Asp Phe Pro Pro Leu Ile Leu Phe Leu Asn His Asn
      530      535      540
Glu Trp Gln Lys Arg Cys Ser Ile Cys Leu Glu Ile Pro Asp Gln Asp
545      550      555      560
Tyr

```

(2) INFORMATIONS POUR LA SEQ ID NO: 246:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 473 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(244479..245897)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 246:

```

Gly Ala Met Asn Lys His Lys Arg Phe Leu Ser Leu Val Leu Leu Thr
1      5      10      15
Phe Ile Leu Leu Gly Ile Trp Phe Cys Pro His Ser Asp Leu Ile Asp
      20      25      30
Ser Lys Ala Trp His Leu Phe Ala Ile Phe Thr Thr Thr Ile Ile Gly
      35      40      45
Ile Ile Val Gln Pro Ala Pro Met Gly Ala Ile Val Ile Met Gly Ile
      50      55      60
Ser Leu Leu Leu Val Thr Lys Thr Leu Thr Leu Asp Gln Ala Leu Ser
65      70      75      80
Gly Phe His Ser Pro Ile Ala Trp Leu Val Phe Leu Ser Phe Ser Ile
      85      90      95
Ala Lys Gly Val Ile Lys Thr Gly Leu Gly Glu Arg Val Ala Tyr Phe
      100      105      110
Phe Val Lys Ile Leu Gly Lys Ser Pro Leu Gly Leu Ser Tyr Gly Leu
      115      120      125
Val Leu Thr Asp Phe Leu Leu Ala Pro Ala Ile Pro Ser Leu Thr Ala
      130      135      140
Arg Ala Gly Gly Ile Leu Phe Pro Val Val Met Gly Leu Ser Glu Ser
145      150      155      160
Phe Gly Ser Ser Val Glu Lys Gly Thr Glu Lys Leu Leu Gly Ser Phe
      165      170      175
Leu Ile Lys Val Ala Tyr Gln Ser Ser Val Ile Thr Ser Ala Met Phe
      180      185      190
Leu Thr Ala Met Ala Gly Asn Pro Ile Ile Ser Ala Leu Ala Ser His
      195      200      205
Ser Gly Val Thr Leu Thr Trp Ala Ile Trp Ala Lys Ala Ala Ile Leu
      210      215      220
Pro Gly Ile Ile Ser Leu Ala Cys Met Pro Phe Val Leu Phe Lys Leu
225      230      235      240
Phe Pro Pro Gln Ile Thr Ser Cys Glu Glu Ala Val Ala Thr Ala Lys
      245      250      255
Thr Arg Leu Lys Glu Met Gly Pro Leu Asn Gln Gly Glu Arg Ile Ile

```



(2) INFORMATION POUR LA SEQ ID NO: 247:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 318 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(245924..246877)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 247:

Cys 1	Gly	Leu	Asp	Ser 5	Pro	Tyr -	Leu	Leu	Arg 10	Leu	Arg	Ala	Pro	Trp 15	Ser
Leu	Leu	Ala	Thr 20	Ala	Cys	Ser	Phe 25	Ser	Glu	Ser	Pro	Ser 30	Phe	Arg	Glu
Arg	Leu	Gly 35	Gly	Leu	His	Ser 40	Tyr	Arg	Val	Val	Asp 45	Arg	Arg	Phe	Leu
Ala	Cys 50	Tyr	Asp	Gln	Glu	Thr 55	Ile	Asp	Tyr	Ser 60	Gln	Ile	Phe	Arg	Thr
Gly 65	Val	Thr	Leu	Thr 70	Met	Glu	Ile	Ser	His 75	Ile	Leu	Glu	Asp	Leu 80	Val
Tyr	Asp	Asn	Gly 85	Val	Leu	Pro	Arg	Glu	Ala 90	Ile	Glu	Ala	Ala 95	Ile	Val
Lys	His	His	Gln 100	Ile	Thr	Pro	Tyr 105	Leu	Leu	Lys	Ile	Leu 110	Glu	Glu	Gly
Ile	Asp	His 115	Val	Ser	Asp	Ile 120	Ile	Asp	Asp	Cys 125	Tyr	Gln	Gly	His	

```

Leu Tyr Ala Met Tyr Leu Leu Ala Gln Phe Arg Glu Thr Arg Ala Leu
130      135      140
Pro Leu Ile Ile Lys Leu Phe Ser Phe Glu Gln Asp Ile Pro His Ala
145      150      155      160
Ile Ala Gly Asp Val Leu Thr Glu Asp Leu Ser Arg Ile Leu Ala Ser
      165      170      175
Val Cys Asp Asp Val Ala Leu Ile Gln Glu Leu Ile Glu Thr Pro His
      180      185      190
Val Asn Pro Tyr Val Gln Ala Ala Ile Ser Ser Leu Val Ala Leu
      195      200      205
Val Gly Val His Lys Leu Ser Arg Glu Thr Ala Ile Arg Tyr Phe Gly
      210      215      220
Glu Leu Leu Asn Tyr Arg Leu Glu Lys Lys Pro Ser Phe Ala Trp Asp
225      230      235      240
Ser Leu Val Ala Ser Ile Cys Ala Leu Tyr Pro Lys Glu Leu Phe Tyr
      245      250      255
Pro Ile Ser Lys Ala Phe Ser Ala Gly Leu Ile Asp Thr Ser Phe Ile
      260      265      270
Ser Met Glu Asp Val Glu Thr Ile His Glu Glu Ser Ile Asp Ser
      275      280      285
Cys Leu Lys Glu Val Phe Ser Ser Thr Asp Leu Ile Asn Asp Thr Leu
      290      295      300
Glu Glu Met Glu Lys Trp Leu Glu Arg Phe Pro Phe Glu Ser
305      310      315

```

(2) INFORMATIONS POUR LA SEQ ID NO: 248:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 249 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(246985..247731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 248:

```

Leu Ala Met Ser Thr Leu Val Ser Ile Lys Asp Leu Ser Leu Thr Ile
1      5      10      15
Arg Lys Gln Pro Ile Leu Arg Asn Val His Leu Glu Ile Cys Arg Gly
      20      25      30
Glu Cys Leu Thr Ile Val Gly Ala Ser Gly Ser Gly Lys Thr Ser Leu
      35      40      45
Ala Leu Ala Ile Leu Gly Leu Leu Pro Pro Asp Ala Gln Asp Ser Ile
      50      55      60
Asp Phe His Leu Pro Pro Lys Thr Pro Arg Thr Lys Ala Val Gln Met
65      70      75      80
Ile Trp Gln Asp Val Tyr Ser Ser Leu Asn Pro Met Met Thr Ile Gln
      85      90      95
Glu Ile Ile Ala Glu Pro Leu His Ile Met Gly Gly Leu Ser Lys Ser
      100      105      110
Xaa Gln Gln Glu Glu Ile Ala His Ala Leu Lys Leu Val His Leu Pro
      115      120      125
Lys Ser Phe Leu Ser Leu Arg Pro Ile Lys Leu Ser Gly Gly Gln Arg
      130      135      140
Gln Arg Ile Ala Ile Ala Lys Ala Leu Val Cys Lys Pro Glu Leu Ile

```

145		150		155		160
Ile Cys Asp Glu Pro Leu Ser Ala Leu Asp Thr Met Asn Gln Lys Leu						
	165		170		175	
Ile Leu Asp Leu Phe Gln Thr Ile Lys Asn Gln Tyr Asn Asn Ala Phe						
	180		185		190	
Leu Phe Ile Thr His Asp Met Ser Ala Ala Tyr Thr Leu Ala Asp Lys						
	195		200		205	
Ile Ala Val Met Asp Arg Gly Tyr Leu Val Glu Ile Ala Ser Lys Gln						
	210		215		220	
Glu Ile Phe Ser Ser Pro Lys His Ile Lys Thr Arg Glu Leu Leu Asp						
225		230		235		240
Ala Ile Pro Ala Phe Thr Phe Ser Phe						
	245					

(2) INFORMATIONS POUR LA SEQ ID NO: 249:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 281 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(247743..248585)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 249:

Arg Lys Ile Pro Leu Ser Glu Asp Leu Leu Lys Ile Asp Asn Leu Val														
1		5		10		15								
Val Ser Val Lys Asn Ser Asn Gln Arg Leu Val Asn His Leu Ser Leu														
	20		25		30									
Thr Ile Lys Arg Cys Gln Ser Met Ala Leu Val Gly Glu Asn Gly Ser														
	35		40		45									
Gly Lys Thr Thr Val Ser Lys Ala Val Leu Gly Phe Leu Pro Asp Asn														
	50		55		60									
Cys Tyr Ile Gln Ser Gly Arg Ile Leu Tyr Ser Ser Thr Asp Ile Thr														
65		70		75		80								
Arg Leu Ser Arg Arg Gln Leu Gln Thr Ile Arg Gly Lys Lys Ile Ala														
	85		90		95									
Thr Ile Phe Gln Asn Ala Met Gly Thr Leu Thr Pro Ser Met Arg Val														
	100		105		110									
Gly Ala Gln Ile Val Glu Thr Leu Arg His His Phe Asp Met Ser Lys														
	115		120		125									
Glu Glu Ala Phe Ser Lys Ala Arg Glu Leu Leu Glu Ser Val His Ile														
	130		135		140									
Glu Ser Pro Asp Arg Cys Leu Gln Leu Tyr Pro Phe Glu Leu Ser Gly														
145		150		155		160								
Gly Met Cys Gln Arg Val Ser Ile Ala Ile Ala Leu Ala Thr Asn Pro														
	165		170		175									
Glu Leu Ile Ile Ala Asp Glu Pro Ser Thr Ala Leu Asp Ser Ile Ser														
	180		185		190									
Gln Ala Gln Val Leu Arg Val Leu Thr Gln Ile His Gln Asn His Ser														
	195		200		205									
Thr Ala Leu Leu Leu Ile Thr His Asn Leu Ala Leu Val Ser Glu Leu														
	210		215		220									
Cys Glu Glu Met Ala Ile Ile Arg Tyr Gly Glu Ile Val Glu Gln Gly														
225		230		235		240								

```

Pro Val Gln Glu Leu Leu His Ser Pro Ser His Pro Tyr Thr Gln Gln
                245                      250                255
Leu Ile Arg Ala Ile Pro Arg Ile Pro Ser Pro Ser Tyr Leu Ser Pro
                260                      265                270
Thr Glu Pro Leu Ala Thr Thr Ala Tyr
                275                      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 250:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(248569..249420)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 250:

```

Asn Lys Leu Met Phe Arg Ser Ser Ser Ser His Thr Trp Arg Tyr Ile
1      5      10      15
Arg Thr Asn Lys Met Leu Val Leu Gly Cys Leu Thr Leu Ala Val Leu
      20      25      30
Val Leu Ala Ala Thr Phe Leu Pro Tyr Leu Tyr Pro Asp Tyr Glu Arg
      35      40      45
Thr Phe Pro Glu His Ala Leu Gln Ser Pro Ser Lys Ala Phe Pro Phe
      50      55      60
Gly Thr Asp Asn Leu Gly Arg Cys Met Leu Ala Arg Thr Leu Gln Gly
65      70      75      80
Ile Arg Leu Ser Leu Leu Ile Ala Val Ser Ala Thr Ile Ile Asp Val
      85      90      95
Cys Leu Gly Leu Leu Trp Ser Thr Leu Ala Leu Ala Ser Gly Lys Lys
      100     105     110
Val Ala Asp Ile Met Ser Arg Ile Thr Glu Ile Leu Phe Ser Ile Pro
      115     120     125
Arg Ile Pro Val Ile Ile Leu Leu Val Ile Phe Asn His Gly Ile
      130     135     140
Leu Pro Leu Ile Leu Ala Met Thr Ile Thr Gly Trp Ile Pro Ile Ala
145     150     155     160
Arg Ile Ile Tyr Gly Gln Phe Leu Leu Leu Glu Asn Lys Glu Phe Val
      165     170     175
Leu Ser Ala Arg Ala Leu Gln Ala Ser Thr Phe His Ile Leu Arg Lys
      180     185     190
His Leu Leu Pro Asn Ser Leu Gly Pro Ile Ile Ser Thr Leu Ile Phe
      195     200     205
Thr Ile Pro Asn Ala Val Tyr Thr Glu Ala Phe Ile Ser Phe Leu Gly
      210     215     220
Leu Gly Xaa Gln Pro Pro Tyr Ala Ser Leu Gly Thr Leu Val Lys Glu
225     230     235     240
Gly Ile His Ser Leu Ala Tyr His Pro Trp Leu Phe Phe Ile Pro Ser
      245     250     255
Phe Phe Met Ile Ile Val Ser Val Ser Phe Asn Cys Ile Gly Glu Gly
      260     265     270
Leu Gln Thr Lys Leu Leu Glu Glu Asn Thr Leu Val
      275     280

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 251:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 206 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(249766..250383)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 251:

```

Met Leu Ser Tyr Ile Lys Arg Arg Leu Leu Phe Asn Leu Leu Ser Leu
1      5      10      15
Trp Val Val Val Thr Leu Thr Phe Phe Ile Ile Lys Thr Ile Pro Gly
      20      25      30
Asp Pro Phe Asn Asp Glu Asn Gly Asn Ile Leu Ser Pro Glu Thr Leu
      35      40      45
Ala Leu Leu Lys Asn Arg Tyr Gly Leu Asp Lys Pro Leu Phe Thr Gln
      50      55      60
Tyr Leu Ile Tyr Leu Lys Cys Leu Leu Thr Leu Asp Phe Gly Glu Ser
65      70      75      80
Leu Ile Tyr Lys Asp Arg Thr Val Ile Ser Ile Ile Ala Ala Ala Leu
      85      90      95
Pro Ser Ser Ala Ile Leu Gly Leu Glu Ser Leu Cys Leu Ser Leu Phe
      100     105     110
Gly Gly Ile Thr Leu Gly Ile Leu Ala Ala Phe Tyr Lys Lys Ser Cys
      115     120     125
Gly Arg Thr Ile Phe Phe Ser Ser Val Ile Gln Ile Ser Val Pro Ala
      130     135     140
Phe Val Ile Gly Ala Phe Leu Gln Tyr Val Phe Ala Ile Lys Tyr Ser
145     150     155     160
Cys Leu Pro Ile Ala Cys Trp Gly Asn Phe Ser His Thr Leu Leu Pro
      165     170     175
Ser Ile Ala Leu Ala Ile Thr Pro Met Ala Phe Ile Thr Gln Leu Thr
      180     185     190
Tyr Ala Ser Val Ser Ala Asn Leu Lys Lys Xaa Thr Ser Tyr
      195     200     205

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 252:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 214 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(250545..251186)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 252:

```

Thr Lys Lys Leu Leu Pro Pro Trp Leu Leu Xaa Xaa Pro Ala Lys His
1      5      10      15

```

```

Leu Leu Pro Ala His Leu His Thr Tyr Pro Glu Gln Pro Ser Tyr Lys
      20      25      30
Gln Gln Glu Ala Ile Thr Leu Ala Lys Ser Leu Leu Glu Glu Ala Leu
      35      40      45
Thr Glu Leu Asn Met Thr Ile Lys Asp Leu Glu Lys Tyr Pro Leu Thr
      50      55      60
Phe Ser Ala Thr Ser Thr Val Asn Ser Gln Ile Ala Gln Met Leu Arg
      65      70      75      80
Asp Gln Trp Arg Arg Ser Leu Gly Ile Thr Phe Pro Ile Cys Gly Lys
      85      90      95
Glu Tyr Ala Leu Leu Gln Asn Asp Leu Ile Gly Asn Thr Phe Phe Met
      100      105      110
Ser Ile Gly Gly Trp Phe Ala Asp Phe Ser Asp Pro Leu Ala Phe Leu
      115      120      125
Ser Ile Phe Ser Ser Lys Gly Val Lys Pro Tyr Ala Leu Gln Asp Pro
      130      135      140
Gln Phe Asp Gln Leu Ile Leu Ser Ile Glu Thr Glu Lys Asn Pro Gln
      145      150      155      160
Lys Arg Ser Ala Leu Ile Ser Glu Ala Ser Leu Tyr Ile Glu Arg Gln
      165      170      175
Asn Val Ile Glu Pro Leu Tyr His Asp Val Phe His Tyr Thr Thr Asn
      180      185      190
Asn Lys Leu Ser Phe Val Arg Leu His Pro Ser Gly Leu Val Asp Met
      195      200      205
Arg Tyr Ala Lys Asn Ser
      210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 253:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 339 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(251095..252111)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 253:

```

Gly Gly His Ser Met Arg Lys Ile Ser Val Gly Ile Cys Leu Leu Leu
1      5      10      15
Ala Leu Ala Thr Ser Gly Cys Ser Lys Ser Ser Ser Asn Ala Thr His
      20      25      30
Arg Ser Pro Ala Thr His Thr Val Ala Val Ser Val Lys Asp Asp Pro
      35      40      45
Arg Thr Phe Asp Pro Arg Glu Val Arg Leu Leu Ser Asp Ile Asn Leu
      50      55      60
Ile His His Leu Tyr Glu Gly Leu Val Gln Glu Thr Pro Ser Gly Glu
      65      70      75      80
Val Phe Pro Ala Leu Ala Glu Ser Phe Phe Leu Ser Glu Asp Lys Lys
      85      90      95
Thr Tyr Thr Phe Asn Leu Lys Lys Ala Phe Trp Ser Asn Gly Asp Leu
      100      105      110
Ile Thr Ala His Asp Phe Val Arg Ser Trp Asn Asp Val Leu Gln Asn
      115      120      125
Arg Val Ala Ser Ile Tyr Ser Phe Ala Phe Leu Pro Ile Asp Val Asn

```

130		135		140
Lys Asp Ser Gly Phe Phe Ala Lys Asp Asp His Thr Leu Val Ile Asn				
145		150		155
Leu Leu Thr Pro Thr Pro His Phe Leu Lys Leu Leu Thr Leu Pro Val				
	165		170	175
Phe Tyr Pro Val His Ser Gln His Gln Ile Trp Lys Glu Glu Lys Ser				
	180		185	190
Leu Pro Ile Ser Thr Gly Ala Phe Phe Leu Lys Glu Lys Lys Asp Arg				
	195	200		205
Arg Trp Leu Lys Leu Glu Lys Ser Pro Tyr Tyr Tyr Asn Lys Asp Gln				
	210	215		220
Val Ala Val Gln Glu Ile Cys Ile His Ile Ile Pro Asp Gln Gln Thr				
225		230		235
Ala Ser Ala Leu Phe Asn Gln Gly Lys Leu Asp Trp Gln Gly Leu Pro				
	245		250	255
Trp Gly His Ser Ile Pro Gln Glu Thr Leu Ala Thr Ala Asn Lys Arg				
	260		265	270
Arg Ala Pro Gln Ser Phe Asp Ile Ser Gly Thr Ser Trp Leu Thr Phe				
	275	280		285
Asn Thr Ala Lys Lys Pro Phe Ser His Ser Lys Leu Arg Gln Ala Leu				
	290	295		300
Ser Leu Val Leu Asn Lys Glu Ala Leu Ala Ser Leu Ala Phe Val Xaa				
305		310		315
Xaa Cys Lys Thr Ser Pro Ser Cys Thr Phe Ala His Leu Pro Arg Ala				
	325		330	335
Ala Phe Leu				

(2) INFORMATIONS POUR LA SEQ ID NO: 254:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 341 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(252066..253088)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 254:

Val Phe Ala Met Leu Thr Leu Gly Leu Glu Ser Ser Cys Asp Glu Thr				
1	5		10	15
Ser Cys Ser Leu Val Gln Asn Gly Lys Ile Leu Ala Asn Lys Ile Ala				
	20		25	30
Ser Gln Asp Ile His Ala Ser Tyr Gly Gly Val Ile Pro Glu Leu Ala				
	35		40	45
Ser Arg Ala His Leu Gln Thr Phe Pro Glu Leu Leu Thr Ala Ala Thr				
	50		55	60
Gln Ser Ala Gly Val Ser Leu Glu Asp Ile Glu Leu Ile Ser Val Ala				
65		70		75
Asn Thr Pro Gly Leu Ile Gly Ala Leu Ser Ile Gly Val Asn Phe Ala				
	85		90	95
Lys Gly Leu Ala Ser Gly Leu Lys Arg Pro Leu Ile Gly Val Asn His				
	100		105	110
Val Glu Ala His Leu Tyr Ala Ala Cys Met Glu Ala Pro Ala Thr Gln				
	115		120	125

```

Phe Pro Ala Leu Gly Leu Ala Ile Ser Gly Ala His Thr Ser Leu Phe
130      135      140
Leu Met Pro Asp Ala Thr Thr Phe Leu Leu Ile Gly Lys Thr Arg Asp
145      150      155      160
Asp Ala Ile Gly Glu Thr Phe Asp Lys Val Ala Arg Phe Leu Gly Leu
165      170      175
Pro Tyr Pro Gly Gly Gln Lys Leu Glu Glu Leu Ala Arg Glu Gly Asp
180      185      190
Ala Asp Ala Phe Ala Phe Ser Pro Ala Arg Val Ser Gly Tyr Asp Phe
195      200      205
Ser Phe Ser Gly Leu Lys Thr Ala Val Leu Tyr Ala Leu Lys Gly Asn
210      215      220
Asn Ser Ser Ala Lys Ala Pro Phe Pro Glu Val Ser Glu Thr Gln Lys
225      230      235      240
Arg Asn Ile Ala Ala Ser Phe Gln Lys Ala Val Phe Met Thr Ile Ala
245      250      255
Gln Lys Leu Pro Asp Ile Val Lys Ala Phe Ser Cys Glu Ser Leu Ile
260      265      270
Val Gly Gly Gly Val Ala Asn Asn Ser Tyr Phe Arg Arg Leu Leu Asn
275      280      285
Gln Ile Cys Ser Leu Pro Ile Tyr Phe Pro Ser Ser Gln Leu Cys Ser
290      295      300
Asp Asn Ala Ala Met Ile Ala Gly Leu Gly Glu Arg Leu Phe Cys Asn
305      310      315      320
Arg Thr His Val Ser Lys Glu Val Ile Pro Cys Ala Arg Tyr Gln Trp
325      330      335
Glu Ser Ala Cys Ser
340

```

(2) INFORMATIONS POUR LA SEQ ID NO: 255:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 495 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 255234..256718

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 255:

```

Met Asp Ser Lys Thr Ser His Leu Asp Asp Glu Leu Cys Phe Lys Leu
1      5      10
Glu Glu Ala Phe Asp Thr Leu Thr Ala Gly Glu His Ser Gln Asp Leu
20      25      30
Thr Ser Ile Val Ser Val Tyr Asn Pro Ile Asp Leu Ala Tyr Ala Val
35      40      45
Ser Cys Leu Pro Ser Asp Ser Arg Ser Ile Leu Tyr Lys Asn Leu Asp
50      55      60
Ser Ile Ala Ser Lys Ile Ala Phe Ile Ile Asn Thr Asp Ser Ala Ser
65      70      75      80
Arg Trp Ala Ile Phe Arg Asn Leu Ser Asp Gly Glu Ile Cys Ala Leu
85      90      95
Ile Glu Gln Met Pro Pro Asp Glu Ala Ile Trp Val Leu Asp Asp Ile
100      105      110
Pro Asp Arg Arg Tyr Arg Arg Ile Leu Asp Leu Ile Asp Val Lys Lys

```



Ala	Leu	Lys	Ile	Arg	Asp	Leu	Gln	Lys	His	Gly	Arg	Asn	Thr	Ala	Gly
130						135					140				
Arg	Leu	Met	Thr	Asn	Glu	Phe	Phe	Ala	Phe	Leu	Met	Glu	Thr	Thr	Val
145					150					155					160
Lys	Glu	Val	Ala	Thr	Cys	Ile	Arg	Asn	Asn	Pro	Gly	Ile	Asp	Leu	Thr
				165					170					175	
Arg	Leu	Val	Phe	Val	Leu	Asp	Phe	Lys	Gly	Glu	Leu	Gln	Gly	Phe	Val
			180					185					190		
Thr	Asp	Arg	Ser	Leu	Ile	Ile	Ala	Ser	Pro	Glu	Met	Pro	Leu	Lys	Gln
	195						200					205			
Ile	Met	Arg	Pro	Ile	Glu	His	Lys	Val	Leu	Ala	Asp	Thr	Thr	Arg	Glu
210					215					220					
Glu	Val	Val	Asp	Leu	Val	Glu	Arg	Tyr	Lys	Val	Ala	Val	Leu	Pro	Val
225					230					235					240
Val	Asp	Glu	Glu	Asn	Phe	Leu	Ile	Gly	Ala	Ile	Thr	Tyr	Glu	Asp	Val
				245					250					255	
Val	Glu	Thr	Ile	Glu	Asp	Ile	Ala	Asp	Glu	Thr	Ile	Ala	Arg	Met	Ala
			260					265					270		
Gly	Thr	Thr	Glu	Asp	Val	Gly	Tyr	His	Asp	Cys	His	Val	Val	Gln	Arg
		275				280						285			
Phe	Leu	Leu	Arg	Ala	Pro	Trp	Leu	Leu	Ile	Thr	Leu	Cys	Ala	Gly	Leu
290					295					300					
Val	Ser	Ala	Ser	Val	Met	Ala	Tyr	Phe	Gln	Lys	Ile	Ala	Pro	Thr	Leu
305					310					315					320
Leu	Ala	Met	Val	Ile	Phe	Phe	Ile	Pro	Leu	Val	Asn	Gly	Leu	Ser	Gly
				325					330					335	
Asn	Val	Gly	Val	Gln	Cys	Ser	Thr	Ile	Leu	Val	Arg	Ser	Met	Ala	Thr
		340						345					350		
Gly	Thr	Leu	Ser	Phe	Gly	Arg	Arg	Arg	Glu	Thr	Ile	Leu	Lys	Glu	Met
		355				360						365			
Ser	Ile	Gly	Leu	Leu	Thr	Gly	Val	Ala	Leu	Gly	Ile	Leu	Cys	Gly	Leu
370					375					380					
Val	Val	Cys	Cys	Met	Gly	Cys	Leu	Gly	Leu	Gly	Leu	Phe	Ala	Thr	Gly
385					390					395					400
Gly	Val	Gln	Leu	Gly	Val	Thr	Val	Ser	Val	Gly	Ile	Leu	Gly	Ala	Ser
				405					410					415	
Leu	Thr	Ala	Thr	Thr	Leu	Gly	Val	Leu	Ser	Pro	Phe	Phe	Phe	Ala	Lys
			420					425					430		
Ile	Gly	Val	Asp	Pro	Ala	Leu	Ala	Ser	Gly	Pro	Ile	Val	Thr	Ala	Leu
		435				440						445			
Asn	Asp	Ile	Val	Ser	Met	Val	Ile	Phe	Leu	Leu	Ile	Thr	Gly	Thr	Leu
450						455					460				
Asn	Val	Leu	Phe	Leu	Gln	Ile	Val	Gly	Glu	Ser	Glu	Asp	Lys	Gly	Phe
465					470					475					480
Leu	Arg	Ala	Phe	Phe	Thr	Met	Ser	Phe	Leu	Pro	Leu	Ser	Leu	Glu	
				485					490					495	

## (2) INFORMATIONS POUR LA SEQ ID NO: 256:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 361 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 256:

(2) INFORMATION POUR LA SEQ ID NO: 257:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 257911..258690

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 258:

Glu Pro Ser Ser Xaa Ala Phe Cys Glu Gly Arg Cys Ala Cys Ala Tyr  
1 5 10 15

Arg	Arg	Ser	Val	Val	Ser	Phe	Tyr	Pro	Gln	Asn	Leu	Pro	Ser	Phe	Arg
			20					25					30		
Arg	Arg	Lys	Pro	Ser	Arg	Thr	Asp	Ser	Pro	Ile	Lys	His	Ala	Lys	His
		35					40					45			
Phe	Leu	Arg	Asp	His	Leu	Ser	His	Leu	Arg	Lys	Ile	Leu	Ala	Gly	Lys
	50					55					60				
Pro	Gln	Glu	Val	Ile	Glu	Ala	Trp	Tyr	Glu	Ile	Leu	Gly	Lys	Lys	Tyr
65					70					75					80
Asn	Gly	Met	Thr	Gln	Ala	Ile	Gly	Leu	Lys	Asp	Gly	Ile	Leu	Ser	Ile
				85					90					95	
Lys	Val	Arg	Asn	Ala	Ser	Leu	Tyr	Ala	Val	Leu	Lys	Gln	Ser	Ser	Gln
			100					105					110		
Lys	Glu	Leu	Ile	Ser	Arg	Ile	His	Ser	Ala	Val	Pro	Gly	Ala	Lys	Val
		115					120					125			
Lys	Glu	Ile	Arg	Phe	Leu	Leu	Gly								
	130						135								

(2) INFORMATIONS POUR LA SEQ ID NO: 259:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 804 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 259193..261604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 259:

Met	Asp	Ala	Gln	Glu	Lys	Lys	Tyr	Asp	Ala	Ser	Ala	Ile	Thr	Val	Leu
1				5				10						15	
Glu	Gly	Leu	Gln	Ala	Val	Arg	Glu	Arg	Pro	Gly	Met	Tyr	Ile	Gly	Asp
			20					25					30		
Thr	Gly	Val	Thr	Gly	Leu	His	His	Leu	Val	Tyr	Glu	Val	Val	Asp	Asn
		35					40					45			
Ser	Ile	Asp	Glu	Ala	Met	Ala	Gly	Phe	Cys	Thr	Glu	Val	Val	Val	Arg
	50					55				60					
Ile	Leu	Glu	Asp	Gly	Gly	Ile	Ser	Ile	Ser	Asp	Asn	Gly	Arg	Gly	Ile
65				70						75					80
Pro	Ile	Gln	Ile	His	Glu	Lys	Glu	Ser	Ala	Lys	Gln	Gly	Arg	Glu	Ile
			85					90						95	
Ser	Ala	Leu	Glu	Val	Val	Leu	Thr	Val	Leu	His	Ala	Gly	Gly	Lys	Phe
			100					105					110		
Asp	Lys	Asp	Ser	Tyr	Lys	Val	Ser	Gly	Gly	Leu	Xaa	Gly	Val	Gly	Val
		115					120					125			
Ser	Cys	Val	Asn	Ala	Leu	Ser	Glu	Lys	Phe	Ile	Ala	Lys	Val	Phe	Lys
	130					135					140				
Asp	Gly	Gln	Ala	Tyr	Ser	Met	Glu	Phe	Ser	Arg	Gly	Ala	Pro	Leu	Thr
145					150					155					160
Thr	Leu	Gln	Val	Leu	Gly	Pro	Thr	Asp	Lys	Arg	Gly	Thr	Glu	Val	Leu
			165						170					175	
Phe	Tyr	Pro	Asp	Pro	Ala	Ile	Phe	Ser	Thr	Cys	Val	Phe	Asp	Arg	Ala
			180					185					190		
Ile	Leu	Met	Lys	Arg	Leu	Arg	Glu	Leu	Ala	Phe	Leu	Asn	Arg	Gly	Ala
		195					200					205			
Thr	Ile	Val	Phe	Glu	Asp	Asp	Arg	Asp	Thr	Gly	Phe	Asp	Lys	Val	Val

210	215	220
Phe Phe Tyr Glu Gly Gly	Ile Gln Ser Phe Val Ser Tyr Leu Asn Gln	
225	230	235
Asn Lys Glu Ile Leu Phe	Pro Asn Pro Ile Tyr Ile Gln Gly Ser Arg	240
	245	250
Pro Gly Asp Asp Gly Asp	Ile Glu Phe Glu Ala Ala Leu Gln Trp Asn	255
	260	265
Ser Gly Tyr Ser Glu Leu	Ile Tyr Ser Tyr Ala Asn Asn Ile Pro Thr	270
	275	280
Arg Gln Gly Gly Thr His	Leu Thr Gly Phe Ser Thr Ala Leu Thr Arg	285
	290	295
Ala Val Asn Ser Tyr Ile	Lys Ala His Asn Leu Ser Lys Ser Asp Lys	300
305	310	315
Leu Ser Leu Thr Gly Glu	Asp Ile Lys Glu Gly Leu Val Ala Ile Val	320
	325	330
Ser Val Lys Val Pro Asn	Pro Gln Phe Glu Gly Gln Thr Lys Gln Lys	335
	340	345
Leu Gly Asn Ser Asp Val	Gly Ser Val Ser Gln Gln Ile Ser Gly Glu	350
	355	360
Val Leu Thr Thr Phe Phe	Glu Glu Asn Thr Gln Ile Ala Lys Thr Ile	365
	370	375
Val Asp Lys Val Phe Val	Ala Ala Gln Ala Arg Glu Ala Ala Lys Arg	380
385	390	395
Ala Arg Glu Leu Thr Phe	Arg Lys Ser Ala Leu Asp Ser Ala Arg Leu	400
	405	410
Pro Gly Lys Leu Ile Asp	Cys Leu Glu Lys Asp Pro Glu Lys Cys Glu	415
	420	425
Met Tyr Ile Val Glu Gly	Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly	430
	435	440
Arg Asp Arg Arg Phe Gln	Ala Ile Leu Pro Ile Arg Gly Lys Ile Leu	445
	450	455
Asn Val Glu Lys Ala Arg	Leu Gln Lys Val Phe Gln Asn Gln Glu Ile	460
465	470	475
Gly Ser Ile Ile Ala Ala	Leu Gly Cys Gly Ile Gly Lys Asp Asn Phe	480
	485	490
Asn Leu Ser Lys Leu Arg	Tyr Lys Arg Ile Ile Met Thr Asp Ala	495
	500	505
Asp Val Asp Gly Ser His	Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr	510
	515	520
Arg His Met Ser Ala Leu	Ile Glu Asn Glu Cys Val Tyr Ile Ala Gln	525
	530	535
Pro Pro Leu Tyr Arg Val	Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu	540
545	550	555
Ser Glu Lys Glu Met Asp	Gly Tyr Leu Leu Asn Leu Gly Thr Lys Glu	560
	565	570
Ser Gln Ile Val Phe Asp	Asp Thr Leu Arg Asp Leu Arg Gly Glu Ala	575
	580	585
Leu Glu Thr Phe Val Asn	Leu Ile Leu Glu Val Glu Ser Phe Ile Val	590
	595	600
Ser Leu Glu Lys Lys Ala	Ile Pro Phe Ser Glu Phe Leu Asp Met Phe	605
	610	615
Arg Asp Gly Ala Tyr Pro	Leu Tyr Tyr Tyr Pro Glu Ser Gly Lys	620
625	630	635
Gln Gly Gly Ser Tyr Leu	Tyr Ser His Glu Glu Lys Glu Ala Ala Ile	640
	645	650
Ala Ala Asn Glu Glu Ser	Ala Ser Arg Ile Leu Glu Leu Tyr Lys Gly	655
	660	665
Ser Val Leu Glu Glu Leu	Gln Arg Asp Leu Gly Asp Tyr Gly Tyr Asp	670
	675	680
		685

Ile	Arg	Asn	Tyr	Leu	His	Pro	Lys	Gly	Ser	Gly	Ile	Thr	Val	Ser	Thr
690						695					700				
Glu	Asp	Pro	Lys	Ile	Ser	Pro	Tyr	Val	Cys	Tyr	Thr	Leu	Lys	Glu	Val
705				710					715						720
Ile	Asp	Tyr	Leu	Lys	Gly	Leu	Gly	Arg	Lys	Gly	Ile	Glu	Ile	Gln	Arg
			725					730						735	
Tyr	Lys	Gly	Leu	Gly	Glu	Met	Asn	Ala	Asp	Gln	Leu	Trp	Asp	Thr	Thr
			740					745					750		
Met	Asn	Pro	Glu	Gln	Arg	Thr	Leu	Val	Arg	Val	Ser	Leu	Lys	Asp	Ala
		755					760					765			
Val	Glu	Ala	Asp	His	Ile	Phe	Thr	Met	Leu	Met	Gly	Glu	Glu	Val	Pro
	770				775						780				
Pro	Arg	Arg	Glu	Phe	Ile	Lys	Ser	His	Ala	Leu	Ser	Ile	Arg	Met	Asn
785					790					795					800
Asn	Leu	Asp	Ile												

## (2) INFORMATIONS POUR LA SEQ ID NO: 260:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 836 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 261622..264129

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 260:

Met	Leu	Asn	Lys	Glu	Glu	Ile	Ile	Val	Pro	Lys	Asn	Leu	Glu	Glu	Glu
1				5				10					15		
Met	Lys	Glu	Ser	Tyr	Leu	Arg	Tyr	Ser	Met	Ser	Val	Ile	Ile	Ser	Arg
		20						25				30			
Ala	Leu	Pro	Asp	Ala	Arg	Asp	Gly	Leu	Lys	Pro	Ser	Gln	Arg	Arg	Ile
		35					40					45			
Leu	Tyr	Ala	Met	Lys	Gln	Leu	Asn	Leu	Thr	Pro	Gly	Val	Lys	His	Arg
	50					55					60				
Lys	Cys	Ala	Lys	Ile	Cys	Gly	Asp	Thr	Ser	Gly	Asp	Tyr	His	Pro	His
65				70						75				80	
Gly	Glu	Ser	Val	Ile	Tyr	Pro	Thr	Leu	Val	Arg	Met	Ala	Gln	Asp	Trp
			85					90					95		
Ala	Met	Arg	Tyr	Pro	Leu	Val	Asp	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile
			100					105					110		
Asp	Gly	Asp	Pro	Ala	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Leu	Thr
		115					120					125			
His	Ser	Ala	Ile	Phe	Leu	Leu	Glu	Asp	Leu	Asp	Lys	Asp	Thr	Val	Asp
	130				135						140				
Met	Val	Pro	Asn	Tyr	Asp	Glu	Thr	Lys	Tyr	Glu	Pro	Val	Val	Phe	Pro
145				150						155				160	
Ser	Lys	Phe	Pro	Asn	Leu	Leu	Cys	Asn	Gly	Ser	Ser	Gly	Ile	Ala	Val
			165					170					175		
Gly	Met	Ala	Thr	Asn	Ile	Pro	Pro	His	Asn	Leu	Gly	Glu	Leu	Ile	Glu
		180						185					190		
Ala	Thr	Leu	Val	Leu	Ala	Asn	Ser	Gln	Thr	Ser	Ile	Glu	Asp	Ile	
	195					200					205				
Leu	Glu	Val	Met	Pro	Gly	Pro	Asp	Phe	Pro	Thr	Gly	Gly	Ile	Ile	Cys

210					215					220					
Gly 225	Thr	Glu	Gly	Ile	Arg 230	Ser	Thr	Tyr	Tyr	Thr 235	Gly	Arg	Gly	Lys	Leu 240
Arg	Leu	Arg	Ala	Arg 245	Met	His	Val	Glu	Glu	Asn 250	Ser	Asp	Lys	Gln	Arg
Glu	Asn	Ile	Ile	Leu 260	Thr	Glu	Met	Pro	Tyr	Asn 265	Val	Asn	Lys	Ser	Pro
Leu	Ile	Glu	Gln	Ile 275	Ala	Glu	Leu	Ile	Asn	Glu	Lys	Thr	Leu	Thr	Gly
Ile	Ser	Asp	Val	Arg 290	Asp	Glu	Ser	Asp	Lys	Asp	Gly	Asn	Arg	Val	Val
Leu 305	Glu	Leu	Lys	Lys 310	Gly	Glu	Ser	Ser	Glu	Val	Val	Ile	Asn	Arg	Leu
Tyr	Lys	Phe	Thr	Asp 325	Val	Gln	Val	Thr	Phe	Gly	Ala	Asn	Met	Leu	Ala
Leu	Asp	Lys	Asn	Leu 340	Pro	Arg	Thr	Met	Asn	Ile	His	Arg	Met	Ile	Ser
Ala	Trp	Ile	Arg	His 355	Arg	Met	Asp	Val	Ile	Arg	Arg	Arg	Thr	Arg	Tyr
Glu	Leu	Asn	Lys	Ala 370	Glu	Ala	Arg	Ala	His	Ile	Leu	Glu	Gly	Phe	Leu
Lys 385	Ala	Leu	Ser	Cys 390	Met	Asp	Glu	Val	Val	Lys	Thr	Ile	Arg	Glu	Ser
Ser	Asn	Lys	Glu	His 405	Ala	Lys	Gln	Gln	Leu	Val	Glu	Leu	Phe	Ser	Phe
Ser	Glu	Ala	Gln	Ala 420	Leu	Ala	Ile	Leu	Glu	Leu	Arg	Leu	Tyr	Gln	Leu
Thr	Gly	Leu	Glu	Ala 435	Asp	Lys	Val	Gln	Lys	Glu	Tyr	Ser	Glu	Leu	Leu
Glu	Lys	Ile	Thr	Tyr 450	Tyr	Arg	Lys	Val	Leu	Ala	Glu	Glu	Glu	Leu	Val
Lys 465	Asp	Ile	Ile	Arg 470	Glu	Glu	Leu	Gln	Glu	Leu	His	Lys	Val	His	Lys
Thr	Pro	Arg	Arg	Thr 485	Lys	Ile	Glu	Met	Asp	Thr	Gly	Asp	Val	Arg	Asp
Ile	Glu	Asp	Ile	Ile 500	Ser	Asp	Glu	Ser	Val	Ile	Ile	Thr	Ile	Ser	Gly
Asp	Asp	Tyr	Val	Lys 515	Arg	Met	Pro	Val	Lys	Val	Phe	Arg	Glu	Gln	Lys
Arg	Gly	Gly	Gln	Gly 530	Val	Thr	Gly	Phe	Asp	Met	Lys	Lys	Gly	Ser	Asp
Phe 545	Leu	Lys	Ala	Val 550	Tyr	Ser	Ala	Ser	Thr	Lys	Asp	Tyr	Leu	Leu	Ile
Phe	Thr	Asn	Phe	Gly 565	Gln	Cys	Tyr	Trp	Leu	Lys	Val	Trp	Gln	Leu	Pro
Glu	Gly	Glu	Arg	Arg 580	Ala	Lys	Gly	Lys	Pro	Ile	Ile	Asn	Phe	Leu	Glu
Gly	Ile	Arg	Pro	Gly 595	Glu	Gln	Val	Ala	Ala	Val	Leu	Asn	Val	Lys	Arg
Phe	Glu	Gln	Gly	Glu 610	Tyr	Leu	Phe	Leu	Ala	Thr	Lys	Lys	Gly	Val	Val
Lys 625	Lys	Val	Ser	Leu 630	Asp	Ala	Phe	Gly	Ser	Pro	Arg	Lys	Lys	Gly	Ile
Arg	Ala	Leu	Glu	Ile 645	Asp	Asp	Gly	Asp	Glu	Leu	Ile	Ala	Ala	Arg	His
Ile	Ala	Asn	Asp	Glu 660	Glu	Lys	Val	Met	Leu	Phe	Thr	Arg	Leu	Gly	Met
Ala	Val	Arg	Phe	Pro 675	His	Asp	Lys	Val	Arg	Pro	Met	Gly	Arg	Ala	Ala

```

Arg Gly Val Arg Gly Val Ser Leu Lys Asn Glu Gln Asp Phe Val Val
690                               695                               700
Ser Cys Gln Val Val Thr Glu Asp Gln Ser Val Leu Val Val Cys Asp
705                               710                               715                               720
Asn Gly Phe Gly Lys Arg Ser Leu Val Cys Asp Phe Arg Glu Thr Asn
725                               730                               735
Arg Gly Ser Val Gly Val Arg Ser Ile Val Ile Asn Gln Arg Asn Gly
740                               745                               750
Asp Val Leu Gly Ala Ile Ser Val Thr Asp Cys Asp Ser Ile Leu Leu
755                               760                               765
Met Ser Ala Gln Gly Gln Ala Ile Arg Ile Asn Met Gln Asp Val Arg
770                               775                               780
Val Met Gly Arg Ala Thr Gln Gly Val Arg Leu Val Asn Leu Arg Glu
785                               790                               795                               800
Gly Asp Thr Leu Val Ala Met Glu Lys Leu Ser Ile Asn Thr Glu Ser
805                               810                               815
Val Glu Thr Glu Glu Asn Leu Ala Ala Ser Val Gln Ser Gly Gln Asp
820                               825                               830
Thr Ile Glu Glu
835

```

(2) INFORMATIONS POUR LA SEQ ID NO: 261:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 264125..264742

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 261:

```

Arg Asn Ser Val Phe Ile Val Val Glu Gly Gly Glu Gly Ala Gly Lys
1                               5                               10                               15
Thr Gln Phe Ile Gln Ala Leu Ser Lys Arg Leu Ile Glu Glu Gly Arg
20                               25                               30
Glu Ile Val Thr Thr Arg Glu Pro Gly Gly Cys Ser Leu Gly Asp Ser
35                               40                               45
Val Arg Gly Leu Leu Leu Asp Pro Glu Gln Lys Ile Ser Pro Tyr Ala
50                               55                               60
Glu Leu Leu Leu Phe Leu Ala Ala Arg Ala Gln His Ile Gln Glu Lys
65                               70                               75                               80
Ile Ile Pro Ala Leu Lys Ser Gly Lys Thr Val Ile Ser Asp Arg Phe
85                               90                               95
His Asp Ser Thr Ile Val Tyr Gln Gly Ile Ala Gly Gly Leu Gly Glu
100                               105                               110
Ser Phe Val Thr Asn Leu Cys Tyr His Val Val Gly Asp Lys Pro Phe
115                               120                               125
Leu Pro Asp Ile Ile Phe Leu Leu Asp Ile Pro Ala Arg Glu Gly Leu
130                               135                               140
Leu Arg Lys Ala Arg Gln Lys His Leu Asp Lys Phe Glu Gln Lys Pro
145                               150                               155                               160
Gln Ile Phe His Gln Ser Val Arg Glu Gly Phe Leu Ala Leu Ala Glu
165                               170                               175
Lys Ala Pro Asp Arg Tyr Lys Val Leu Asp Ala Leu Leu Pro Thr Glu

```





(2) INFORMATIONS POUR LA SEQ ID NO: 263:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 244 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(265631..266362)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 263:

Met	Leu	Ile	Ala	Asp	Ser	Gln	Glu	Glu	Phe	Leu	Gln	Ile	Ala	Cys	Tyr
1			5					10					15		
Asp	Trp	Ile	Ser	Thr	Ala	Asn	Lys	Ala	Ile	His	Lys	Arg	Gly	Ala	Phe
		20						25					30		
Tyr	Val	Ala	Leu	Ser	Gly	Gly	Lys	Thr	Pro	Leu	Gln	Ile	Phe	Gln	Glu
		35					40					45			
Ile	Val	Lys	Lys	Arg	Ala	Ala	Ile	Ser	Asp	Cys	Ser	Lys	Ile	Val	Val
	50					55				60					
Phe	Trp	Gly	Asp	Glu	Arg	Ala	Asn	Glu	Asp	Val	Glu	Ala	Gly	Ser	Asn
65					70				75						80
Tyr	Leu	Lys	Ala	Met	Asp	Ile	Leu	Lys	Gly	Leu	Arg	Ile	Pro	Glu	Asp
				85					90					95	
Gln	Ile	Phe	Arg	Met	Asp	Thr	Ala	Asp	Pro	Lys	Gly	Asp	Glu	Ala	Tyr
			100					105					110		
Glu	Ala	Leu	Ile	Gln	Lys	Tyr	Val	Pro	Asp	Ala	Ile	Phe	Asp	Met	Val
		115					120					125			
Met	Leu	Gly	Val	Gly	Glu	Asp	Gly	His	Thr	Leu	Ser	Leu	Phe	Pro	Glu
	130					135					140				
Thr	Gln	Ala	Leu	Glu	Glu	Lys	Glu	Arg	Phe	Val	Val	Phe	Asn	Glu	Val
145					150				155						160
Pro	Gln	Leu	His	Thr	Arg	Arg	Met	Thr	Leu	Thr	Phe	Pro	Ile	Val	Arg
				165					170					175	
Gln	Ala	Arg	His	Leu	Val	Ala	Tyr	Val	Gln	Gly	Glu	Asn	Lys	Gln	Asp
			180					185					190		
Leu	Phe	His	Lys	Leu	Val	His	Pro	Leu	Gly	Arg	Asp	Thr	Phe	Pro	Ile
		195					200					205			
Glu	Arg	Val	Gly	Thr	Pro	Leu	Asn	Pro	Val	Gln	Trp	Val	Leu	Ser	Ser
	210					215				220					
Asp	Ser	Cys	Arg	Lys	Thr	Asp	Leu	Ala	Asp	Ile	Pro	Ala	Asp	Cys	Lys
225					230					235					240
Leu	Glu	Met	Phe												

(2) INFORMATIONS POUR LA SEQ ID NO: 264:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(266426..266938)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 264:

```

Lys Leu Phe Ile Asp Asn Pro Arg Trp Lys Gly Val Pro Phe Tyr Leu
1           5           10           15
Gln Ala Gly Lys Arg Leu Pro Lys Arg Thr Thr Asp Ile Ala Val Ile
          20           25           30
Phe Lys Lys Ser Ser Tyr Asn Leu Phe Asn Ala Glu Asn Cys Pro Leu
          35           40           45
Cys Pro Leu Asp Asn Asp Leu Leu Ile Ile Arg Ile Gln Pro Asp Glu
          50           55           60
Gly Val Ala Leu Gln Phe Asn Cys Lys Val Pro Gly Thr Asn Lys Leu
65           70           75           80
Val Arg Pro Val Lys Met Asp Phe Arg Tyr Asp Ser Tyr Phe Asn Thr
          85           90           95
Val Thr Pro Glu Ala Tyr Glu Arg Leu Leu Cys Asp Cys Ile Leu Gly
          100          105          110
Asp Arg Thr Leu Phe Thr Ser Asn Glu Glu Val Leu Ala Ser Trp Glu
          115          120          125
Leu Phe Ser Pro Leu Leu Glu Lys Trp Ser Gln Val His Pro Ile Phe
          130          135          140
Pro Asn Tyr Met Ala Gly Ser Leu Arg Pro Gln Glu Ala Asp Glu Leu
145          150          155          160
Leu Ser Arg Asp Gly Lys Ala Trp Arg Pro Tyr
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 265:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 340 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(266942..267961)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 265:

```

Ile Leu Gly Cys Thr Leu Glu Glu Ile Lys Asp Phe Gly Pro Thr Leu
1           5           10           15
Pro Ala Cys Pro Pro Cys Ile Val Val Ile Phe Gly Ala Thr Gly Asp
          20           25           30
Leu Thr Ser Arg Lys Leu Phe Pro Ala Leu Tyr Asn Leu Thr Lys Glu
          35           40           45
Gly Arg Leu Ser Glu Asn Phe Val Cys Val Gly Phe Ala Arg Arg Pro
          50           55           60
Lys Ser His Glu Gln Phe Arg Glu Glu Met Lys Leu Ala Val Gln His
65           70           75           80
Phe Ser His Ser Ser Glu Ile Asp Ile Arg Val Trp Glu Ser Leu Glu
          85           90           95
Asn Arg Ile Phe Tyr His Gln Ala Asn Phe Ser Asp Ala Glu Gly Tyr
          100          105          110
Ser Ala Leu Lys Ala Tyr Leu Glu Gln Leu Asp Gln Gln Tyr Gly Thr
          115          120          125
Gln Gly Asn Arg Leu Phe Tyr Leu Ser Thr Pro Pro Asp Tyr Phe Gln
130          135          140

```

```

Glu Ile Ile Arg Asn Leu Asn Arg His Gln Leu Phe Tyr His Glu Gln
145                150                155                160
Gly Ala Gln Gln Pro Trp Ser Arg Leu Ile Ile Glu Lys Pro Phe Gly
                165                170                175
Val Asn Leu Glu Thr Ala Arg Glu Leu Gln Gln Cys Ile Asp Ala Asn
                180                185                190
Ile Asp Glu Glu Ser Val Tyr Arg Ile Asp His Tyr Leu Gly Lys Glu
                195                200                205
Thr Val Gln Asn Ile Leu Thr Ile Arg Phe Ala Asn Thr Leu Phe Glu
                210                215                220
Ser Cys Trp Asn Ser Gln Tyr Ile Asp His Val Gln Ile Ser Val Ser
225                230                235                240
Glu Ser Ile Gly Ile Gly Ser Arg Gly Asn Phe Phe Glu Lys Ser Gly
                245                250                255
Met Leu Arg Asp Met Val Gln Asn His Leu Thr Gln Leu Leu Cys Leu
                260                265                270
Leu Thr Met Glu Pro Pro Ser Glu Phe Ser Ser Glu Glu Ile Lys Lys
                275                280                285
Glu Lys Ile Lys Ile Leu Lys Lys Ile Leu Pro Ile Arg Glu Glu Asp
                290                295                300
Ala Val Arg Gly Gln Tyr Gly Glu Gly Ile Val Gln Asp Val Ser Val
305                310                315                320
Leu Gly Tyr Arg Glu Glu Glu Asn Val Asp Pro Asn Ser Ser Val Glu
                325                330                335
Thr Tyr Val Ala
                340

```

(2) INFORMATIONS POUR LA SEQ ID NO: 266:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268066..268320)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 266:

```

Phe Ser Gly Asn Pro Leu Pro Met Gln Lys Ala Tyr Ala Ser Ser Val
1      5      10      15
Gln Ser Glu Ile Gln Glu Leu Ala Ala Leu Ile Gln Glu Met Thr Ala
20     25     30
Ile Glu Val Ile Leu Trp Asp Glu Arg Leu Ser Ser Ala Gln Ala Glu
35     40     45
Arg Met Leu Lys Ser Asp Cys Gly Leu Asn Arg Lys Gln Arg Lys Asn
50     55     60
Ser Ser Asp Ser Leu Ala Ala Thr Leu Ile Leu Ser Ser Phe Leu Asp
65     70     75     80
Ser Arg Lys Leu Tyr
85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 267:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 102 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268205..268510)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 267:

Met	Asn	Ile	Ala	Lys	Gln	Gln	Gln	Ala	Phe	Leu	Gly	Ile	Asp	Tyr	Gly
1				5				10					15		
Lys	Lys	Arg	Ile	Gly	Leu	Ala	Phe	Ala	Ser	Ser	Pro	Leu	Leu	Ile	Pro
		20					25					30			
Leu	Pro	Ile	Gly	Asn	Val	Glu	Ala	Arg	Ser	Ser	Leu	Thr	Leu	Thr	Ala
		35				40					45				
Gln	Ala	Leu	Val	Ser	Ile	Ile	Lys	Glu	Arg	Ala	Val	Thr	Thr	Val	Val
	50				55					60					
Phe	Gly	Glu	Ser	Ile	Thr	Tyr	Ala	Lys	Ser	Leu	Cys	Phe	Lys	Arg	Ala
65				70				75						80	
Ile	Arg	Asn	Ser	Arg	Thr	Ser	Arg	Thr	His	Pro	Arg	Asn	Asp	Cys	Tyr
		85						90				95			
Arg	Ser	His	Ser	Leu	Gly										
				100											

(2) INFORMATIONS POUR LA SEQ ID NO: 268:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 539 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268500..270116)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 268:

Met	Ser	Phe	Lys	Ser	Ile	Phe	Leu	Thr	Gly	Gly	Val	Val	Ser	Ser	Leu
1			5					10					15		
Gly	Lys	Gly	Leu	Thr	Ala	Ala	Ser	Leu	Ala	Leu	Leu	Leu	Glu	Arg	Gln
		20					25					30			
Asp	Leu	Lys	Val	Ala	Met	Leu	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	Val	Asp
		35				40					45				
Pro	Gly	Thr	Met	Asn	Pro	Tyr	Glu	His	Gly	Glu	Val	Tyr	Val	Thr	Asp
	50			55						60					
Asp	Gly	Val	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	His	Arg	Phe	Ser
65			70					75						80	
Ser	Val	Gln	Leu	Ser	Lys	Tyr	Ser	Ile	Ala	Thr	Ser	Gly	Gln	Ile	Tyr
		85				90						95			
Thr	Lys	Val	Leu	Thr	Lys	Glu	Arg	Asn	Gly	Glu	Phe	Leu	Gly	Ser	Thr
		100				105						110			
Val	Gln	Val	Ile	Pro	His	Val	Thr	Asn	Glu	Ile	Ile	Asn	Val	Ile	Gln
	115			120						125					
Ser	Cys	Ala	Asp	His	His	Lys	Pro	Asp	Ile	Leu	Ile	Val	Glu	Ile	Gly
	130					135				140					

Gly	Thr	Ile	Gly	Asp	Ile	Glu	Ser	Leu	Pro	Phe	Leu	Glu	Ala	Val	Arg
145					150					155					160
Gln	Phe	Arg	Cys	Glu	His	Pro	Gln	Asp	Cys	Leu	Ser	Ile	His	Met	Thr
			165						170					175	
Tyr	Val	Pro	Tyr	Leu	Arg	Ala	Ala	Lys	Glu	Ile	Lys	Thr	Lys	Pro	Thr
			180					185					190		
Gln	His	Ser	Val	Gln	Asn	Leu	Arg	Ser	Ile	Gly	Ile	Ser	Pro	Asp	Val
		195					200					205			
Ile	Leu	Cys	Arg	Ser	Glu	Ala	Pro	Leu	Ser	Thr	Glu	Val	Lys	Arg	Lys
	210					215					220				
Ile	Ser	Leu	Phe	Cys	Asn	Val	Pro	Glu	His	Ala	Val	Phe	Asn	Ala	Ile
225					230					235					240
Asp	Leu	Glu	Arg	Ser	Ile	Tyr	Glu	Met	Pro	Leu	Leu	Leu	Ala	Lys	Glu
				245					250					255	
Asn	Ile	Ser	Asp	Phe	Leu	Leu	Asn	Lys	Leu	Gly	Phe	Ser	Pro	Lys	Pro
			260					265					270		
Leu	Asp	Leu	Ser	Asp	Trp	Gln	Asp	Leu	Val	Glu	Ala	Leu	Cys	Asp	Lys
	275						280					285			
Glu	Arg	Gln	His	Val	Arg	Ile	Gly	Leu	Val	Gly	Lys	Tyr	Leu	Glu	His
	290					295					300				
Lys	Asp	Ala	Tyr	Lys	Ser	Val	Phe	Glu	Ala	Leu	Phe	His	Ala	Ser	Val
305					310					315					320
Pro	Ala	Asn	Cys	Ser	Leu	Glu	Leu	Val	Pro	Ile	Ala	Pro	Glu	Ser	Glu
				325					330					335	
Asp	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Cys	Asp	Gly	Cys	Leu	Ile	Pro	Gly
			340					345					350		
Gly	Phe	Gly	Thr	Arg	Ser	Trp	Glu	Gly	Lys	Ile	Ser	Ala	Ala	Arg	Tyr
	355						360					365			
Cys	Arg	Glu	Gln	Asn	Ile	Pro	Cys	Phe	Gly	Ile	Cys	Leu	Gly	Met	Gln
	370					375					380				
Ala	Leu	Val	Val	Glu	Tyr	Ala	Arg	Asn	Val	Leu	Asp	Lys	Pro	Leu	Ala
385					390					395					400
Asn	Ser	Met	Glu	Met	Asn	Pro	Glu	Thr	Pro	Asp	Pro	Val	Val	Cys	Met
			405						410					415	
Met	Glu	Gly	Gln	Asp	Ser	Val	Val	Lys	Gly	Gly	Thr	Met	Arg	Leu	Gly
			420					425					430		
Ala	Tyr	Pro	Cys	Arg	Ile	Ala	Pro	Gly	Ser	Leu	Ala	Ser	Ala	Ala	Tyr
	435						440					445			
Lys	Thr	Asp	Leu	Val	Gln	Glu	Arg	His	Arg	His	Arg	Tyr	Glu	Val	Asn
	450					455					460				
Pro	Ser	Tyr	Ile	Glu	Arg	Leu	Glu	Glu	His	Gly	Leu	Lys	Ile	Ala	Gly
465					470					475					480
Val	Cys	Pro	Leu	Gly	Glu	Leu	Cys	Glu	Ile	Val	Glu	Ile	Pro	Asn	His
				485					490					495	
Arg	Trp	Met	Leu	Gly	Val	Gln	Phe	His	Pro	Glu	Phe	Leu	Ser	Lys	Leu
			500					505					510		
Ala	Lys	Pro	His	Pro	Leu	Phe	Ile	Glu	Phe	Ile	Arg	Ala	Ala	Lys	Ala
	515						520					525			
Tyr	Ser	Leu	Glu	Lys	Ala	Asn	His	Glu	His	Arg					
	530						535								

## (2) INFORMATIONS POUR LA SEQ ID NO: 269:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 254 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 269:

(2) INFORMATIONS POUR LA SEQ ID NO: 270:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 271191..271613

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 270:

Ser Asn Glu Lys Leu Leu Tyr Phe Ile Ile Ile Met Leu Ser Lys Phe  
1 5 10 15  
Cys Lys Leu Ser Leu Ser Ala Ile Leu Leu Ile Asn Thr Leu Ala Pro  
20 25 30

Ser	Glu	Ala	Phe	Ser	Glu	Glu	Gly	Thr	Ser	Gly	Phe	Leu	Gly	Arg	Met
		35					40					45			
Lys	Ser	Trp	Ile	Leu	Lys	Asp	Lys	Thr	Ile	Leu	Ser	Thr	Thr	Glu	Glu
	50					55					60				
Ser	Gln	Thr	Ser	Ala	Ile	Glu	Lys	Val	Ser	Asp	Leu	Leu	Ser	Trp	Lys
65					70					75					80
Arg	Tyr	Asp	Tyr	Thr	Gln	Glu	Ser	Gly	Phe	Ala	Ile	Gln	Phe	Pro	Glu
				85					90					95	
Ser	Pro	Glu	His	Ser	Glu	Gln	Val	Ile	Glu	Val	Pro	Gln	Ser	Asp	Leu
			100					105					110		
Ala	Ile	Arg	Tyr	Asp	Thr	Tyr	Val	Ala	Glu	Thr	Pro	Ser	Asp	Ser	Thr
		115					120						125		
Val	Tyr	Val	Val	Ser	Val	Leu	Gly	Ile	Ser	Arg	Glu	Asn			
	130						135					140			

(2) INFORMATIONS POUR LA SEQ ID NO: 271:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 238 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 272219..272932

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 271:

Phe	Leu	Phe	Arg	Ser	Cys	Phe	Pro	Met	Leu	Asp	Val	Lys	Ser	Leu	Tyr
1				5					10					15	
Tyr	Ser	His	Ala	Ser	His	Ser	Val	Phe	Glu	Asp	Ala	Ser	Ala	Gly	Phe
			20					25					30		
Ala	Ser	Gly	Gln	Ile	Ser	Met	Val	Leu	Gly	Ala	Ser	Gly	Ser	Gly	Lys
		35					40					45			
Thr	Thr	Leu	Phe	Arg	Ile	Ile	Val	Gly	Leu	Leu	Ser	Cys	Ser	Leu	Gly
	50					55					60				
Glu	Ile	Leu	Trp	Lys	Gly	Gln	Pro	Ile	Gln	Gln	Glu	Gln	Ile	Ala	Tyr
65				70					75						80
Met	Gln	Gln	Lys	Glu	Ala	Leu	Leu	Pro	Trp	Arg	Thr	Val	Arg	Lys	Asn
			85					90						95	
Ile	Leu	Leu	Leu	Thr	Glu	Leu	Gly	Ser	Arg	Lys	Gln	Lys	Thr	Thr	Ile
			100				105						110		
Glu	Glu	Glu	Cys	Phe	Tyr	Asn	Val	Val	His	Ser	Phe	Gly	Leu	Ser	Ser
		115				120						125			
Leu	Leu	Asp	Arg	Phe	Pro	Asp	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg
	130					135					140				
Val	Val	Phe	Ala	Met	Gln	Ser	Leu	Ser	Pro	Lys	Pro	Ile	Leu	Leu	Leu
145					150					155					160
Asp	Glu	Pro	Phe	Thr	Ser	Leu	Asp	Pro	Ile	Thr	Lys	Xaa	Ile	Leu	Tyr
			165					170						175	
Gln	Asp	Val	Lys	Arg	Leu	Ala	Lys	Glu	Glu	Gly	Lys	Thr	Ile	Ile	Leu
		180					185						190		
Ala	Ser	His	Asp	Val	Gln	Asp	Cys	Leu	Gly	Val	Gly	Glu	Ala	Phe	Phe
		195				200						205			
Ala	Ile	Lys	Asn	Gln	Lys	Leu	His	Ser	Ile	Ala	Leu	Asn	Lys	Glu	Gln
	210					215					220				
Gly	Ile	Ala	Gly	Leu	Leu	Gln	Gln	Met	Lys	Asp	His	Leu	Val		



235

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(273596..274816)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 273:

Ser	Trp	Cys	Met	Glu	Lys	Asp	Phe	Leu	Glu	Asn	Val	Tyr	Arg	His	Phe
1				5					10					15	
Arg	Tyr	Arg	Phe	Phe	Lys	Leu	Ser	Ile	Leu	Pro	Ala	Leu	Leu	Gly	Leu
			20					25					30		
Trp	Leu	Phe	Phe	Thr	Pro	Asn	Ile	Leu	Asn	Tyr	Leu	Asp	Ser	Ser	Val
		35					40					45			
Ile	Leu	Ser	Asp	Lys	Ile	Cys	Gly	Val	Leu	Leu	Ile	Leu	Leu	Ser	Ala
	50					55					60				
Leu	Ser	Phe	Tyr	Asn	Pro	Val	Ile	Leu	Gln	Leu	Gly	Ile	Phe	Ile	Gly
65				70					75						80
Leu	Trp	Val	Ser	Phe	Phe	Ser	Cys	Ser	Ser	Asp	Leu	Leu	Pro	Leu	Val
			85					90					95		
Phe	Ala	His	Asp	Ser	Leu	Leu	Gly	Phe	Ala	Thr	Leu	Ala	Ile	Ile	Phe
			100					105					110		
Leu	Ile	Pro	Asn	Arg	Pro	Glu	Asp	Leu	Glu	Val	Gly	Pro	Thr	Ile	Pro
		115				120						125			
Glu	Thr	Cys	His	Tyr	Asn	Pro	Ser	Ser	Gly	Gly	Lys	Arg	Ala	Ala	Val
	130				135						140				
Leu	Ile	Phe	Ala	Phe	Val	Gly	Trp	Leu	Gln	Ser	Arg	Tyr	Leu	Thr	Ser
145				150					155						160
Ala	Ala	Leu	Asn	Ile	Ala	Asp	Ala	Asp	Thr	Ser	Cys	Ser	Leu	Phe	Phe
			165					170					175		
Ser	Ser	Thr	Leu	Met	Val	Ile	Tyr	Ser	Met	Leu	Ile	Val	Leu	Ser	Leu
			180					185					190		
Thr	Gly	Gly	Glu	Arg	Arg	Trp	His	Thr	Gln	Pro	Lys	Val	Val	Phe	Ile
		195				200						205			
Thr	Ala	Ile	Leu	Leu	Phe	Ile	Ala	Ile	Gly	Leu	Thr	Leu	Ala	Ala	Ile
	210				215						220				
Leu	Leu	Ser	Gln	Leu	Phe	Leu	Thr	Asn	Tyr	Glu	Gly	Val	Cys	Leu	Thr
225				230					235						240
Val	Ala	Pro	Val	Phe	Ser	Leu	Ala	Phe	Phe	Tyr	Asp	Glu	Ile	Arg	Ala
			245					250					255		
Thr	Trp	Asn	Tyr	Leu	Ser	Gln	Asn	Tyr	Ser	Asn	Arg	Lys	Gln	Leu	Ala
		260					265						270		
Ile	Thr	Ala	Phe	Tyr	Gly	Ser	Glu	Tyr	Tyr	Lys	Glu	Ser	Leu	Phe	Trp
	275				280							285			
Glu	Glu	Arg	Ser	Val	Leu	Pro	Phe	Ser	Gln	Ala	Cys	Lys	Gln	Ala	Phe
	290				295						300				
Ala	Gly	Leu	Ser	Phe	Pro	Leu	Asn	Leu	Ile	Phe	Ala	Cys	Ile	Phe	Ser
305				310					315						320
Ile	Phe	Phe	Val	Gln	Leu	Asn	Val	Asn	Leu	Ser	Ile	Pro	Asp	Thr	Cys
			325					330					335		
Arg	Phe	Phe	Val	Asn	Ser	Ala	Cys	Trp	Phe	Ile	Leu	Val	Leu	Ser	Ile
			340				345						350		
Phe	Ser	Phe	Ala	Glu	Ser	Leu	Arg	His	Leu	Arg	Trp	Leu	Ser	Leu	Leu
		355				360						365			
Phe	Ala	Ala	Gly	Ile	Ile	Leu	Ser	Pro	Val	Ile	Phe	His	Leu	Pro	Leu
	370				375						380				
Glu	Ala	Ser	Thr	Leu	Leu	Ser	Ile	Ile	Val	Ser	Gly	Ile	Ala	Phe	Ile
385				390					395						400
Ile	Leu	Ser	Met	Gly	Arg	Leu									
			405												

(2) INFORMATIONS POUR LA SEQ ID NO: 274:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 274821..275666

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 274:

```

Leu Ser Phe Leu Thr His Lys Lys Ser Glu Arg Lys Glu Lys Val Phe
1          5          10          15
Phe Asn Lys Glu Ala Ser Phe Ile Ser Ala Arg Lys Arg Phe Arg Phe
20          25          30
Phe Tyr Phe Cys Leu Ile Ser Ile Leu Asn Gly Arg Met Asp Thr Arg
35          40          45
Thr Pro Leu Arg Lys Lys Ile Leu Ile Ile Ser Thr Ala Leu Gly Phe
50          55          60
Val Leu Cys Val Gly Leu Met Ile His Thr Lys Arg Ser Ile Met Pro
65          70          75          80
Pro Lys Thr His Ile Pro Thr Thr Ala Lys Tyr Phe Pro Thr Ile Gly
85          90          95
Asp Pro Tyr Ala Pro Ile Asn Ile Thr Val Phe Glu Glu Pro Ser Cys
100          105          110
Ser Ala Cys Glu Glu Phe Ser Ser Glu Val Phe Pro Leu Ile Lys Lys
115          120          125
His Phe Val Asp Thr Gly Glu Ala Ser Leu Thr Leu Val Pro Val Cys
130          135          140
Phe Ile Arg Gly Ser Met Pro Ala Ala Gln Ala Leu Leu Cys Val Tyr
145          150          155          160
His His Asp Pro Lys Arg Pro Asp Pro Glu Ala Tyr Met Glu Tyr Phe
165          170          175
His Arg Ile Leu Thr Tyr Lys Lys Thr Lys Gly Ser His Trp Ala Thr
180          185          190
Pro Glu Val Leu Ala Lys Leu Ala Glu Lys Ile Pro Thr His Ser Gly
195          200          205
Arg Glu Ile Asn Pro Lys Gly Leu Ile Gln Cys Ile Asn Ser Gln Arg
210          215          220
Phe Thr Glu Gln Leu Lys Lys Asn Asn Ile Tyr Gly Ser Gln Ile Met
225          230          235          240
Gly Gly Gln Leu Ala Thr Pro Thr Ala Val Val Gly Asp Tyr Leu Ile
245          250          255
Glu Asp Pro Thr Phe Asp Glu Ile Glu Arg Val Ile Thr Gln Leu Arg
260          265          270
His Leu Gln Ala Ile Glu Glu Glu Val Arg
275          280

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(2) INFORMATIONS POUR LA SEQ ID NO: 275:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 529 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(276103..277689)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 275:

Met	His	His	Arg	Lys	Phe	Leu	Ala	Val	Ser	Ile	Ala	Phe	Val	Ser	Leu
1				5					10					15	
Ala	Phe	Gly	Leu	Thr	Ser	Cys	Tyr	His	Gln	Lys	Glu	Glu	Pro	Lys	Asp
			20					25					30		
Val	Leu	Arg	Ile	Ala	Ile	Cys	His	Asp	Pro	Met	Ser	Leu	Asp	Pro	Arg
		35					40					45			
Gln	Val	Phe	Leu	Ser	Lys	Asp	Val	Ser	Ile	Val	Lys	Ala	Leu	Tyr	Glu
	50					55					60				
Gly	Leu	Val	Arg	Glu	Lys	Glu	Ala	Ala	Phe	Gln	Leu	Ala	Leu	Ala	Glu
65					70					75					80
Arg	Tyr	His	Gln	Ser	Asp	Asp	Gly	Cys	Val	Tyr	Thr	Phe	Phe	Leu	Lys
			85						90					95	
Asn	Thr	Phe	Trp	Ser	Asn	Gly	Asp	Val	Val	Thr	Ala	Tyr	Asp	Phe	Glu
			100					105					110		
Glu	Ser	Ile	Lys	Gln	Ile	Tyr	Phe	Arg	Glu	Ile	Asp	Asn	Pro	Ser	Leu
		115					120					125			
Arg	Ser	Leu	Ala	Leu	Ile	Lys	Asn	Ser	His	Ala	Val	Leu	Thr	Gly	Ala
	130					135					140				
Leu	Pro	Val	Glu	Asp	Leu	Gly	Val	Arg	Ala	Leu	Asn	Ala	Lys	Ser	Leu
145					150					155					160
Glu	Ile	Val	Leu	Glu	Asn	Pro	Phe	Pro	Tyr	Phe	Leu	Glu	Ile	Leu	Ala
			165						170					175	
His	Pro	Val	Phe	Tyr	Pro	Val	His	Thr	Ser	Leu	Arg	Glu	Tyr	Tyr	Lys
			180					185					190		
Asp	Lys	Arg	Asn	Lys	Arg	Val	Phe	Pro	Met	Ile	Ser	Asn	Gly	Pro	Phe
		195					200					205			
Ala	Ile	Gln	Cys	Tyr	Glu	Pro	Gln	Arg	Tyr	Leu	Leu	Ile	Asn	Lys	Asn
	210					215					220				
Pro	Leu	Tyr	His	Ala	Lys	His	Asp	Val	Leu	Leu	Asn	Ser	Val	Cys	Leu
225					230					235					240
Gln	Ile	Val	Pro	Asp	Ile	His	Thr	Ala	Met	Gln	Leu	Phe	Gln	Lys	Asn
			245						250					255	
His	Ile	Asp	Leu	Val	Gly	Leu	Pro	Trp	Ser	Ser	Ser	Phe	Ser	Leu	Glu
		260						265					270		
Glu	Gln	Arg	Asn	Leu	Pro	Arg	Glu	Lys	Leu	Phe	Asp	Tyr	Pro	Val	Leu
		275					280					285			
Ser	Cys	Ser	Val	Leu	Phe	Cys	Asn	Ile	His	Gln	Thr	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Ser	Leu	Arg	Thr	Ala	Leu	Ser	Leu	Ala	Ile	Asn	Arg	Glu	Thr	Leu
305					310					315					320
Leu	Lys	Leu	Ala	Gly	Lys	Gly	Cys	Ser	Ala	Thr	Ser	Phe	Val	His	Pro
			325						330					335	
Gln	Leu	Ser	Gln	Ile	Pro	Ala	Thr	Thr	Leu	Ser	Gln	Asp	Glu	Arg	Ile
		340						345					350		
Ala	Leu	Ala	Lys	Gly	Tyr	Leu	Thr	Glu	Ala	Leu	Lys	Thr	Leu	Ser	Gln
		355					360					365			
Glu	Asp	Leu	Glu	Lys	Ile	Thr	Leu	Ile	Tyr	Pro	Ile	Glu	Ser	Val	Cys
	370					375					380				
Leu	Arg	Ala	Val	Val	Gln	Glu	Ile	Arg	Gln	Gln	Leu	Phe	Asp	Val	Leu
385					390					395					400
Gly	Phe	Lys	Ile	Ser	Thr	Leu	Gly	Leu	Glu	Tyr	His	Cys	Phe	Leu	Asp
			405						410					415	
Lys	Arg	Ser	Arg	Gly	Glu	Phe	Ser	Leu	Ala	Thr	Gly	Asn	Trp	Ile	Ala

Asp	Tyr	His	Gln	Ala	Ser	Ala	Phe	Leu	Ser	Val	Leu	Gly	Asn	Gly	Thr
		435					440					445			
Arg	Tyr	Lys	Asp	Phe	Gln	Leu	Ile	Asn	Trp	Gln	Asn	Gln	Lys	Tyr	Thr
	450					455					460				
Asn	Ile	Val	Ala	Gln	Leu	Leu	Ile	Gln	Glu	Ser	Ser	Asp	Leu	Gln	Leu
465					470					475					480
Met	Ala	Glu	Gln	Leu	Leu	Lys	Glu	Ser	Pro	Leu	Ile	Pro	Leu	Tyr	
			485					490						495	
His	Leu	Asp	Tyr	Val	Tyr	Ala	Lys	Gln	Pro	Arg	Val	Ser	Asp	Leu	Gln
		500						505					510		
Thr	Ser	Ser	Leu	Gly	Glu	Ile	Asp	Leu	Lys	Arg	Val	Ser	Leu	Ala	Glu
		515					520					525			
Gly															

(2) INFORMATIONS POUR LA SEQ ID NO: 276:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 278268..278816

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 276:

Ile	Ile	Thr	Thr	Leu	Phe	Val	Lys	Thr	Ser	Met	Phe	Phe	Leu	Ala	Lys
1				5					10					15	
Arg	Leu	Val	Gln	Leu	Asn	Lys	Asn	Pro	Phe	Leu	Leu	Lys	Lys	Phe	Ser
			20					25					30		
Glu	Thr	Thr	Val	Leu	Phe	Ile	Phe	Glu	Arg	Gln	Leu	Lys	Met	Trp	Glu
		35					40					45			
Gly	Tyr	Ser	Ile	Asp	Glu	Asn	Asn	Tyr	Ile	Ser	Asp	Tyr	Asn	Met	Glu
	50					55					60				
Phe	Gly	Arg	Pro	Leu	Leu	Gln	Lys	Leu	Ala	Asn	Pro	Val	Cys	Lys	Ala
65					70					75					80
Leu	Leu	Gln	Lys	Gln	Leu	Glu	Ala	Glu	Gln	Ala	Met	Thr	Leu	Ser	Asn
				85					90					95	
Gln	Val	Thr	Val	Gly	Asp	Ile	Val	Leu	Met	Arg	Ser	Pro	Ile	Phe	Glu
		100						105					110		
Lys	Ser	Val	Leu	Leu	Glu	Ala	Leu	Ile	Asn	Glu	Ile	Ile	Tyr	Gln	Glu
		115					120				125				
Ser	Leu	Phe	Leu	Phe	Lys	Lys	Pro	Glu	Asn	Cys	Ser	Met	Ser	Glu	Asp
	130					135					140				
Glu	Phe	Arg	Ala	Arg	Cys	Thr	Arg	Asn	Leu	Val	Glu	Asp	Leu	Phe	Asp
145					150					155					160
Gly	Leu	Met	Asn	Leu	Trp	Val	Gln	Ile	Lys	Leu	Ile	Lys	Gly	Tyr	Asp
			165						170					175	
Ser	Met	Gln	Asp	Tyr	Gln	Glu									

(2) INFORMATIONS POUR LA SEQ ID NO: 277:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 253 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(279013..279771)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 277:

Met	Ser	Lys	Leu	Thr	Gln	Val	Phe	Lys	Gln	Thr	Lys	Pro	Cys	Ile	Gly	1	5	10	15
Tyr	Leu	Thr	Ala	Gly	Asp	Gly	Gly	Thr	Ser	Tyr	Thr	Ile	Glu	Ala	Ala	20	25	30	
Lys	Ala	Leu	Ile	Gln	Gly	Gly	Val	Asp	Ile	Leu	Glu	Leu	Gly	Phe	Pro	35	40	45	
Phe	Ser	Asp	Pro	Val	Ala	Asp	Asn	Pro	Glu	Ile	Gln	Val	Ser	His	Asp	50	55	60	
Arg	Ala	Leu	Ala	Glu	Asn	Leu	Thr	Ser	Glu	Thr	Leu	Leu	Glu	Ile	Val	65	70	75	80
Glu	Gly	Ile	Arg	Ala	Phe	Asn	Gln	Glu	Val	Pro	Leu	Ile	Leu	Tyr	Ser	85	90	95	
Tyr	Tyr	Asn	Pro	Leu	Leu	Gln	Arg	Asp	Leu	Asp	Tyr	Leu	Arg	Arg	Leu	100	105	110	
Lys	Asp	Ala	Gly	Ile	Asn	Gly	Val	Cys	Val	Ile	Asp	Leu	Pro	Ala	Pro	115	120	125	
Leu	Ser	His	Gly	Glu	Lys	Ser	Pro	Phe	Phe	Glu	Asp	Leu	Leu	Ala	Val	130	135	140	
Gly	Leu	Asp	Pro	Ile	Leu	Leu	Ile	Ser	Ala	Gly	Thr	Thr	Pro	Glu	Arg	145	150	155	160
Met	Ser	Leu	Ile	Gln	Glu	Tyr	Ala	Arg	Gly	Phe	Leu	Tyr	Tyr	Ile	Pro	165	170	175	
Tyr	Glu	Ala	Thr	Arg	Asp	Ser	Glu	Val	Gly	Ile	Lys	Glu	Glu	Phe	Arg	180	185	190	
Lys	Val	Arg	Glu	His	Phe	Asp	Leu	Pro	Ile	Val	Asp	Arg	Arg	Asp	Ile	195	200	205	
Cys	Asp	Lys	Lys	Glu	Ala	Ala	His	Val	Leu	Asn	Tyr	Ser	Asp	Gly	Phe	210	215	220	
Ile	Val	Lys	Thr	Ala	Phe	Val	His	Gln	Thr	Thr	Met	Asp	Ser	Ser	Val	225	230	235	240
Glu	Thr	Leu	Thr	Ala	Leu	Ala	Gln	Thr	Val	Ile	Pro	Gly				245	250		

## (2) INFORMATIONS POUR LA SEQ ID NO: 278:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(279767..280777)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 278:

Leu	Lys	Leu	Arg	Ile	Leu	Leu	Gly	Ala	Ile	Asp	Gly	Pro	Arg	Val	Phe
1				5					10					15	
Leu	Lys	Arg	Glu	Asp	Leu	Leu	His	Thr	Gly	Ala	His	Lys	Leu	Asn	Asn
			20					25					30		
Ala	Leu	Gly	Gln	Cys	Leu	Leu	Ala	Lys	Tyr	Leu	Gly	Lys	Thr	Arg	Val
		35					40					45			
Val	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Val	Ala	Thr	Ala	Thr	Ala
	50					55				60					
Cys	Ala	Tyr	Leu	Gly	Leu	Asp	Cys	Val	Val	Tyr	Met	Gly	Ala	Lys	Asp
65					70					75					80
Val	Glu	Arg	Gln	Lys	Pro	Asn	Val	Glu	Lys	Met	Arg	Phe	Leu	Gly	Ala
			85					90						95	
Glu	Val	Val	Ser	Val	Thr	Lys	Gly	Ser	Cys	Gly	Leu	Lys	Asp	Ala	Val
			100					105					110		
Asn	Gln	Ala	Leu	Gln	Asp	Trp	Ala	Thr	Thr	His	Ser	Phe	Thr	His	Tyr
		115					120					125			
Cys	Leu	Gly	Ser	Ala	Leu	Gly	Pro	Leu	Pro	Tyr	Pro	Asp	Ile	Val	Arg
	130					135					140				
Phe	Phe	Gln	Ser	Val	Ile	Ser	Ala	Glu	Val	Lys	Glu	Gln	Ile	His	Ala
145					150					155					160
Val	Ala	Gly	Arg	Asp	Pro	Asp	Ile	Leu	Ile	Ala	Cys	Ile	Gly	Gly	Gly
			165					170						175	
Ser	Asn	Ala	Ile	Gly	Phe	Phe	His	His	Phe	Ile	Pro	Asn	Pro	Lys	Val
		180					185					190			
Gln	Leu	Ile	Gly	Val	Glu	Gly	Gly	Gly	Leu	Gly	Ile	Ser	Ser	Gly	Lys
	195						200					205			
His	Ala	Ala	Arg	Phe	Ala	Thr	Gly	Arg	Pro	Gly	Val	Phe	His	Gly	Phe
	210					215					220				
Tyr	Ser	Tyr	Leu	Leu	Gln	Asp	Asp	Asp	Gly	Gln	Val	Leu	Gln	Thr	His
225					230					235					240
Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Ser	Val	Gly	Pro	Asp	His	Ala
			245					250						255	
Glu	Met	His	Glu	Ser	Gly	Arg	Ala	Phe	Tyr	Thr	Leu	Ala	Thr	Asp	Glu
		260					265						270		
Glu	Ala	Leu	Arg	Ala	Phe	Phe	Leu	Thr	Arg	Asn	Glu	Gly	Ile	Ile	
	275						280				285				
Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Leu	Ala	His	Leu	Val	Ser	Ile	Ala
	290					295					300				
Pro	Ser	Leu	Pro	Lys	Glu	Gln	Ile	Val	Ile	Val	Asn	Leu	Ser	Gly	Arg
305					310					315					320
Gly	Asp	Lys	Asp	Leu	Pro	Gln	Ile	Ile	Arg	Arg	Asn	Arg	Gly	Ile	Tyr
				325					330					335	
Glu															

(2) INFORMATIONS POUR LA SEQ ID NO: 279:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 103 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(281295..281603)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 279:

```

Tyr Tyr Ser Ile Thr Lys Arg Cys Asp Met Lys Asn Gln Glu Glu Ser
1      5      10      15
Gly Trp Gln Ala Phe Leu Thr Leu Cys Ser Lys Met Gln Lys Glu Lys
      20      25      30
Phe Leu Gln Asp Leu Phe Ser Leu Phe Leu Ser Phe Gly Glu Arg Lys
      35      40      45
Asp Val Ala Ser Arg Tyr His Ile Ile Arg Ala Leu Leu Glu Gly Glu
      50      55      60
Leu Thr Gln Arg Glu Ile Ala Glu Lys Tyr Gly Val Ser Ile Ala Gln
65      70      75      80
Ile Thr Arg Gly Ser Asn Ala Leu Lys Gly Ser Asp Pro Gln Phe Lys
      85      90      95
Glu Phe Leu Gln Lys Glu Ile
      100

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 280:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 106 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(281787..282104)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 280:

```

Leu Pro Ser Glu Ala Cys Met Ser Leu Asp Thr Ala Gly Lys Pro His
1      5      10      15
Trp Lys Ile Pro Glu Gly Phe Leu Gln Phe Ala Phe Ala Tyr Tyr Arg
      20      25      30
Ser Trp Val Glu His Trp Val Lys Ser Leu Arg Arg Gly Ser Leu
      35      40      45
Ile Gln Leu Pro Ala Arg Ser Ile Gln Val Ser Leu Ile Thr Thr Gln
      50      55      60
Thr Gly Tyr Phe Ala Arg Gln Asn Arg Arg Gly Gly Phe Gln Val Phe
65      70      75      80
Tyr Ser Ile Tyr Gly Leu Glu Gly Lys Val Gln Pro His Gln Ala Pro
      85      90      95
Gly Asp Met Leu Cys Asp Ile Thr Glu Asp
      100      105

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 281:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 514 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(282794..284335)



(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 281:

Ser	Glu	Gly	Leu	Glu	Met	Phe	Val	Ser	Phe	Asp	Lys	Ser	Arg	Cys	Arg	1	5	10	15
Ala	Asp	Val	Pro	Asp	Phe	Phe	Glu	Arg	Thr	Gly	Asn	Phe	Leu	Leu	His	20	25	30	
Cys	Val	Ala	Arg	Gly	Ile	Asn	Val	Leu	Tyr	Arg	Val	Lys	Gln	Ile	Pro	35	40	45	
Asn	Tyr	Pro	Ser	Cys	Tyr	Phe	Ser	His	Lys	Glu	Ile	Ser	Cys	Cys	Arg	50	55	60	
Arg	Ile	Ala	Asn	Ile	Val	Ile	Cys	Ile	Leu	Thr	Gly	Pro	Leu	Met	Leu	65	70	75	80
Leu	Ala	Thr	Val	Leu	Gly	Leu	Leu	Ala	Tyr	Arg	Phe	Ser	Ser	Thr	Tyr	85	90	95	
Gln	Thr	Ser	Leu	Gln	Glu	Arg	Phe	Arg	Tyr	Lys	Tyr	Glu	Gln	Lys	Gln	100	105	110	
Ala	Leu	Asp	Glu	Tyr	Arg	Asp	Arg	Glu	Glu	Lys	Val	Ile	Thr	Leu	Gln	115	120	125	
Lys	Phe	Cys	Arg	Gly	Phe	Leu	Val	Arg	Asn	His	Leu	Leu	Asn	Gln	Glu	130	135	140	
Thr	Leu	Thr	Thr	Cys	Lys	Gln	Trp	Gly	Gln	Lys	Leu	Leu	Glu	Gly	Glu	145	150	155	160
Lys	Phe	Pro	Arg	Val	Pro	Glu	Gly	Arg	Ser	Leu	Val	Tyr	Ile	Ser	Lys	165	170	175	
Gln	Phe	Pro	Ser	Leu	Val	Glu	Asn	Phe	Leu	Phe	Glu	Glu	Lys	Leu	Pro	180	185	190	
Val	Ser	Arg	Ile	Ser	Val	Asp	Ser	Met	Cys	Leu	Tyr	Lys	Glu	Asn	Pro	195	200	205	
Gln	Ala	Phe	Asp	Glu	Ala	Ile	Lys	Glu	Leu	Leu	Phe	Leu	Phe	Lys	Glu	210	215	220	
Val	His	Phe	Arg	Asp	Phe	Val	Val	Glu	Thr	Glu	Ser	Pro	Thr	Asp	Asp	225	230	235	240
Phe	Pro	Leu	Ala	Val	Lys	Val	His	Asn	Tyr	Trp	Val	Cys	Pro	Arg	Tyr	245	250	255	
Asp	Asn	Leu	Pro	Leu	Phe	Ile	Gln	Glu	Gly	Lys	Asp	Gly	Ser	Pro	Glu	260	265	270	
Gly	Arg	Ile	Gly	Leu	Val	Asp	Leu	Glu	Thr	Phe	Ser	Trp	Ser	Pro	His	275	280	285	
Pro	Cys	Pro	Val	Glu	Glu	Leu	Ala	Val	Met	Phe	Pro	Met	Ser	Lys	Glu	290	295	300	
Leu	Leu	Met	Thr	Glu	Ala	Lys	Lys	Leu	Gln	Ile	Pro	Phe	Ser	Thr	Lys	305	310	315	320
Glu	Val	Glu	Arg	Ser	Val	Glu	Lys	Gly	Leu	Ala	Phe	Phe	Glu	His	Met	325	330	335	
Leu	Gly	His	Pro	Asp	Phe	Cys	Ser	Gln	Lys	Ser	Val	Thr	Pro	Leu	Arg	340	345	350	
Asn	Cys	Ala	Pro	Tyr	Leu	His	Leu	Glu	Val	Trp	Arg	Phe	Ser	Leu	Lys	355	360	365	
Ile	Phe	Asp	Ile	Leu	Lys	Ala	Ala	Ile	Arg	Leu	Asn	Gly	Ala	Leu	Asn	370	375	380	
Val	Leu	Leu	Ser	Pro	Asp	Ile	Arg	Glu	Arg	Leu	Ser	Ala	Ile	Ser	Asp	385	390	395	400
Lys	Gln	Trp	Leu	Ala	Ile	Ser	Ser	Gln	Val	Thr	Ser	Ser	Leu	Leu	Glu	405	410	415	
Gln	Val	Ser	Thr	Asn	Ile	Tyr	Gln	Ser	His	Thr	Glu	Glu	Ala	Lys	Arg	420	425	430	
Val	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Met	Cys	Arg	Ser	Pro	Ile	Phe	Arg	435	440	445	

Lys Ser Ile Phe Ile Lys Asn Leu Pro Glu Leu Leu Asn Lys Lys Leu  
 450 455 460  
 Gln Leu Leu Pro Glu Glu Lys Glu Ile Ser Glu Ala Leu Ala Ser Leu  
 465 470 475 480  
 Cys Leu Arg Ala Val Met Glu Glu Leu Val Ala Thr Gly Asn Ile Tyr  
 485 490 495  
 Ser Tyr Asp Ser Met Asp Asp Phe Phe Glu Gly Gln Tyr Cys Arg Ile  
 500 505 510  
 Arg Tyr

## (2) INFORMATIONS POUR LA SEQ ID NO: 282:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 112 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 284460..284795

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 282:

Lys Ile His Lys Lys Ile Lys Lys Cys Leu Thr Thr Thr Leu Leu Pro  
 1 5 10 15  
 Asn Leu Phe Ser Leu Phe Thr Asn Arg Asn Arg Glu Thr Leu Met Ile  
 20 25 30  
 Val Thr Phe Asp Lys Tyr Leu Ala Pro Glu Leu Gly Pro Asp Pro Leu  
 35 40 45  
 Glu Arg Leu Gly Asn Val Leu Leu Tyr Pro Ile Ile Arg Gly Phe Gly  
 50 55 60  
 Ser Leu Val Ser Val Lys Thr Leu Gly Glu Lys Arg Phe Leu Cys Phe  
 65 70 75 80  
 Ser Asp Lys Val Val Ser Leu Cys Val Asn Ala Phe Phe Val Trp Tyr  
 85 90 95  
 Ala Ile Phe Ser Gln His Leu Leu Arg Val Cys Ser Leu Cys Glu Gly  
 100 105 110

## (2) INFORMATIONS POUR LA SEQ ID NO: 283:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 286 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 284817..285674

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 283:

Arg Pro Ile Lys Leu His Glu Leu Phe Leu Ile Val Leu Leu Lys Arg  
 1 5 10 15  
 Glu Thr Arg Leu Arg Ser Leu Ser Lys Asn Asn Ala Pro Pro Leu Ser

(2) INFORMATION POUR LA SEQ ID NO: 284:

(A) LONGUEUR: 167 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 285637..286137

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 284:

Lys	Ala	Leu	Pro	Leu	Gln	Lys	Trp	Lys	Ile	Phe	Met	Thr	Glu	Gln	Pro
1				5					10					15	
His	Arg	Leu	Ser	Glu	Glu	Ala	Arg	Ser	Ile	Ala	Asn	Glu	Ala	Lys	Glu
			20					25					30		
Arg	Leu	Leu	Lys	Leu	Asn	Asp	Lys	Pro	Glu	Leu	Ser	Arg	Pro	Tyr	Leu
			35				40					45			
Val	Lys	Gly	Phe	Leu	Ser	Lys	Ile	Ser	Arg	Gly	Ile	Ser	Asp	Lys	Glu
	50					55					60				
Ala	Ala	Ser	Lys	Phe	Ser	Lys	Ala	Ile	Val	Thr	Ser	Leu	Leu	Gly	Tyr
65					70					75					80



(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 287:

```

Ser Leu Ile Leu Glu Asp Ala Val Ala Leu Asp Pro Pro Pro Pro Pro
1      5      10      15
Pro His Thr Ser Gln Asn Thr Pro Ser Pro Lys Asp Ser Ser Leu Val
20      25      30
Ala Arg Thr Asp Lys Ala Ala Thr Asp Ile Phe Asn Ser Ala Lys His
35      40      45
Lys Ala Ile Glu Thr Thr Lys Arg Ser Asp Gln Gln Ser Arg Ser Leu
50      55      60
Pro Ile Leu His Leu Leu Ala Ala Asp Pro Glu Pro Ile Val Phe His
65      70      75      80
Ser Thr His Gln Thr Asn His Asn Asp Pro Gln Arg Met Leu Cys Asp
85      90      95
Ala Ile Leu Gln Ala Asn Arg Ile Ile Thr Met Arg Ile Phe Asn Ile
100     105     110
Gly Ser Pro Glu Ile Ile Arg Ala Leu Ile Arg Ala Val Arg Arg Asn
115     120     125
Ile Pro Val Ile Val Ser Ala Trp Asn Phe Pro Asn Leu Ser Asn Trp
130     135     140
Asp Arg Glu Ser Lys Leu Tyr Val Glu Leu Arg Gly Asn Pro Gln Ile
145     150     155     160
Cys Leu His Lys Lys Thr Thr Leu Ile Asp Asn Gln Leu Thr Ile Ile
165     170     175
Gly Thr Ala Asn Tyr Thr Lys Ser Ser Phe Phe Lys Asp Ile Asn Leu
180     185     190
Thr Ala Leu Ile Gln Asn Pro Ala Leu Tyr Ser Leu Ile Leu Ser Gly
195     200     205
Thr Arg Gly Ser Val Ser Ile Gly Ser Gln Thr Ile Ser Tyr Tyr Pro
210     215     220
Leu Pro Phe Pro Gln Ser Asn Thr Lys Thr Leu Pro Ile Ile Gln Glu
225     230     235     240
Ile Gln Lys Ala Gln Arg Thr Ile Lys Ile Ala Met Asn Ile Phe Ser
245     250     255
His Pro Glu Ile Phe Leu Ala Leu Glu Gln Ala Arg Leu Arg Gly Val
260     265     270
Thr Ile Thr Ile Val Ile Asn Lys Lys Glu Ser Ala His Thr Leu Asp
275     280     285
Ile Leu His Arg Ile Ser Ala Leu Leu Leu Leu Lys Ser Val Thr Thr
290     295     300
Val Asp Ser Leu His Ala Lys Ile Cys Leu Ile Asp Asp Gln Thr Leu
305     310     315     320
Ile Phe Gly Ser Pro Asn Trp Thr Tyr His Gly Met His Lys Asn Leu
325     330     335
Glu Asp Leu Leu Ile Val Thr Pro Leu Thr Pro Lys Gln Ile His Ser
340     345     350
Ile Gln Glu Ile Trp Ala Phe Leu Leu Lys Asn Ser Ser Pro Val
355     360     365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 288:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 312 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 289744..290679

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 288:

Met	Leu	Ala	Gly	Ser	Lys	Arg	Lys	His	Lys	Thr	Pro	Glu	Asp	Thr	Ser	1	5	10	15
Ser	Ser	Ser	Ser	Lys	Arg	Ala	Arg	Ser	Ser	Ser	Ser	Gln	Val	Val	Pro	20	25	30	
Arg	Leu	Leu	Gln	His	His	Glu	Leu	Ile	Gln	Leu	Tyr	Ser	Ala	His	Gln	35	40	45	
Gln	Arg	Asn	Asn	Glu	Pro	Val	Lys	Met	Ile	Cys	Glu	Thr	Ile	Leu	Gln	50	55	60	
Ala	Lys	Arg	Ser	Val	Leu	Leu	Lys	Val	Phe	Asn	Ile	Gly	Ser	Pro	Arg	65	70	75	80
Ile	Leu	Ala	Ala	Leu	Ala	Glu	Ala	Ser	Asn	Arg	Ala	Pro	Val	Ser	Val	85	90	95	
His	Tyr	Gln	Met	Gly	Pro	Phe	Ser	Lys	His	Cys	Thr	Glu	Gly	Asn	Val	100	105	110	
Gln	Phe	Arg	Pro	Arg	Arg	Gly	Cys	Ser	Leu	Leu	His	Arg	Lys	Thr	Leu	115	120	125	
Leu	Ile	Asp	Asn	Asn	Ile	Val	Val	Thr	Gly	Thr	Ala	Asn	Tyr	Thr	Glu	130	135	140	
Ala	Ser	Leu	Glu	Lys	Asp	Val	Asn	Leu	Thr	Ala	Lys	Ile	Phe	Ser	Glu	145	150	155	160
His	Leu	Tyr	Arg	Trp	Ala	Phe	Arg	His	Asp	Arg	Gly	Glu	Val	Arg	Val	165	170	175	
Gly	Ser	Gln	Gln	Val	Ser	Tyr	Tyr	Ser	Leu	Ser	Gln	Ile	Arg	Arg	Asp	180	185	190	
Leu	Cys	Val	Lys	Ala	Ile	Leu	Glu	Ala	Asn	Gly	Ile	Val	Leu	Arg	Glu	195	200	205	
Arg	Thr	Cys	Glu	Gly	Ile	Leu	His	Thr	Lys	Val	Cys	Cys	Ile	Asp	Ser	210	215	220	
Ser	Thr	Leu	Ile	Ile	Gly	Ser	Val	Asn	Trp	Ser	Arg	Gly	Gly	Leu	Thr	225	230	235	240
Leu	Asn	Leu	Glu	Glu	Phe	Leu	Ile	Ile	Asn	Pro	Leu	Thr	Glu	Thr	Gln	245	250	255	
Leu	Glu	Cys	Tyr	Asn	Glu	Leu	Trp	Ala	Tyr	Ile	Glu	Thr	Asn	Ser	Arg	260	265	270	
Leu	Met	Thr	Lys	Glu	Leu	Ile	Gln	Leu	His	Glu	Lys	Arg	Lys	Lys	Ser	275	280	285	
Ile	Thr	Asp	Pro	Lys	Gln	Thr	Ser	Ser	Ser	Thr	Gln	Asp	Glu	Glu	Asn	290	295	300	
Ala	Ser	Thr	Ser	Ala	Gln	Gln										305	310		

## (2) INFORMATIONS POUR LA SEQ ID NO: 289:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 290828..291535

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 289:

```

Leu Phe Ser Ser Ala Ser Pro Arg Thr Phe Thr Ser Pro Phe Phe Cys
1      5      10      15
Arg Ile Ile Ser Tyr Ser Ser Val Arg Phe Lys Ser Leu Ser Ile Phe
20      25      30
Thr Ala Phe Arg Gln Ser Ser Glu Ser Arg Asn Ser Pro Leu Arg Glu
35      40      45
Thr Thr Gly Ser Ser Ser Arg His Arg Tyr His Arg His Gly Glu Thr
50      55      60
Ser Ser Ser Ser Arg Ile Glu Thr Val Gly Ser Arg His Phe Ser Ser
65      70      75      80
Arg Arg Glu Ser Ser Arg Thr Gly Ser Arg Ser Ser Arg His Ser Glu
85      90      95
Arg Ala Arg His His Glu Ser Arg Ser His Arg His Ser Ser Ser Ser
100     105     110
Arg His His Val Thr Arg Ser Gln Ser Ser Ala Leu Pro Gln Leu Gln
115     120     125
Glu Arg Pro Val Pro His Pro Leu Ala Glu Arg Glu Leu Ile Thr Phe
130     135     140
His Ser Val His Gln Gln Gln Asn Asn Asn Pro Leu Arg Met Ile Cys
145     150     155     160
Asp Thr Ile Arg Gln Ala Gln Arg Gly Ile Phe Met Arg Ile Tyr Ala
165     170     175
Ile Ser Ser Asp Asp Ile Ile Gln Ser Leu Ile Gln Thr Ser His His
180     185     190
Val Pro Val Glu Val Lys Tyr His Cys Gly Glu Ser Leu Pro Val Ala
195     200     205
Cys Gln Asn Ser Arg Val Val Leu Arg Pro Thr Asn Gly Arg Thr Leu
210     215     220
Gln His Lys Lys Leu Cys Trp Leu Ile Ser Lys Gln
225     230     235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 290:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 209 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 291604..292230

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 290:

```

Glu Ser Ser Glu Leu His Asp Ala Val Phe Ser Glu Arg Pro Gln Leu
1      5      10      15
Val His Val Gly Pro Gln Leu Leu Asn Tyr Ile Pro Ile Gln Arg Leu
20      25      30
Ile Pro Asn Ala Ala Ser Lys Met Ile Leu Asn Ala Ile Asn Gln Ala
35      40      45
Thr Asp Ser Ile Phe Val Leu Met Tyr Ile Phe Leu Ser Pro Glu Phe
50      55      60
Phe Leu Ala Leu Ala Gln Ala Met Arg Arg Gly Val Arg Val Lys Val
65      70      75      80
Ile Ile Asp Asn His Ser Lys Gln Asp Thr Cys Lys Leu Leu Ser Lys
85      90      95
Leu Gly Ile Gln Leu Pro Leu Tyr Glu Arg Lys Thr Glu Gly Ile Leu

```



			100					105					110				
His	Thr	Lys	Ile	Cys	Cys	Ile	Asp	Asn	Lys	Thr	Pro	Ile	Phe	Gly	Ser		
		115					120					125					
Ala	Asn	Trp	Ser	Gly	Ala	Gly	Met	Ile	Lys	Asn	Phe	Glu	Asp	Leu	Phe		
	130						135				140						
Ile	Leu	Arg	Pro	Ile	Thr	Glu	Thr	Gln	Leu	Gln	Ala	Phe	Met	Asp	Val		
145					150					155					160		
Trp	Ser	Leu	Leu	Glu	Thr	Asn	Ser	Ser	Tyr	Leu	Ser	Pro	Glu	Ser	Val		
			165						170						175		
Leu	Thr	Ala	Pro	Thr	Pro	Ser	Ser	Arg	Pro	Thr	Gln	Gln	Asp	Thr	Asp		
		180						185					190				
Ser	Asp	Asp	Glu	Gln	Pro	Ser	Thr	Ser	Gln	Gln	Ala	Ile	Arg	Met	Arg		
		195					200					205					
Lys																	

(2) INFORMATIONS POUR LA SEQ ID NO: 291:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 241 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 292326..293048

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 291:

Arg	Leu	Ser	Ser	Ser	Ser	Val	Ser	Leu	Leu	Phe	Phe	Lys	Ala	Ser	Ser		
1				5					10					15			
Phe	His	Tyr	Arg	Val	Ser	Ile	Thr	Val	Gln	Pro	Gly	Glu	Phe	Leu	Met		
		20						25					30				
Thr	Lys	Pro	Ser	Xaa	Leu	Tyr	Val	Ile	Gln	Pro	Phe	Ser	Val	Phe	Asn		
		35					40					45					
Pro	Arg	Leu	Gly	Arg	Phe	Ser	Ile	Asp	Ser	Asp	Thr	Tyr	Ile	Glu	Glu		
	50					55					60						
Glu	Asn	Arg	Leu	Ala	Ser	Phe	Ile	Glu	Ser	Leu	Pro	Leu	Glu	Ile	Phe		
65				70						75				80			
Asp	Ile	Pro	Ser	Phe	Met	Glu	Thr	Ala	Ile	Ser	Asn	Ser	Pro	Tyr	Ile		
			85					90					95				
Leu	Ser	Trp	Glu	Thr	Thr	Lys	Asp	Gly	Ala	Leu	Phe	Thr	Ile	Leu	Glu		
		100						105					110				
Pro	Lys	Leu	Ser	Ala	Cys	Ala	Ala	Thr	Cys	Leu	Val	Ala	Pro	Ser	Ile		
		115					120					125					
Gln	Met	Lys	Ser	Asp	Ala	Glu	Leu	Leu	Glu	Glu	Ile	Lys	Gln	Ala	Leu		
	130					135					140						
Leu	Arg	Ser	Ser	His	Asp	Gly	Val	Lys	Tyr	Arg	Ile	Thr	Arg	Glu	Ser		
145				150						155				160			
Phe	Ser	Pro	Glu	Lys	Lys	Thr	Pro	Lys	Val	Ala	Leu	Val	Asp	Asn	Asp		
			165					170					175				
Ile	Glu	Leu	Ile	Arg	Asn	Val	Asp	Phe	Leu	Gly	Arg	Ala	Val	Asp	Ile		
		180						185					190				
Val	Lys	Leu	Asp	Pro	Ile	Asn	Ile	Leu	Asn	Thr	Val	Ser	Glu	Glu	Asn		
		195				200						205					
Ile	Leu	Asp	Tyr	Ser	Phe	Thr	Arg	Glu	Thr	Ala	Gln	Leu	Ser	Ala	Asp		
	210					215					220						

Gly Arg Phe Gly Ile Pro Pro Gly Thr Lys Leu Phe Ser Lys Pro Ser  
 225 230 235 240  
 Phe

(2) INFORMATIONS POUR LA SEQ ID NO: 292:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 508 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 293330..294853

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 292:

Lys Pro Asn Pro His Arg Gly Lys Arg Pro Ser Arg Leu Thr Arg Ile  
 1 5 10 15  
 His Arg Ile Glu Val Gln Leu Pro Asp Ser Ser Arg Ile Pro Tyr Asp  
 20 25 30  
 Cys Ser Cys Ile Asn Arg Tyr Gly Ile Phe Pro Arg Phe Asn Pro Asn  
 35 40 45  
 Gln Asn Lys Leu Asn Val Ile Arg Lys Ile Lys Ser Gly Phe Gln Arg  
 50 55 60  
 Ser Leu Asp Asp Tyr His Ile Tyr Gln Ile Glu Arg Lys Xaa Xaa Phe  
 65 70 75 80  
 Ser Phe Ser Pro Lys His Arg Ser Leu Ser Ser Thr Ser His Ser Glu  
 85 90 95  
 Asp Ser Asp Leu Asp Leu Ser Glu Ala Ala Phe Ser Gly Ser Leu  
 100 105 110  
 Thr Cys Glu Phe Val Lys Lys Ser Thr Gln His Ala Lys Asn Thr Val  
 115 120 125  
 Thr Cys Ser Thr Ala Ala His Ser Leu Tyr Thr Leu Lys Glu Asp Asp  
 130 135 140  
 Ser Ser Asn Pro Ser Glu Lys Arg Leu Glu Asn Cys Phe Arg Asn Trp  
 145 150 155 160  
 Ile Asp Asn Lys Leu Ser Ala Asn Ser Pro Asp Ser Trp Ser Ala Phe  
 165 170 175  
 Ile Gln Lys Phe Gly Thr His Tyr Ile Ala Ser Ala Thr Phe Gly Gly  
 180 185 190  
 Ile Gly Phe Gln Val Leu Lys Leu Ser Phe Glu Gln Val Glu Asp Leu  
 195 200 205  
 His Ser Lys Lys Ile Ser Leu Glu Thr Ala Ala Ala Asn Ser Leu Leu  
 210 215 220  
 Lys Gly Ser Val Ser Ser Ser Thr Glu Ser Gly Tyr Ser Ser Tyr Ser  
 225 230 235 240  
 Ser Thr Ser Ser Ser His Thr Val Phe Leu Gly Gly Thr Val Leu Pro  
 245 250 255  
 Ser Val His Asp Glu Arg Leu Asp Phe Lys Asp Trp Ser Glu Ser Val  
 260 265 270  
 His Leu Glu Pro Val Pro Ile Gln Val Ser Leu Gln Pro Ile Thr Asn  
 275 280 285  
 Leu Leu Val Pro Leu His Phe Pro Asn Ile Gly Ala Ala Glu Leu Ser  
 290 295 300  
 Asn Lys Arg Glu Ser Leu Gln Gln Ala Ile Arg Val Tyr Leu Lys Glu

305					310					315					320
His	Lys	Val	Asp	Glu	Arg	Gly	Glu	Arg	Thr	Thr	Phe	Thr	Ser	Gly	Ile
				325					330					335	
Asp	Asn	Pro	Ser	Ser	Trp	Phe	Thr	Leu	Glu	Ala	Ala	His	Ser	Pro	Leu
			340					345					350		
Val	Val	Ser	Thr	Pro	Tyr	Val	Ala	Ser	Trp	Ser	Thr	Leu	Pro	Tyr	Leu
		355					360					365			
Phe	Pro	Thr	Leu	Arg	Glu	Arg	Ser	Ser	Ala	Thr	Pro	Ile	Val	Phe	Tyr
	370					375					380				
Phe	Cys	Val	Asp	Asn	Asn	Glu	His	Ala	Ser	Gln	Lys	Ile	Leu	Asn	Gln
385				390					395					400	
Ser	Tyr	Cys	Phe	Leu	Gly	Ser	Leu	Pro	Ile	Arg	Gln	Lys	Ile	Phe	Gly
			405					410					415		
Ser	Glu	Phe	Ala	Ser	Phe	Pro	Tyr	Leu	Ser	Phe	Tyr	Gly	Asn	Ala	Lys
		420					425					430			
Glu	Ala	Tyr	Phe	Asp	Asn	Thr	Tyr	Tyr	Pro	Thr	Arg	Cys	Gly	Trp	Ile
		435					440					445			
Val	Glu	Lys	Leu	Asn	Thr	Thr	Gln	Asp	Gln	Phe	Leu	Arg	Asp	Gly	Asp
	450				455					460					
Glu	Val	Arg	Leu	Lys	His	Val	Ser	Ser	Gly	Lys	Tyr	Leu	Ala	Thr	Thr
465					470				475					480	
Pro	Leu	Lys	Asp	Thr	His	Gly	Thr	Leu	Thr	Arg	Thr	Thr	Asn	Cys	Glu
			485					490					495		
Asp	Ala	Ile	Phe	Ile	Ile	Lys	Lys	Ser	Ser	Gly	Tyr				
		500					505								

(2) INFORMATIONS POUR LA SEQ ID NO: 293:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 225 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(295010..295684)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 293:

Met	Val	Ile	Leu	Val	Glu	Ala	Lys	His	Ile	Ser	Lys	Val	Ile	Gln	Gln
1			5						10					15	
Gln	Asp	Val	Cys	Ile	Pro	Ile	Leu	Lys	Asp	Val	Ser	Phe	Gln	Leu	His
		20					25						30		
Ala	Gly	Glu	Val	Val	Ala	Ile	Thr	Gly	Ala	Ser	Gly	Ser	Gly	Lys	Ser
	35					40					45				
Ser	Leu	Leu	His	Leu	Leu	Gly	Thr	Leu	Asp	Gln	Pro	Ser	Ser	Gly	Gln
	50				55				60						
Ile	Leu	Phe	Phe	Gly	Lys	Gln	Val	Arg	Arg	Glu	Glu	Leu	Pro	Ile	Phe
65				70					75					80	
Arg	Asn	Cys	Arg	Ile	Gly	Phe	Ile	Phe	Gln	Asn	Phe	Tyr	Leu	Leu	Glu
			85					90					95		
Asp	Asp	Ser	Val	Ile	Asn	Asn	Val	Leu	Met	Pro	Ala	Gln	Ile	Ala	Arg
		100					105					110			
Lys	Asp	Thr	Gly	Gln	Lys	Ser	Lys	Ala	Arg	Glu	Arg	Ala	Leu	Ala	Leu
	115					120						125			
Leu	Glu	Ser	Val	Gly	Leu	Val	Asp	Arg	Arg	Asp	Glu	Lys	Gly	Ser	Leu
130						135					140				

Leu Ser Gly Gly Glu Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Met  
 145 150 155 160  
 Asn Asp Pro Glu Ile Val Leu Ala Asp Glu Pro Ser Gly Asn Leu Asp  
 165 170 175  
 His Arg Thr Ala Asp Thr Ile His Glu Leu Leu Leu Ala Leu Ala Glu  
 180 185 190  
 Lys His Arg Gly Val Leu Ile Val Thr His Asp Arg Glu Leu Ala Glu  
 195 200 205  
 Lys Cys His Arg Glu Glu Ile Leu Arg Asp Gly Thr Leu Met Gln Arg  
 210 215 220  
 Gln  
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 294:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 215 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(295692..296336)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 294:

Gly Ile Gly Cys Ile His Pro Leu Gly Ile Arg Arg Leu Gly Met His  
 1 5 10 15  
 Asn Gly Trp Gln Val Phe Leu Pro Ser Val Gln Asp Ile Pro Val Met  
 20 25 30  
 Lys Gln Ser Ile Gln Lys Ile Phe Lys Glu Ser Glu Val Ser Ser Tyr  
 35 40 45  
 Trp Glu Ile Ser Ser Leu Tyr Asp Tyr Glu Phe Phe Lys Pro Ile Leu  
 50 55 60  
 Asp Gln Leu Gln Ser Asp Gln Val Leu Phe Ser Ile Val Ser Phe Ile  
 65 70 75 80  
 Val Leu Ile Val Ala Cys Ser Asn Ile Val Thr Met Ser Ile Leu Leu  
 85 90 95  
 Val Asn Asn Lys Lys Lys Glu Ile Gly Ile Leu Lys Ala Met Gly Val  
 100 105 110  
 Ser Ser Ser Arg Leu Gln Leu Val Phe Gly Leu Cys Gly Ala Cys Ser  
 115 120 125  
 Gly Leu Val Gly Ala Leu Leu Gly Ser Ile Leu Ala Ala Leu Thr Leu  
 130 135 140  
 Lys Asn Leu Gly Val Leu Thr His Trp Leu Ser Lys Leu Gln Gly Arg  
 145 150 155 160  
 Glu Ala Phe Asn Pro Ser Phe Phe Gly Glu Gln Leu Pro Gln Asp Phe  
 165 170 175  
 His Leu Pro Thr Val Ile Cys Leu Ser Leu Gly Ala Leu Val Leu Ala  
 180 185 190  
 Ala Ile Ser Gly Ala Ile Pro Ala Gln His Val Ala Arg Met Gln Val  
 195 200 205  
 Ser Asp Ile Leu Lys Ser Glu  
 210 215

(2) INFORMATIONS POUR LA SEQ ID NO: 295:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 332 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(296243..297238)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 295:

Val	Gly	Phe	Tyr	Leu	Ala	Ser	Lys	Ile	Pro	Lys	Gly	Val	Met	Lys	Leu	1	5	10	15
Glu	Leu	Leu	Leu	Ala	Phe	Lys	Tyr	Leu	Ile	Pro	Lys	Arg	Lys	Arg	Leu	20	25	30	
Ser	Ser	Ser	Ile	Val	Ser	Ala	Phe	Ser	Ile	Gly	Ile	Val	Ala	Leu	Val	35	40	45	
Val	Trp	Leu	Ser	Val	Val	Phe	Met	Ser	Val	Ile	His	Gly	Leu	Gln	Gln	50	55	60	
Arg	Trp	Val	Gly	Asp	Leu	Ala	Ser	Leu	His	Ser	Ser	Ile	Arg	Ile	Glu	65	70	75	80
Pro	Ser	Asp	Lys	Tyr	Tyr	Glu	Ser	Tyr	Tyr	Tyr	Gln	Ile	Asp	Ser	His	85	90	95	
Ala	Glu	Ala	Ser	Gln	Tyr	Ile	Tyr	Lys	Thr	Ile	Gly	Glu	Lys	Leu	Leu	100	105	110	
Cys	Glu	Gln	Thr	Asp	Pro	Tyr	Asp	Pro	Asp	Val	Asp	Phe	Leu	Leu	Pro	115	120	125	
Glu	Ala	Phe	Pro	Asp	Pro	Glu	Phe	Ser	Asp	Asn	Gly	Glu	Met	Ile	Asp	130	135	140	
Pro	Val	Arg	Thr	Ala	Asn	Glu	Arg	Met	Leu	Ser	Leu	Phe	Ser	Ser	Arg	145	150	155	160
Lys	Gly	Ser	Phe	Val	Glu	Phe	Glu	Glu	Gly	Met	Gly	His	Val	His	Met	165	170	175	
Asp	Arg	Ala	Phe	Arg	Gly	His	Lys	Gly	Glu	Pro	Arg	Ala	Leu	Ser	Gln	180	185	190	
Tyr	Ile	Ala	Tyr	Ser	Ser	Asp	Ile	Leu	Tyr	Gln	Gln	Arg	Val	Leu	Pro	195	200	205	
Phe	Glu	Glu	Thr	Asp	Tyr	Ser	Thr	Glu	Val	Leu	Asn	Arg	Phe	Asn	Ala	210	215	220	
Ser	Ser	Glu	Gly	Trp	Leu	Ala	Asp	Phe	Leu	Val	Leu	Gln	Glu	Lys	Phe	225	230	235	240
Arg	Gly	Met	Ser	Val	Ile	Leu	Pro	Val	Val	Tyr	Arg	Asp	Gln	Gly	Tyr	245	250	255	
Arg	Val	Gly	Asp	Thr	Ala	Ser	Leu	Ser	Val	Phe	Ser	Val	Lys	Lys	Glu	260	265	270	
Gly	Glu	Val	Arg	Phe	Pro	Leu	Arg	Val	Ile	Gly	Phe	Tyr	Asn	Pro	Gly	275	280	285	
Val	Ser	Pro	Phe	Gly	Gly	Lys	Thr	Ile	Phe	Ile	Asp	Lys	Glu	Leu	Ala	290	295	300	
Ala	Ser	Ile	Arg	Ser	Glu	Ser	Glu	Gly	Leu	Val	Cys	Ile	Met	Ala	Gly	305	310	315	320
Arg	Tyr	Phe	Phe	Leu	Val	Phe	Lys	Ile	Ser	Leu	Ser					325	330		

(2) INFORMATIONS POUR LA SEQ ID NO: 296:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 315 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 297791..298735

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 296:

```

Met Lys Lys Phe Ala Thr Phe Leu Cys Val Leu Leu Ser Gly Ser Gly
1      5      10      15
Phe Ala Ala Pro Val Glu Ala Pro Gly Phe Pro Ser Ile Pro Glu Thr
20      25      30
Tyr Ile Thr Ile Asn Asp Lys Glu Leu Gly Leu Gln Glu His Cys Arg
35      40      45
Gly Val Asn Val Leu Ser Cys Gly Tyr Asn Leu Val Gly Met Phe His
50      55      60
Thr Pro Thr Thr Pro Met Pro Leu Gly Gly Tyr Pro Thr Val Ile Phe
65      70      75      80
Phe His Gly Phe Arg Gly Asn Cys Thr Gly Lys Asp Gly Val Tyr Arg
85      90      95
Asp Leu Ala Arg Leu Leu Thr Ala Asn Gly Ile Ala Val Ala Arg Phe
100     105     110
Asp Met Ala Gly Cys Gly Asn Ser Glu Gly Ile Cys Asp Gln Ile Pro
115     120     125
Ala Arg Thr Tyr Leu Arg Asn Gly Glu Asp Ile Leu Ala Thr Val Ala
130     135     140
Lys Tyr Pro Glu Val Asn Pro His Arg Ile Gly Ile Ala Gly Val Ser
145     150     155     160
Leu Gly Cys His Thr Thr Ile His Leu Ala Ser Thr Tyr Arg Pro Arg
165     170     175
Asp Tyr Thr Val Gln Ala Ile Ser Val Trp Ala Pro Ile Ala Asp Gly
180     185     190
Val Ile Leu Leu Lys Glu Ile Cys Ala Thr Ile Gly Leu Thr Met Thr
195     200     205
Gln Phe Ser Asp Met Gly Glu Val Gly Lys Ala Phe Gly Phe Lys Gln
210     215     220
Leu Pro Leu Lys Leu Cys Arg Asp Asp Ile Asp Phe Phe Leu Gly Ile
225     230     235     240
Gln Asp His Ile Leu Leu Ser Leu Pro Arg Arg Ile Pro Val Leu
245     250     255
His Gln Gln Gly Leu Glu Asp Arg Val Val Ser Thr Ala His Gln Arg
260     265     270
Leu Phe Leu Gly Ala Ala Pro Ala Gln Met Leu Ser Lys Ser Tyr Pro
275     280     285
Glu Thr Pro His Glu Ile Ala Leu Ser Pro Tyr Arg Gln Glu Val Leu
290     295     300
Gln Glu Ile Leu Thr His Phe Gln Ser Xaa Leu
305     310     315

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 297:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 518 acides aminés  
 (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 298905..300458

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 297:

Glu	Lys	Ser	Thr	Phe	Leu	Leu	Val	Arg	Ile	Thr	Met	Ile	Asp	Val	Leu	1	5	10	15
Ile	Met	Gly	Ala	Asn	Pro	Ser	Gly	Leu	Ile	Leu	Ala	Ser	Ile	Leu	Gln	20	25	30	
Gln	His	Arg	Ala	Arg	Ile	Lys	Val	Ile	Asp	Ser	Arg	Asp	Ser	Ile	Thr	35	40	45	
Ala	Ser	Leu	Pro	Leu	Pro	Leu	His	Ser	Leu	Pro	Val	Val	Leu	Ser	Ser	50	55	60	
Ser	Ser	Leu	Glu	Leu	Leu	Asp	Asn	Ile	Asn	Leu	Leu	Gly	Asp	Leu	Leu	65	70	75	80
Asp	Lys	Gly	Arg	Lys	Ile	Phe	Gly	Ala	Arg	Tyr	His	Trp	Lys	Gln	Arg	85	90	95	
Thr	Val	Leu	Phe	Lys	Phe	Asn	Gln	Ser	Ser	Ala	Ser	Arg	Cys	Pro	Phe	100	105	110	
Ser	Leu	Leu	Ile	Ser	Tyr	Asn	Glu	Leu	Val	Thr	His	Leu	Leu	Glu	Glu	115	120	125	
Phe	Glu	Arg	Leu	Gly	Gly	Val	Val	Asn	Trp	Ala	Thr	Arg	Pro	Val	Thr	130	135	140	
Gln	Val	Glu	Gln	Asn	Leu	Phe	Ile	Glu	Ser	Thr	Lys	Ser	Ser	Ser	Gln	145	150	155	160
Val	Tyr	Glu	Gly	Arg	Glu	Ile	Phe	Thr	Pro	Lys	Trp	Ile	Ile	Ala	Cys	165	170	175	
Glu	Met	Asp	Ala	Asp	Pro	Asp	Leu	Lys	Asp	Leu	Leu	Lys	Thr	Gln	Ile	180	185	190	
Lys	Thr	Lys	Lys	Ile	His	Lys	Glu	Ala	Leu	Phe	Val	Asp	Cys	Glu	Glu	195	200	205	
Gly	Glu	Pro	Phe	Glu	Glu	Ser	His	Ile	His	Leu	Leu	Pro	Val	Thr	Lys	210	215	220	
Ser	Phe	Val	Asn	Phe	Val	Phe	Tyr	Asn	Pro	Tyr	Arg	Gly	Ser	Arg	Gln	225	230	235	240
Leu	Tyr	Leu	Ala	Asn	Thr	Ser	Gly	Ser	Leu	Ser	Ser	Lys	Phe	Lys	Asn	245	250	255	
Lys	Leu	Leu	Tyr	Thr	Tyr	Ser	Leu	Ala	Leu	Ala	Glu	Asp	Pro	Leu	Ser	260	265	270	
Ile	Ser	Ser	Ser	Leu	Leu	Gln	Tyr	Pro	Phe	Cys	His	Asp	Arg	Tyr	Ile	275	280	285	
Phe	Leu	Gly	Ser	Ile	Ala	Asn	Asn	Leu	Ser	Phe	Ser	Tyr	Leu	Ser	Gly	290	295	300	
Val	Asn	Ser	Asn	Ile	His	Asp	Ala	Phe	Asn	Leu	Gly	Trp	Lys	Leu	Leu	305	310	315	320
Pro	Val	Ile	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Leu	Ile	Leu	Ser	Lys	Glu	325	330	335	
Leu	Lys	Thr	Ser	His	Val	Leu	Pro	His	Phe	Asn	Glu	Val	His	Gln	Lys	340	345	350	
Arg	Ala	Thr	Lys	Leu	Leu	Phe	Ser	Asn	Met	Tyr	Thr	Pro	Ala	Leu	Met	355	360	365	
Tyr	Tyr	Tyr	Leu	Lys	Gly	Cys	Lys	Gln	Leu	Asp	Ala	Ala	Glu	Gly	Glu	370	375	380	
Leu	Tyr	Tyr	Pro	Ser	His	Arg	Ala	Ser	Lys	Tyr	Glu	Ala	Ser	Asp	Ile	385	390	395	400

```

Ile Lys Val Ser Pro Asn Asp Lys Glu Ile Gln Gly Pro Arg Pro Gly
      405                               410           415
Ser Arg Ala Leu Asp Ile Arg Leu Asp Thr Gly Asn Tyr Leu Leu Asp
      420                               425           430
Ser Leu Lys Asn Ala Lys His Leu Leu Val Phe Phe Lys Glu Arg Pro
      435                               440           445
Asp Leu Val His Ala Leu Leu Glu Glu Tyr Gly Glu Trp Val Asp Val
      450                               455           460
Ile Val Thr Glu Asp Pro Lys Val His Lys Leu Tyr His Ala Asn Pro
      465                               470           475           480
Glu Ser Leu Phe Ile Ile Arg Pro Asp Arg Tyr Ile Gly Tyr Arg Thr
      485                               490           495
His Thr Phe Lys Leu His Glu Leu Ile Ser Tyr Leu Leu Arg Ile Phe
      500                               505           510
Ala Ala Glu Asn Ala Asn
      515

```

(2) INFORMATIONS POUR LA SEQ ID NO: 298:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 542 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(300527..302152)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 298:

```

Gly Cys Leu Phe Ser Glu Glu Leu Val Ser Asp Gly Arg Lys Leu Pro
1      5      10      15
Tyr Pro Asp Leu Gly Asp Gln Asn Ile Lys His Leu Glu Lys Ile Arg
      20      25      30
Asp Val Tyr Gly Leu Asp Gly Val Ala Glu Leu Arg Val Ala Glu Ala
      35      40      45
Ala Leu Leu Gly Val Gln Lys Leu Pro Glu Glu Gln Lys Gln Glu Ser
      50      55      60
Leu Lys Ser Ala Val Lys Ala Leu Arg Ala Asp Ala Lys Val Leu Asn
65      70      75      80
Lys Lys Phe Lys Lys Leu Pro Glu Ser Tyr Gln Pro Gln His Ser Glu
      85      90      95
Val Thr Gly Val Gln Gly Val Thr Glu Gln Glu Ser Arg Asp Asp Val
      100     105     110
Leu Val Ala Gln Asp Met Ala Ala Ile Glu Glu Leu Gln Asp Gln Tyr
      115     120     125
His Ala Ala Cys Leu Gln Phe Glu Ser Val Ser Met Arg Phe Leu Ala
      130     135     140
Glu Gln Arg Lys Ala Lys Phe Leu Glu Lys Leu Leu Ile Gln Lys Arg
145     150     155     160
Arg Asp Val Ser His Leu Ser His Gln Glu Ala His Tyr Thr Gln Val
      165     170     175
Val Ser His Leu Lys Glu Arg Ile Ser Met Arg Lys Gly Ala Ser Thr
      180     185     190
Gln His Ala Ser Lys Glu Glu Ile Ser Thr Lys Met Arg Glu Leu Leu
      195     200     205
Ser Leu Asp Asp Gln Leu Leu Lys Ala His Thr Ala Gln Asp Val Asn

```



(2) INFORMATIONS POUR LA SEQ ID NO: 299:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 949 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(302071..304917)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 299:

Glu Tyr Gly Ile Ile Leu Pro Ser Lys Ile Val Phe Gln Glu Ser Met  
1 5 10 15

Ala	Asn	Pro	Ser	Thr	Pro	Pro	Ser	Asn	His	Ser	Gly	Leu	Ser	Leu	Gln
			20					25					30		
Gly	Arg	Leu	Arg	Ala	Ser	Ser	Gln	Gln	Cys	Thr	Gln	Ala	Gly	Gln	Gly
		35					40					45			
Asp	Pro	Gln	Pro	Leu	Ser	Pro	Glu	Ser	Arg	Gly	Leu	Thr	Ser	Asn	Phe
	50					55					60				
Ser	Thr	Arg	Arg	Asp	Leu	Ile	Asp	Val	Val	Glu	Glu	Ser	Ile	Glu	Thr
65					70					75					80
Ala	Lys	Gly	Ser	Glu	Leu	Lys	Lys	Leu	Arg	Ile	Tyr	Glu	Ile	Ala	Leu
				85					90					95	
Lys	Ile	Leu	Thr	Ile	Ile	Gly	Ala	Ala	Ile	Leu	Phe	Ala	Val	Pro	Leu
			100					105					110		
Cys	Met	Leu	Leu	Gly	Val	Pro	Leu	Trp	Ile	Pro	Ile	Val	Thr	Cys	Ile
		115					120					125			
Gly	Val	Gly	Ile	Ala	Phe	Ser	Ile	Ala	Lys	Gly	Cys	Leu	Gln	Lys	Arg
	130					135					140				
Cys	Gln	Gln	Ile	Arg	Glu	Glu	Tyr	Arg	Ala	Leu	His	Leu	Tyr	His	Arg
145					150					155					160
Tyr	Leu	Leu	Ser	Asn	Lys	Asp	Ser	Ile	Asp	Gly	Thr	Leu	Leu	Ser	Arg
				165					170					175	
Phe	Asp	Ile	Arg	Phe	Arg	Lys	Ala	Glu	Lys	Leu	His	Gly	Leu	Leu	Asp
			180					185				190			
Leu	Asp	Lys	Arg	Glu	Ala	Asn	His	Pro	Leu	Glu	Ala	Asp	Lys	Arg	Tyr
		195					200					205			
Asp	Phe	Ala	Gly	Leu	Ala	His	Gln	Arg	Tyr	Gln	Val	Asp	Ala	Ala	Leu
	210					215					220				
Gly	Ile	Ser	Ser	Ser	Gln	Asp	Ala	Phe	Trp	Arg	Gly	Val	Ala	Gln	Gln
225					230					235					240
Val	Lys	Ser	Val	Lys	Asp	Asp	Val	Val	Leu	Gly	Asp	Lys	Ala	Ser	Thr
				245					250					255	
Asp	Leu	Tyr	Pro	Ile	Ala	Gln	Gln	Ala	Leu	Gln	Ala	Ala	Gly	Val	Gly
			260					265					270		
Phe	Ser	Gly	Ala	Ala	Gly	Lys	Glu	Ser	Leu	Leu	Asp	Leu	Ala	Lys	Ser
		275					280					285			
Leu	Ser	Ser	Leu	Phe	Ala	Trp	Gly	Ser	Gln	Val	Gly	Lys	Asp	Ser	His
	290					295					300				
Glu	Ala	Leu	Gln	Arg	Tyr	Gln	Met	Arg	Phe	Leu	Ser	Ser	Pro	Ile	Leu
305					310					315					320
Ala	Thr	Trp	Cys	Gly	Ala	Gly	Phe	Ser	Thr	Ser	Ala	Gln	Asp	Phe	Val
				325					330					335	
Leu	Lys	Gly	Lys	Asn	Val	Leu	Asp	Ile	Ala	Ser	Glu	Asn	His	Thr	Lys
			340					345				350			
Met	Gln	Asn	Ala	Ile	Lys	Cys	Val	Gln	Leu	Val	Ser	Val	Leu	Gly	Lys
		355					360					365			
Met	Arg	Asn	Trp	Lys	Glu	Lys	Ile	Asp	Thr	Leu	Ile	Gln	Asn	Lys	Asn
	370					375					380				
Leu	Asp	Gln	Asp	Ser	Leu	Arg	Lys	Leu	Tyr	Gln	Asp	Ile	Glu	Lys	Ala
385					390					395					400
Met	His	Lys	Val	Cys	Ile	Glu	Asp	Gly	Val	Ser	Ala	Ser	Ile	Gln	Ala
				405					410					415	
Arg	Val	Arg	Lys	Val	Thr	Gln	Lys	Tyr	Leu	Arg	Gln	Asp	Leu	Gln	Glu
			420					425					430		
Leu	Leu	Asn	Lys	Lys	Ala	Pro	Leu	Asn	Glu	Ser	Asp	Leu	Ser	Lys	Met
		435					440					445			
Gln	Lys	Gly	Ile	Ser	Ser	Cys	Ala	Asn	Leu	Val	Val	Thr	Leu	Leu	Glu
	450					455					460				
Ser	Gln	Leu	Gly	Ile	Ser	Glu	Gln	Thr	Ser	Ile	Lys	Glu	Val	Glu	Glu
465					470					475					480
Ser	Ile	Tyr	Arg	Asp	Leu	Ile	Asp	Thr	Ile	Leu	Gln	Met	Gly	Ser	Ala

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 300:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 395 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(304973..306157)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 300:

Arg	Arg	Cys	Gly	Ala	Val	Leu	Arg	Met	Ala	Ile	Asp	Gly	Val	Val	Ile
1			5					10					15		
Lys	Val	Asp	Asn	Ile	Ala	His	Gln	Asp	Arg	Leu	Gly	Leu	Thr	Ser	Lys
		20					25					30			
His	Tyr	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Tyr	Ala	Pro	Glu	Arg	Ala	Glu
		35					40					45			
Thr	Ile	Leu	Glu	Asp	Ile	Val	Phe	Gln	Val	Gly	Lys	Thr	Gly	Ile	Leu
	50					55				60					
Thr	Pro	Val	Ala	Glu	Leu	Ala	Pro	Val	Phe	Leu	Ser	Gly	Ser	Arg	Val
65					70				75					80	
Ser	Arg	Ala	Ser	Leu	Tyr	Asn	Gln	Asp	Glu	Ile	Glu	Lys	Lys	Asp	Ile
			85					90						95	
Arg	Ile	Gly	Asp	Ser	Val	Tyr	Val	Glu	Lys	Gly	Gly	Glu	Val	Ile	Pro
		100						105				110			
Lys	Ile	Val	Gly	Ile	Asn	Leu	Ala	Lys	Arg	Ser	Leu	Glu	Ser	Glu	Pro
		115					120					125			
Trp	Lys	Met	Pro	Ser	Leu	Cys	Pro	Val	Cys	His	Glu	Pro	Val	Val	Lys
	130					135					140				
Glu	Lys	Val	Ser	Val	Arg	Cys	Ile	Asn	Pro	Leu	Cys	Ser	Gly	Gly	Met
145					150				155						160
Leu	Glu	Lys	Ile	Cys	Phe	Phe	Ala	Ser	Lys	Ser	Ala	Leu	Asn	Ile	Asp
				165					170					175	
His	Leu	Gly	Glu	Lys	Val	Val	Thr	Lys	Leu	Phe	Glu	Val	Gly	Leu	Ile
		180						185					190		
Ser	Ser	Cys	Ser	Asp	Ile	Phe	Ala	Leu	Thr	Glu	Glu	Asp	Leu	Lys	Gln
		195					200					205			
Val	Pro	Gly	Phe	Lys	Asp	Arg	Ser	Ile	Gln	Asn	Leu	Leu	Ala	Ser	Ile
	210					215					220				
Ala	Gly	Ala	Lys	Lys	Val	Ala	Leu	Asp	Arg	Leu	Leu	Thr	Ala	Leu	Ser
225					230				235						240
Ile	Pro	Phe	Val	Gly	Ser	Ser	Gly	Ala	Ile	Ala	Leu	Ala	Asp	His	Phe
				245					250					255	
Gly	Thr	Leu	Asp	Lys	Val	Ile	Glu	Ala	Ser	Leu	Asp	Glu	Leu	Met	Ser
		260					265					270			
Ile	Glu	Gly	Ile	Gly	Pro	Lys	Val	Ala	Ala	Ser	Ile	Val	Ala	Phe	Phe
		275					280					285			
Ser	Lys	His	Glu	Asn	Arg	Glu	Glu	Ile	Arg	Arg	Met	Gln	Glu	Leu	Gly
	290					295					300				
Val	Gln	Val	Leu	Ser	Lys	Gln	Ser	Asp	Lys	Glu	Ala	Pro	Leu	Gln	Gly
305					310					315					320
Lys	Val	Phe	Val	Leu	Thr	Gly	Thr	Leu	Gln	Gln	Met	Thr	Arg	Thr	Gln
				325					330					335	
Ala	Glu	Glu	Arg	Ile	Arg	Ser	Leu	Gly	Gly	Lys	Val	Ser	Ser	Ser	Val

(2) INFORMATION POUR LA SEQ ID NO: 301:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306111..306494)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 301:

(2) INFORMATION POUR LA SEQ ID NO: 302:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306436..306963)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 302:

Met Gly Ala Val Ser Arg Asp Asp Tyr Ile Ala Leu Cys Thr Glu Leu  
1 5 10 15  
Val Glu His Asp Arg Arg Tyr Tyr Ala Leu Asn Gln Pro Thr Ile Ser  
20 25 30

Asp	Tyr	Ser	Tyr	Asp	Met	Lys	Met	Arg	Glu	Leu	Gln	Glu	Ile	Glu	Val
		35					40					45			
Gln	His	Pro	Glu	Trp	Lys	Val	Ser	Trp	Ser	Pro	Thr	Met	Tyr	Leu	Gly
	50				55						60				
Asp	Arg	Pro	Ser	Gly	Gln	Phe	Pro	Val	Val	Pro	His	Ser	Ser	Pro	Met
65					70					75					80
Leu	Ser	Ile	Ala	Asn	Val	Tyr	Ser	Leu	Gln	Glu	Leu	Glu	Glu	Phe	Phe
				85					90					95	
Ser	Arg	Thr	Glu	Lys	Leu	Leu	Gly	Tyr	Ser	Pro	Gly	Tyr	Ser	Leu	Glu
			100					105					110		
Leu	Lys	Ile	Asp	Gly	Ile	Ala	Val	Ala	Ile	Arg	Tyr	Glu	Lys	Arg	Leu
		115					120					125			
Phe	Ala	Gln	Ala	Leu	Ser	Arg	Gly	Asn	Gly	Val	Lys	Gly	Glu	Asp	Ile
	130					135					140				
Thr	Ala	Asn	Val	Ser	Thr	Ile	Arg	Ser	Leu	Pro	Met	Arg	Leu	Pro	Gln
145					150					155					160
Glu	Gly	Ser	Arg	Gly	Ser	Arg	Ser	Ala	Arg	Arg	Ser	Val	Ser	Phe	Ile
				165					170					175	

(2) INFORMATIONS POUR LA SEQ ID NO: 303:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 599 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306977..308773)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 303:

Ser	Gln	Asn	Ser	Asp	Met	Asp	Leu	Trp	Ser	Arg	Asp	Val	Leu	Ala	Glu
1				5					10					15	
His	Arg	Phe	Ile	Lys	Lys	Arg	Tyr	Ile	Leu	Lys	Ile	Leu	Pro	Ser	Glu
			20					25					30		
Leu	Ser	Ser	Ser	Glu	Asn	Phe	Met	Arg	Val	Phe	Gln	Glu	Val	Ile	Val
		35					40					45			
Gln	Leu	Ala	Ala	Ile	Arg	His	Ala	Ser	Leu	Val	Ala	Ile	Glu	Asn	Val
	50					55					60				
Ser	Arg	Glu	Gly	Asp	Arg	Tyr	Phe	Val	Val	Thr	Glu	Glu	Asn	Gly	Gly
65				70						75					80
Thr	Ile	Ser	Leu	Ala	Gln	Tyr	Leu	Ser	Gly	Arg	Lys	Leu	Ser	Glu	Glu
				85					90					95	
Glu	Val	Val	His	Leu	Ile	Gln	Gln	Leu	Cys	Asp	Ala	Leu	Glu	Leu	Val
			100					105					110		
His	Ser	Ile	Gly	Leu	Ala	His	Gly	Gln	Ile	His	Leu	His	Ser	Val	His
		115					120					125			
Val	Ser	Phe	Phe	Asn	Gly	Ile	Ala	Asn	Ile	Tyr	Leu	Pro	Glu	Val	Gly
	130					135					140				
Phe	Ala	Ser	Leu	Leu	Arg	Glu	Arg	Met	Phe	Ser	Thr	Ile	Met	Gln	Ser
145					150					155					160
Gly	Ser	Ala	Arg	Glu	Ser	Ile	Thr	Arg	Ile	Arg	Asp	Leu	Leu	Met	Phe
				165					170					175	
Glu	Ala	Pro	Glu	Glu	Gln	Glu	Val	Phe	Gly	Arg	Glu	Ala	Asp	Val	Tyr
		180						185				190			
Ser	Val	Gly	Val	Leu	Ala	Tyr	Tyr	Leu	Leu	Val	Gly	Ser	Phe	Pro	Trp

		195				200				205					
Gly	Ser	Phe	Pro	Lys	Pro	Ser	Leu	Cys	Met	Pro	Asp	Ser	Trp	Tyr	Asp
	210					215					220				
Trp	Asp	Gly	Phe	Ile	Leu	Ser	Cys	Leu	Gln	Gln	Gln	Arg	Glu	Ala	Arg
225					230					235					240
Pro	Lys	Cys	Leu	Arg	Glu	Ala	Leu	Arg	Arg	Lys	Thr	Ser	Gly	Glu	Gln
				245				250						255	
Leu	Gln	Val	Thr	Leu	Asp	Ser	Cys	Arg	Glu	Pro	Leu	Arg	Glu	Met	Glu
			260					265					270		
Ile	Glu	Asp	Thr	Pro	Thr	Glu	Leu	Gly	Pro	Pro	Ser	Ala	Leu	Ile	Arg
	275						280					285			
Glu	Gly	Glu	Arg	Leu	Cys	Glu	Val	Lys	Glu	Glu	Gln	His	Ala	Phe	Val
	290					295					300				
Leu	Val	Glu	Ala	Lys	Ser	Ile	Asp	Glu	Ala	Met	Val	Thr	Thr	Val	Asp
305					310					315					320
Ser	Glu	Glu	Glu	Leu	Glu	Ser	Ser	Glu	Gly	Tyr	Ala	Asn	Pro	Leu	Gln
				325					330					335	
Ser	Leu	Leu	Ala	Arg	Glu	Pro	Val	Val	Ser	Arg	Tyr	Val	Glu	Val	Glu
			340					345					350		
Arg	Glu	Glu	Ile	Lys	Pro	Gln	Pro	Leu	Leu	Thr	Glu	Met	Ile	Phe	Ile
	355						360					365			
Glu	Gly	Gly	Glu	Phe	Ser	Arg	Gly	Ser	Gly	Asp	Gly	Gln	Arg	Asp	Glu
	370					375					380				
Leu	Pro	Val	His	Asn	Ile	Thr	Leu	Pro	Gly	Phe	Phe	Leu	Asp	Ile	His
385					390					395					400
Pro	Val	Thr	Asn	Glu	Gln	Phe	Val	Arg	Phe	Leu	Glu	Cys	Val	Gly	Ser
			405						410					415	
Glu	Gln	Asp	Glu	His	Tyr	Asn	Glu	Leu	Ile	Arg	Leu	Lys	Asp	Ser	Arg
			420					425					430		
Ile	Gln	Arg	Arg	Ser	Gly	Arg	Leu	Ile	Ile	Glu	Pro	Gly	Tyr	Ala	Lys
	435						440					445			
His	Pro	Val	Val	Gly	Val	Thr	Trp	Tyr	Gly	Ala	Ser	Ser	Tyr	Ala	Cys
	450					455					460				
Trp	Ile	Gly	Lys	Arg	Leu	Pro	Ser	Glu	Ala	Glu	Trp	Glu	Val	Ala	Ala
465					470					475					480
Ser	Gly	Gly	Lys	Leu	Gly	Leu	Arg	Tyr	Pro	Thr	Gly	Glu	Glu	Ile	Asp
			485						490					495	
Lys	Ser	Lys	Ala	Asn	Phe	Phe	Ser	Ser	Asp	Thr	Thr	Pro	Val	Met	Ser
			500					505					510		
Tyr	Pro	Ser	Ser	Ile	Leu	Gly	Leu	Tyr	Asp	Met	Ala	Gly	Asn	Val	Tyr
	515						520					525			
Glu	Trp	Cys	Gln	Asp	Trp	Tyr	Ser	Tyr	Asp	Phe	Tyr	Glu	Ser	Ser	Ala
	530					535					540				
Leu	Asp	Pro	Asp	Ala	Pro	Leu	Gly	Pro	Pro	Gln	Gly	Val	Tyr	Arg	Val
545					550					555					560
Leu	Arg	Gly	Gly	Cys	Trp	Lys	Ser	Leu	Lys	Asp	Asp	Leu	Arg	Cys	Ala
				565					570					575	
His	Arg	His	Arg	Asn	Asn	Pro	Gly	Ala	Ile	Asn	Ser	Thr	Tyr	Gly	Phe
			580					585					590		
Arg	Cys	Ala	Lys	Asp	Val	Lys									
			595												

(2) INFORMATIONS POUR LA SEQ ID NO: 304:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 202 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(309276..309881)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 304:

Gly	Gly	Arg	Leu	Met	Thr	Thr	Pro	Asp	Asn	Asn	Thr	Ile	Asp	Val	Ser
1				5					10					15	
Phe	Pro	Thr	Phe	Val	Arg	Leu	Asn	Val	Ala	Thr	Thr	Asp	Leu	Ala	Asp
			20					25					30		
Gly	Asn	Lys	Ser	Asn	Ala	Val	Thr	Ile	Thr	Glu	Thr	Ala	Thr	Ala	Asn
		35					40					45			
Tyr	Val	Asn	Val	Thr	Gln	Asp	Leu	Thr	Ser	Ser	Thr	Ala	Lys	Leu	Glu
	50					55					60				
Cys	Thr	Gln	Asp	Leu	Ile	Ala	Gln	Gly	Lys	Leu	Ile	Val	Thr	Asn	Pro
65					70					75					80
Lys	Ser	Asp	Ile	Ser	Phe	Gly	Gly	Arg	Val	Asn	Leu	Ala	Asp	Asn	Thr
				85					90					95	
Ile	Thr	Tyr	Asn	Pro	Tyr	Asn	Asn	Gly	Gly	Gly	Glu	Val	Ala	Phe	Thr
			100					105					110		
Asp	Ile	Asn	Ser	Arg	Gln	Gly	Lys	Gln	Tyr	Val	Pro	Tyr	Gly	Leu	Tyr
		115					120					125			
Lys	Asn	Gly	Ala	Pro	Lys	Ile	Ser	Met	Arg	Ser	Ala	Leu	Ser	Gly	Gly
	130					135					140				
His	Val	Gly	Ser	Gly	Asp	Thr	Arg	Gly	Trp	Gly	Ala	Glu	Val	Leu	Trp
145					150					155					160
Asp	Ala	Tyr	Thr	Gln	Arg	Glu	Asp	Leu	Glu	Asp	Lys	Ala	Val	Thr	
				165				170					175		
Phe	Ser	Pro	Ala	Asn	Arg	Gly	Lys	Leu	Tyr	Phe	Glu	Ala	Ser	Leu	Arg
			180					185					190		
Leu	Pro	Phe	Cys	Ser	Val	Ser	Pro	Ser	Leu						
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 305:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 283 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(309872..310720)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 305:

Glu	Asp	Asn	Met	Lys	Lys	Pro	Val	Phe	Thr	Gly	Gly	Ala	Pro	Ile	Pro
1				5					10					15	
Gly	Ile	Ser	Thr	Glu	Glu	Gly	Thr	Gly	Val	Lys	Asp	Gln	Asn	Leu	Trp
			20					25					30		
Met	Arg	Asn	Ala	Thr	Leu	Lys	Val	Glu	Gly	Asp	Ala	Thr	Ile	Asp	Asp
		35				40					45				
Thr	Leu	Thr	Ser	Arg	Asp	Leu	Lys	Val	Thr	Gly	Pro	Thr	Ile	His	Thr
	50					55				60					
Asp	Leu	Asp	Leu	Ser	Val	Gly	Gly	Asp	Val	Lys	Gly	Gly	Arg	Thr	Val



65					70					75					80
Leu	Gly	Glu	Thr	Val	Leu	Glu	Gly	Asp	Phe	Asn	Ile	Lys	Cys	Asn	Gln
				85					90					95	
Gly	Gln	Val	Pro	Gln	Phe	Thr	Asn	Leu	Ser	Asp	Pro	Leu	Ser	Ala	Arg
			100					105					110		
Asp	Ala	Ile	Thr	Phe	Asp	Tyr	Tyr	Arg	Asp	Arg	Ser	Thr	Gln	Ala	Tyr
		115					120					125			
Asn	Cys	Ala	Thr	His	Arg	Asn	Gly	Ala	Leu	Val	Lys	Gly	Asn	Arg	Phe
	130					135					140				
Ile	Asp	Leu	Arg	Met	His	Asn	Ile	Asp	Asp	Ser	Glu	Ser	Tyr	Thr	Pro
145					150					155					160
Met	Tyr	Gln	Asn	Arg	Phe	Tyr	Trp	Lys	Asp	Asn	Asp	Gln	Lys	Lys	Leu
			165					170					175		
Tyr	Leu	Lys	Ser	Pro	Gly	Ile	Tyr	Gln	Val	Ala	Phe	Gln	Ile	Phe	Arg
			180					185					190		
Ser	Gly	Gly	Tyr	His	Ser	Gly	Asn	Glu	Asp	Pro	Thr	Ile	Phe	Leu	Arg
	195						200					205			
Leu	Tyr	Thr	Ser	Ala	Tyr	Glu	Tyr	Thr	Asn	Leu	Cys	Thr	Gly	Asp	Thr
	210					215					220				
Arg	Gly	Phe	Asn	Pro	Glu	His	Thr	Thr	Asn	Thr	Ser	Leu	Tyr	Ser	Ile
225					230					235					240
Phe	Ser	Ile	Pro	Ser	Ile	Gly	Asn	Glu	His	Pro	Phe	Ile	Gln	Val	Phe
			245					250					255		
Thr	Lys	Ile	His	Val	Asn	Ile	Ala	Tyr	Ser	Met	Ile	Asn	Val	Ile	Trp
			260				265						270		
Phe	Pro	Phe	Gly	Ser	Ser	Tyr	Lys	Glu	Ala	Asp					
		275					280								

(2) INFORMATIONS POUR LA SEQ ID NO: 306:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 285 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(310716..311570)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 306:

Met	Ser	Asp	Ser	Asp	Lys	Ile	Ile	Asn	Asp	Cys	Arg	Phe	Asp	Phe	Asn
1				5					10					15	
Thr	Thr	Val	His	Gly	Asp	Leu	Leu	Ala	Ser	Asn	Leu	Thr	Thr	Glu	Gly
			20					25					30		
Asp	Val	Thr	Val	Lys	Ser	Ile	Ser	Ala	Lys	Glu	Ser	Phe	Ser	Val	Lys
		35					40					45			
Arg	Lys	Val	Asp	Val	Asn	Glu	Asn	Asp	Ile	Ile	Val	Asn	Gly	Phe	Thr
	50					55					60				
Gly	Ala	Ala	Gly	Tyr	Asp	Leu	Thr	Thr	Arg	Gly	Lys	Ile	Ser	Ile	Asn
65					70					75					80
Leu	Asn	Gly	Asn	Arg	Leu	Ser	Asn	Val	Lys	Cys	Pro	Glu	Lys	Asp	Ser
			85					90					95		
Gln	Pro	Val	Pro	Ala	Asn	Tyr	Ile	Arg	Thr	Pro	Glu	Tyr	Tyr	Phe	Cys
			100					105					110		
Ser	Leu	Gln	Asp	Gly	Ala	Arg	Ile	Glu	Trp	Lys	Arg	Gly	Gln	Lys	Leu
		115					120					125			

Pro	Leu	Ile	Gly	Pro	Ser	Arg	Leu	Val	Tyr	Gln	Ser	Ser	Arg	Ile	Asn
130						135					140				
Glu	Phe	Ile	Arg	Phe	Val	Ser	Phe	Glu	Glu	Asn	Lys	Thr	Arg	Thr	Gln
145					150					155					160
Val	Lys	Ile	Asn	Leu	Ser	Gly	Thr	Thr	Gly	Leu	Gln	Met	Leu	Ala	Lys
				165					170						175
Gly	Val	Tyr	Ile	Ile	Asn	Val	Gly	Val	Gly	Lys	Arg	Trp	Gly	Trp	Asn
			180					185					190		
Asn	Gly	Tyr	Gly	Gly	Asp	Tyr	Cys	Leu	Ala	Val	Pro	Leu	Gly	Lys	Glu
		195					200					205			
Tyr	Ser	Glu	Ser	Ser	Thr	Phe	Ser	Arg	Gly	Gly	Tyr	Tyr	Ala	Ser	Thr
	210					215					220				
Ala	Val	Gly	Thr	Ala	Ile	His	Ile	Arg	Lys	Glu	Ser	Thr	Asn	Pro	Asp
225					230					235					240
Gly	Pro	Phe	Ser	Ser	Ser	Asp	Thr	Glu	Leu	Met	Lys	Thr	Leu	Leu	Glu
				245					250						255
Val	Arg	Tyr	Lys	Gly	Gly	Asp	Tyr	Val	Asp	Lys	Ser	Ala	Leu	Ser	Thr
			260					265					270		
Leu	Tyr	Phe	Gly	Val	Leu	Val	Tyr	Pro	Glu	Ile	Gly	Gly			
		275					280					285			

(2) INFORMATIONS POUR LA SEQ ID NO: 307:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(311972..312451)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 307:

Leu	Ile	Leu	Arg	Met	Arg	Arg	Asp	Arg	Lys	Glu	Leu	Met	Leu	Lys	Lys
1				5					10					15	
Pro	Asn	Arg	Asn	Asp	Pro	Cys	Pro	Cys	Gly	Ser	Gly	Lys	Lys	Tyr	Lys
			20					25					30		
Gln	Cys	Cys	Leu	Lys	Xaa	Gln	Ala	Leu	Thr	Ala	Arg	His	Thr	Pro	Glu
		35				40					45				
Gly	Lys	Phe	Lys	Phe	Ser	Ile	Thr	Ala	Ser	Pro	Ala	Ala	Gly	Ala	Ser
	50					55				60					
Thr	Glu	Gly	Phe	Thr	Lys	Leu	Phe	Arg	Gln	Ser	Val	Asp	Ser	Tyr	Thr
65					70				75					80	
Ser	Glu	Gln	Lys	Glu	Gly	Met	Ser	Arg	Phe	Leu	Ile	Thr	Lys	Asn	Lys
				85				90						95	
Glu	Pro	Ile	Gly	Lys	Arg	Ala	Ile	Arg	Lys	Ala	Lys	Ala	Lys	Glu	Glu
			100					105				110			
Arg	Ile	Ile	Ser	Glu	Lys	Leu	Ser	Gln	His	Glu	Phe	Gln	Val	Met	Asp
		115					120					125			
Thr	Glu	Val	Ser	Gly	Glu	Asp	Ile	Gln	Ser	Ser	Leu	Asp	Tyr	Glu	Gln
	130					135					140				
Phe	Leu	Pro	Thr	Glu	Glu	Asp	Tyr	Arg	Val	Gln	Lys	Glu	Glu	Asp	Ser
145					150					155					160

(2) INFORMATIONS POUR LA SEQ ID NO: 308:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 310 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 313435..314364

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 308:

Phe	Tyr	Arg	Asn	Thr	Gln	Lys	Tyr	Phe	Met	Tyr	Val	Arg	Ser	Ile	Phe	1	5	10	15
Phe	Ser	Ile	Ile	Ala	Phe	Leu	Thr	Val	Gly	Cys	Ser	Phe	Ser	Pro	Pro	20	25	30	
Glu	Ser	Gly	Leu	Ile	Ile	Ala	Ile	His	Asp	Asp	Pro	Arg	Ser	Leu	Ser	35	40	45	
Pro	Glu	Lys	Gly	Glu	Asn	Ala	Phe	His	Phe	Ser	Leu	Ser	Lys	Ala	Leu	50	55	60	
Phe	Ala	Thr	Leu	Phe	Arg	Glu	Glu	Leu	Ser	Gly	Leu	Thr	Pro	Ala	Leu	65	70	75	80
Val	Ser	Ser	Tyr	Gln	Ile	Ser	Glu	Asp	Gly	Arg	Phe	Tyr	Arg	Phe	Cys	85	90	95	
Ile	Arg	Lys	Asp	Ala	Lys	Trp	Ser	Asp	Gly	Ser	Leu	Leu	Leu	Ala	Glu	100	105	110	
Asp	Val	Ile	Ala	Ala	Trp	Glu	His	Thr	Lys	Gln	Ala	Gly	Arg	Tyr	Ser	115	120	125	
Leu	Leu	Phe	Glu	Lys	Leu	Ser	Phe	Arg	Ala	Ser	Ser	Ser	Ser	Glu	Ile	130	135	140	
Leu	Ile	Glu	Leu	Lys	Glu	Pro	Glu	Pro	Gln	Leu	Leu	Ala	Ile	Leu	Ala	145	150	155	160
Ser	Pro	Phe	Phe	Ala	Val	Tyr	Arg	Pro	Glu	Asn	Pro	Phe	Leu	Ser	Ser	165	170	175	
Gly	Pro	Phe	Met	Pro	Lys	Thr	Tyr	Val	Gln	Gly	Gln	Thr	Leu	Val	Leu	180	185	190	
Gln	Lys	Asn	Pro	Tyr	Tyr	Tyr	Asp	His	Ala	His	Val	Glu	Leu	His	Ser	195	200	205	
Ile	Asp	Phe	Arg	Ile	Ile	Pro	Asn	Ile	Tyr	Thr	Ala	Leu	His	Leu	Leu	210	215	220	
Arg	Arg	Gly	Asp	Val	Asp	Trp	Val	Gly	Gln	Pro	Trp	His	Gln	Gly	Ile	225	230	235	240
Pro	Phe	Glu	Leu	Arg	Thr	Thr	Ser	Ala	Leu	Tyr	Thr	His	Tyr	Pro	Val	245	250	255	
Asp	Gly	Thr	Phe	Trp	Leu	Ile	Leu	Asn	Pro	Lys	Asp	Pro	Val	Leu	Ser	260	265	270	
Ser	Leu	Ser	Asn	Arg	Gln	Arg	Leu	Ile	Ala	Ala	Ile	Gln	Lys	Glu	Lys	275	280	285	
Leu	Val	Lys	Gln	Ala	Leu	Gly	Thr	Gln	Tyr	Arg	Val	Ala	Glu	Ser	Leu	290	295	300	
His	Leu	Gln	Arg	Glu	Ser											305	310		

(2) INFORMATIONS POUR LA SEQ ID NO: 309:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 314340..314738

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 309:

Lys	Ser	Pro	Ser	Pro	Glu	Gly	Ile	Ile	Ala	His	Gln	Glu	Ala	Ser	Thr
1				5					10					15	
Pro	Phe	Pro	Gly	Lys	Ile	Thr	Leu	Ile	Tyr	Pro	Asn	Asn	Ile	Thr	Arg
			20					25					30		
Cys	Gln	Arg	Leu	Ala	Glu	Val	Leu	Gln	Glu	Gln	Cys	Arg	Asp	Ala	Gly
		35					40					45			
Ile	Gln	Leu	Thr	Leu	Glu	Gly	Leu	Glu	Tyr	His	Val	Phe	Val	Gln	Lys
	50					55					60				
Arg	Ala	Thr	Gln	Asp	Phe	Ser	Val	Ser	Thr	Ala	Thr	Ser	Ile	Ala	Phe
65					70				75						80
His	Pro	Leu	Ala	Lys	Ser	Lys	Phe	Asp	Gln	Thr	Ala	Leu	Asp	Asn	Phe
				85					90					95	
Thr	Cys	Leu	Pro	Leu	Tyr	His	Ile	Glu	Tyr	Asp	Tyr	Ile	Leu	Ser	Arg
			100					105					110		
Pro	Leu	Asp	Gln	Ile	Val	His	Tyr	Pro	Ser	Gly	Ser	Val	Asp	Leu	Thr
		115					120					125			
Tyr	Ala	His	Phe	His											
															130

(2) INFORMATIONS POUR LA SEQ ID NO: 310:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 262 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(314741..315526)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 310:

Thr	Lys	Pro	Ile	Phe	Phe	Ser	Leu	Ile	Glu	Gln	Asp	Glu	Arg	Leu	Thr
1				5					10					15	
Pro	Leu	Ser	Tyr	Glu	Pro	Gln	Val	Glu	Ser	Ser	Leu	Gln	Val	Val	Arg
			20					25					30		
Ser	Ile	Glu	Asn	Ala	Ser	Gly	Leu	Gly	Ser	Asp	Ala	Gln	Pro	Leu	Gln
		35					40					45			
Glu	Leu	Phe	Arg	Lys	Leu	Leu	Leu	His	Glu	Gln	Gly	Pro	Leu	Ala	
	50					55				60					
Tyr	Ile	Gly	Leu	Val	Trp	Asn	Phe	Ala	Asn	Arg	Phe	Gly	Gly	Gly	Ile
65					70				75						80
Leu	Glu	Pro	Lys	Arg	Leu	Ser	Arg	Asp	Gly	Lys	Asn	Leu	Leu	Glu	Leu
				85					90					95	
Leu	His	Ala	Leu	Ala	Ile	Pro	Val	Asp	Leu	Ser	His	Cys	Ser	Asp	Pro
			100					105					110		
Leu	Ala	Asp	Asp	Ile	Leu	Asp	Phe	Thr	Ala	Asp	Lys	Met	Pro	Asp	Met

(2) INFORMATION POUR LA SEQ ID NO: 311:

(A) LONGUEUR: 281 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(315665..316507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 311:

Val	Phe	Ser	Gln	Gln	Ile	Glu	Glu	Ser	Ile	Lys	Ala	Gly	Gln	Val	Phe
1				5					10					15	
Ala	Phe	Pro	Thr	Asp	Thr	Val	Tyr	Gly	Leu	Gly	Val	Ser	Phe	His	Ile
			20					25					30		
Leu	Asp	Ala	Asp	Gln	Arg	Leu	Phe	Ala	Leu	Lys	His	Arg	Ser	Ser	Gln
		35					40					45			
Lys	Ala	Leu	Ser	Val	Tyr	Val	Ser	Ser	Leu	Glu	Glu	Leu	Glu	Ala	Val
	50					55					60				
Ala	Gln	Gln	Ser	Leu	Gly	Ala	Ser	Ser	Arg	Lys	Ile	Ile	Gln	Lys	Phe
65					70					75					80
Leu	Pro	Gly	Pro	Leu	Thr	Leu	Ile	Thr	Lys	His	Asn	Asn	Pro	Arg	Phe
				85					90					95	
Pro	Gln	Lys	Thr	Leu	Gly	Phe	Arg	Ile	Val	Asn	His	Pro	Ile	Val	Gln
			100					105					110		
Gln	Ile	Ile	Gln	Lys	Val	Gly	Pro	Phe	Leu	Ala	Thr	Ser	Ala	Asn	Leu
		115					120					125			
Ser	Gly	Phe	Pro	Ser	Ala	Val	Ser	Ala	Asp	Glu	Val	Lys	Gln	Asp	Phe
	130					135					140				
Pro	Glu	Glu	Asp	Ile	Val	Met	Ile	Ser	Gly	Glu	Cys	Ser	Ile	Gly	Leu
145					150					155					160
Glu	Ser	Thr	Val	Ile	Asp	Pro	Glu	Glu	Arg	Ile	Val	Tyr	Arg	Glu	Gly
				165					170					175	
Ala	Ile	Ser	Ile	Ala	Glu	Ile	Glu	Thr	Val	Leu	Gly	Ala	Pro	Cys	Ala
			180					185					190		

[illegible]

## (2) INFORMATIONS POUR LA SEQ ID NO: 313:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 85 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(317338..317592)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 313:

```

Ser Arg Thr Ala Arg Cys Ile Gln Arg Gly Ala Leu Tyr Ala Leu Val
1      5      10      15
Leu Glu Lys Met Gln Arg Phe Pro Lys Glu Phe Leu Lys Asp Gly Val
      20      25      30
Ala Lys Ser Val Val Ala Ile Gln Ala Gly Glu Ser Leu Asp Thr Gly
      35      40      45
Glu Leu Ala Trp Glu Glu Met Pro Ser Ile Thr Ala Cys Leu Gly Arg
      50      55      60
Glu Gly Ile Asp Ala Gln Ala Tyr Ser Phe Leu Ser Val Ser Pro Leu
65      70      75      80
Asp Ala Arg Ile Glu
      85

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 314:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 324 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(317499..318470)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 314:

```

Asn Ser Leu Lys Lys Ile Trp Gly Asn Glu Ile Lys Glu Val Lys Leu
1      5      10      15
Leu Lys Met Val Ser Phe Asp Leu Asn Asp Pro Val Arg Asn Thr Asp
      20      25      30
Asn His Tyr Arg Asn Ile Asn Arg Met Leu Asn Ser Ala Thr Cys Ala
      35      40      45
Ala Gly Gly Ile Gly Leu Leu Thr Pro Val Val Cys Ser Pro Met Gly
      50      55      60
Ala Phe Cys Phe Ala Gln Gly Pro Ser Ser Ala Glu Asp Leu Gly His
65      70      75      80
Arg Ile Gln His Phe Val Ala Cys Leu Gly Pro Ala Ala Gly Phe Tyr
      85      90      95
Ser Leu Ser Asn Glu Arg Ile Met Phe Glu Glu Ala Ala Val Pro Ser
      100      105      110
Val Leu Glu Ala Val Glu Ala Thr Phe Trp Ile Ser Ala Phe Ala Arg
      115      120      125

```

```

Leu Arg Gly Asn Lys Pro Ser Thr Cys Asp Thr Val Met Met Ser Cys
130 135 140
Leu Ile Gly Cys Ile Ser Leu Val Cys Gly Ala Met Phe Val Ala Ile
145 150 155 160
Val Ser Cys Ala Val Lys Ile Ser Arg Ile Val Arg Thr Met Thr Gln
165 170 175
Ala His Ala Leu Arg Glu Thr Ile Gln Arg Gln Leu Ala Ala Arg Ala
180 185 190
Thr Asp Met Arg Ser Ala Tyr Ser Lys Leu Lys Gly Ile Ile Ala Ile
195 200 205
Arg Ala Leu Asn Glu Val Glu Arg Gly His Arg Lys Leu Arg Asn Lys
210 215 220
Met Ile Thr Ala Phe Val Ala Asn Ala Leu Ile Thr Leu Ala Phe Cys
225 230 235 240
Ala Leu Leu Ala Ser Ala Val Ile Ala Ala Phe Phe Leu Gly Ala Ala
245 250 255
Ser Ala Gly Leu Ala Ser Val Phe Phe Gly Cys Leu Trp Gly Gly Ile
260 265 270
Gly Ala Leu Ala Val Gly Val Leu Val Gly Ile Val Ser Gly Ile Cys
275 280 285
Gln Arg Asn Tyr Lys Val Glu Leu Arg Gly Val Phe Ser Glu Val Leu
290 295 300
Phe Met Arg Leu Phe Leu Arg Lys Cys Ser Asp Ser Leu Lys Asn Ser
305 310 315 320
Leu Lys Met Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 315:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 317599..317874

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 315:

```

Leu Arg Trp Gln Ile Pro Glu Thr Met Pro Thr Lys Thr Pro Thr Ala
1 5 10 15
Lys Ala Pro Met Pro Pro His Lys His Pro Lys Lys Thr Leu Ala Ser
20 25 30
Pro Ala Leu Ala Ala Pro Lys Lys Asn Ala Ala Ile Thr Ala Glu Ala
35 40 45
Asn Lys Ala Gln Lys Ala Ser Val Met Ser Ala Phe Ala Thr Lys Ala
50 55 60
Val Ile Ile Leu Phe Leu Asn Phe Arg Trp Pro Leu Ser Thr Ser Leu
65 70 75 80
Arg Ala Leu Met Ala Ile Met Pro Leu Ser Leu Glu
85 90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 316:

(i) CARACTERISTIQUES DE LA SEQUENCE:



(iii) HYPOTHETIQUE: cui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 316:

(2) INFORMATION POUR LA SEQ ID NO: 317:

(A) . LONGUEUR: 267 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 319342..320142

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 317:

Met	Ser	Arg	Lys	Pro	Ala	Ser	Asn	Ser	Ser	Arg	Asn	Thr	Lys	Arg	Ser
1				5					10					15	
Ser	Asp	Thr	Ser	Trp	Glu	Val	Ile	Ala	Gln	Asp	Tyr	Asn	Lys	Ala	Val
			20					25					30		
Asp	Arg	Asp	Gly	His	Phe	Tyr	His	Lys	Glu	Val	Ile	Leu	Pro	Asn	Leu
			35				40					45			
Leu	Ser	Lys	Leu	His	Ile	Ser	Arg	Ser	Ser	Ser	Leu	Val	Asp	Val	Gly
	50					55					60				
Cys	Gly	Gln	Gly	Ile	Leu	Glu	Lys	His	Leu	Pro	Lys	Tyr	Leu	Pro	Tyr
65					70					75					80
Leu	Gly	Ile	Asp	Leu	Ser	Pro	Ser	Leu	Leu	Arg	Phe	Ala	Lys	Lys	Ser
				85					90					95	

Ala	Ser	Ser	Lys	Ser	Arg	Arg	Phe	Leu	His	His	Asp	Met	Thr	Gln	Pro
			100					105					110		
Val	Pro	Ala	Asp	His	His	Glu	Gln	Phe	Ser	His	Xaa	Thr	Ala	Ile	Leu
		115					120					125			
Ser	Xaa	Gln	Xaa	Met	Glu	Ser	Pro	Glu	Gln	Ala	Ile	Ala	His	Thr	Ala
	130					135					140				
Asn	Leu	Leu	Ala	Pro	Gln	Gly	Arg	Leu	Phe	Ile	Val	Leu	Asn	His	Pro
145					150					155					160
Cys	Phe	Arg	Ile	Pro	Arg	Leu	Ser	Ser	Trp	Leu	Tyr	Asp	Glu	Pro	Lys
				165					170					175	
Lys	Leu	Leu	Ser	Arg	Lys	Ile	Asp	Arg	Tyr	Leu	Ser	Pro	Val	Ala	Val
			180					185					190		
Pro	Ile	Val	Val	His	Pro	Gly	Glu	Lys	His	Ser	Glu	Thr	Thr	Tyr	Ser
		195					200					205			
Phe	His	Phe	Pro	Leu	Ser	Tyr	Trp	Val	Gln	Ala	Leu	Ser	Asn	His	Asn
	210					215					220				
Leu	Leu	Ile	Asp	Ser	Met	Glu	Glu	Trp	Ile	Ser	Pro	Lys	Lys	Ser	Ser
225					230					235					240
Gly	Lys	Arg	Ala	Arg	Ala	Glu	Asn	Leu	Ser	Arg	Lys	Glu	Phe	Pro	Leu
				245					250					255	
Phe	Leu	Phe	Ile	Ser	Ala	Leu	Lys	Ile	Ser	Lys					
			260					265							

(2) INFORMATIONS POUR LA SEQ ID NO: 318:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 318 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 320544..321497

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 318:

Phe	Leu	Cys	Leu	Leu	Leu	Gly	Arg	Tyr	Ser	Asp	Ala	Thr	Ile	Phe	Arg
1			5						10					15	
Ser	Gly	Leu	Asn	Lys	Ile	Phe	Cys	Ser	Gly	Ile	Thr	Gln	Ala	Ser	Leu
			20					25					30		
Lys	Arg	Leu	Ile	Ser	Tyr	Leu	Val	Ile	Thr	Leu	Val	Ser	Pro	Met	Ile
		35				40					45				
Phe	Ile	Ile	Val	Cys	Gly	Ser	Trp	Ile	Tyr	Ile	Thr	Gln	Ile	Leu	Pro
	50				55						60				
Ile	Asn	Tyr	Pro	Gln	Leu	Phe	Ser	Phe	Ser	His	Ser	Met	Ala	Phe	Ile
65				70						75				80	
Tyr	Ile	Val	Ser	Arg	Leu	Leu	Pro	Tyr	Ala	Leu	Leu	Tyr	Gly	Ile	Leu
				85				90					95		
Phe	Cys	Cys	Tyr	Ala	Phe	Leu	Ser	Arg	Val	Pro	Thr	Lys	Lys	Ser	Ala
			100					105					110		
Ala	Phe	Phe	Ala	Ala	Thr	Ile	Ala	Gly	Ser	Ala	Trp	Ile	Leu	Ser	Gln
		115					120					125			
Lys	Ile	Phe	Phe	Cys	Leu	Gln	Leu	His	Leu	Phe	Asn	Tyr	Ser	Phe	Thr
	130					135					140				
Tyr	Gly	Ala	Leu	Val	Ala	Leu	Pro	Ser	Phe	Leu	Leu	Leu	Leu	Tyr	Leu
145					150					155					160
Tyr	Ala	Ile	Ile	Tyr	Leu	Phe	Gly	Gly	Ala	Leu	Thr	Phe	Leu	Phe	Gln

				165					170					175					
Asn	Lys	Gly	Phe	Ser	Ile	Leu	Ile	Pro	Lys	Glu	Glu	Ile	Phe	Pro	Ser				
			180					185					190						
Ser	Tyr	Phe	Lys	Phe	Ile	Leu	Cys	Val	Tyr	Val	Leu	Ser	Leu	Ile	Thr				
		195					200						205						
Glu	His	Phe	Asp	Asn	Ala	Leu	Pro	Pro	Pro	Ser	Ala	Asn	Tyr	Leu	Ala				
	210					215					220								
Asn	Lys	Ala	Lys	Ala	Ser	Ile	Gly	Glu	Thr	Ser	Gln	Cys	Leu	Asp	Ile				
225					230					235					240				
Leu	Glu	Arg	Glu	Gly	Met	Ile	Leu	Lys	Tyr	Lys	Glu	Gly	Tyr	Lys	Pro				
			245					250						255					
Ser	His	Asn	Ile	Ala	Asn	Leu	His	Ile	Asn	Thr	Ile	Phe	Asp	Gln	Leu				
		260						265					270						
Thr	Lys	Ser	Pro	Ala	Phe	Ser	Lys	Ile	Cys	Ser	Pro	Ser	Leu	Ile	Pro				
		275					280						285						
Ile	Gln	Asp	Ala	Leu	Thr	His	Ile	Leu	Thr	Glu	Ile	Lys	Lys	Asn	Ser				
	290					295					300								
His	Asn	Leu	Ser	Leu	Ser	Glu	Ile	Ala	Lys	Lys	Val	Asn	Ser						
305						310					315								

(2) INFORMATIONS POUR LA SEQ ID NO: 319:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 151 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 321485..321937

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 319:

Lys	Ser	Glu	Phe	Met	Lys	Arg	Ser	Pro	Trp	Tyr	Lys	Ile	Phe	Gly	Tyr				
1				5					10					15					
Tyr	Leu	Leu	Val	Gly	Val	Pro	Leu	Ala	Leu	Leu	Ala	Leu	Leu	Pro	Lys				
			20					25						30					
Phe	Leu	Ser	Ser	Glu	Ser	Gly	Lys	Tyr	Leu	Phe	Leu	Ser	Val	Leu	Asn				
		35					40						45						
Lys	Glu	Thr	Gly	Leu	Gln	Cys	Glu	Ile	Glu	Gln	Leu	His	Leu	Ser	Trp				
	50					55					60								
Phe	Gly	Ser	Gln	Thr	Ala	Lys	Lys	Ile	Arg	Ile	Arg	Gly	Ile	Asp	Ser				
65					70					75				80					
Glu	Ser	Glu	Ile	Phe	Ala	Ala	Glu	Lys	Ile	Ile	Val	Lys	Gly	Ser	Leu				
				85					90					95					
Pro	Arg	Leu	Leu	Leu	Tyr	Arg	Phe	Pro	Lys	Ala	Leu	Thr	Leu	Thr	Gly				
			100					105					110						
Trp	Ser	Leu	Gln	Ile	Asp	Glu	Ser	Leu	Ser	Met	Asn	Ser	Pro	Ser	Leu				
		115					120						125						
Tyr	His	Leu	Asp	Pro	Gly	Val	Leu	Leu	Ser	Lys	Ile	Glu	Arg	Arg	Leu				
	130					135						140							
Ser	Leu	Gln	Asn	Leu	Asp	Pro													
145						150													

(2) INFORMATIONS POUR LA SEQ ID NO: 320:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 321901..322362

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 320:

Asn	Arg	Ala	Gln	Val	Ile	Thr	Ser	Glu	Leu	Gly	Ser	Ile	Thr	Met	Lys
1				5					10					15	
Thr	Ile	Asn	Gly	Ser	Thr	Leu	Ser	Val	Ser	Gly	Phe	Tyr	Val	Lys	Lys
		20						25					30		
Thr	Ala	Glu	Gln	Leu	Leu	Ile	Arg	Ala	Leu	Thr	Lys	Glu	Asn	Asp	Val
		35					40					45			
Pro	Gly	Ser	Val	Ala	Val	Glu	Gly	Ala	Leu	Ser	Pro	Asn	Phe	Val	Leu
	50					55					60				
Asn	Val	Glu	Leu	Ser	Ser	Val	Pro	Ala	Ser	Leu	Phe	Lys	Leu	Phe	Ile
65					70					75					80
Ala	Ser	Pro	Ser	Leu	Asp	Arg	Ile	Leu	Ser	Thr	Glu	Asn	Leu	Ile	Asn
				85					90					95	
Leu	Thr	Ala	Lys	Ala	His	Gln	Glu	Lys	Asp	Ser	Thr	Leu	Ile	Thr	Leu
		100						105					110		
Thr	Ala	Glu	Gly	Asn	Gln	Ile	Ser	Ala	Lys	Leu	Arg	Gly	Tyr	Val	Arg
		115					120					125			
Asp	Arg	Val	Phe	Leu	Ile	Thr	Gln	Gly	Gly	Ala	Ser	Phe	Cys	Ala	Leu
	130					135					140				
Thr	Ala	Tyr	Asn	Asn	Phe	Ser	Asn	Ser	Leu						
145						150									

(2) INFORMATIONS POUR LA SEQ ID NO: 321:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 280 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 322301..323140

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 321:

Ser	His	Lys	Ala	Glu	Pro	Pro	Ser	Val	Leu	Leu	Gln	Pro	Thr	Ile	Thr
1				5					10					15	
Ser	Arg	Ile	Leu	Ser	Glu	Leu	Ser	Pro	Leu	Asp	Thr	Pro	Ile	Arg	Ser
		20						25					30		
Gln	Glu	Ala	Tyr	Leu	Phe	Ile	Ser	Glu	Ala	Lys	Leu	Pro	Leu	Ser	Ile
		35					40					45			
Ser	Lys	Trp	Ser	Ala	Ser	Asp	Phe	Ser	Leu	Gln	Ala	Asn	Leu	Pro	Gln
	50					55					60				
Ile	Ser	Val	Asp	Thr	Leu	Asp	Pro	Asn	Leu	Ser	Ile	Arg	Thr	Glu	Asn
65					70					75					80
Thr	Lys	Ile	Ser	Ile	Arg	Lys	Ser	Asp	His	Leu	Thr	Val	Met	Arg	Ser

				85					90					95					
Ser	Ser	Ser	Ala	Ile	Leu	Gly	Gly	Ala	Ser	Pro	Ser	Tyr	Ile	His	Ser				
			100					105					110						
Thr	Leu	Ser	Met	Asp	Asn	His	Lys	His	Val	Ala	Glu	Phe	His	Ile	Gln				
		115					120					125							
His	Ser	Leu	Leu	Pro	His	Thr	Tyr	Leu	Arg	Ala	Leu	Leu	Pro	Lys	Pro				
	130					135					140								
Ile	Glu	Ile	Asn	Thr	Pro	Leu	Glu	Val	Pro	Tyr	Tyr	Thr	Leu	Asp	Ile				
145					150					155					160				
Lys	Gly	Lys	Tyr	Arg	Asn	Thr	Gln	Leu	Ser	Cys	Glu	Ala	Leu	Leu	Asp				
				165					170					175					
Asn	Pro	Leu	Leu	Arg	Leu	Ser	Cys	Asn	Leu	Ser	Gly	Pro	Leu	Tyr	Ala				
		180						185					190						
Leu	Gln	Phe	Ser	Gly	Glu	Gly	Ala	Tyr	Thr	Leu	Ser	Glu	Arg	Trp	Lys				
		195					200					205							
Glu	Arg	Leu	Ala	Pro	His	Phe	Leu	Gln	Ile	Gln	Ala	Ile	Phe	Ser	Gly				
	210					215				220									
Lys	Met	His	Phe	Ser	Gln	Lys	His	Val	Phe	Phe	Pro	Lys	Leu	Ser	Gly				
225					230					235					240				
Lys	Leu	Ile	Ala	Gly	Asp	Asn	Glu	Ile	Phe	Ile	His	Gly	Lys	Cys	Gly				
				245					250					255					
Arg	Ala	Ser	Glu	Met	Lys	Pro	Ser	Asn	Ser	Ser	Leu	Leu	Val	Tyr					
			260				265						270						
Gly	Asn	Thr	Leu	Leu	Ser	Ser	Phe												
		275					280												

(2) INFORMATIONS POUR LA SEQ ID NO: 322:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 590 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 323144..324913

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 322:

Ile	Tyr	Tyr	Pro	Pro	Lys	Phe	Ala	Pro	Leu	Gln	Met	Thr	Xaa	Ser	Ser				
1				5					10					15					
Phe	Ser	Leu	His	Ser	Asp	Gly	Gly	Lys	Ala	Leu	Leu	Lys	Gly	Asn	Val				
			20					25					30						
Lys	Leu	Phe	Ile	Thr	Asp	Pro	Glu	Ser	Pro	His	Xaa	Glu	Xaa	Thr	Lys				
		35					40					45							
Ile	Leu	Ile	Pro	Asp	Ile	Val	Ile	Xaa	Ser	Leu	Asp	Pro	Ser	Ala	Pro				
	50					55					60								
Trp	Thr	Ala	Asp	Asn	Xaa	Ser	Val	Gln	Ala	Ser	Gly	Glu	Leu	Leu	Gln				
65				70					75					80					
Leu	Pro	Val	Asp	Arg	Leu	Ile	Arg	Leu	Gln	His	Lys	Asp	Leu	Ser	Leu				
				85				90					95						
Ser	Arg	Tyr	Ile	Gly	Glu	Thr	Ser	Glu	Ala	Ser	Phe	Gln	Leu	Leu	Tyr				
			100					105				110							
Ser	Pro	Asp	Lys	Glu	Glu	Thr	Val	Asp	Ile	Ser	Ser	Arg	Phe	Lys	Thr				
		115					120					125							
Asp	Ala	Leu	Thr	Gly	Asp	Phe	Arg	Phe	Val	Met	Asn	Lys	Glu	Leu	Ser				
	130						135					140							

Leu	Thr	Glu	Lys	Ala	His	Gly	Ser	Leu	Gln	Trp	Glu	Ile	Ser	Pro	Glu
145					150					155					160
Arg	Tyr	Ser	Ser	Phe	Phe	Glu	Lys	Ala	Ser	Cys	Pro	Pro	Ser	Cys	Ile
				165					170					175	
Leu	His	Arg	Pro	Thr	Thr	Phe	Arg	Leu	Asp	Leu	Ser	Lys	Ile	Ser	Cys
			180					185					190		
Leu	Asp	Lys	Lys	Thr	Gly	Tyr	Ser	Cys	Leu	Ser	Leu	Leu	Ser	Gln	Gly
		195					200					205			
Gly	Ile	Glu	Gly	Lys	Leu	Ser	Ser	Thr	Pro	Leu	Val	Phe	Tyr	Asp	His
	210					215					220				
Leu	Ser	Lys	Glu	Asn	Phe	Ile	Val	Asn	Asn	Ile	Gly	Gly	Ser	Val	Tyr
225					230					235					240
Ala	Gln	Asn	Val	Asn	Asp	Leu	Ile	Gln	Tyr	Gln	Leu	Asn	Gly	Asn	Cys
				245					250					255	
Leu	Ala	Pro	Asn	Gln	Asp	Asn	Lys	Thr	Pro	Val	Ser	Phe	Ile	Ile	Glu
			260					265					270		
Gly	Glu	Ala	Arg	Asn	Ile	Phe	Ser	Asp	Glu	Thr	Arg	Ala	Cys	Ser	Gln
		275					280					285			
Thr	Ala	Thr	Trp	Val	Asn	Ile	Pro	Thr	Ser	Phe	Ile	Thr	Gly	Ile	Phe
	290					295					300				
Pro	Ile	Ser	Pro	Gly	Val	Arg	Ser	Lys	Leu	Thr	Ser	Leu	Ala	Gly	Pro
305					310					315					320
Lys	Ile	His	Val	Ser	Ile	His	Asn	Asp	Phe	Ser	Arg	Gly	Glu	Gly	Pro
				325					330					335	
Val	Thr	Ile	Lys	Val	Asp	Ser	Glu	Asn	Leu	Thr	Ala	Tyr	Phe	Pro	Leu
			340					345					350		
Val	Leu	Thr	Glu	Gln	Ala	Ile	Leu	Leu	Glu	Asp	Asp	Leu	Thr	Ala	Ser
		355					360					365			
Leu	His	Ile	Asn	Glu	Glu	Ile	Asn	Lys	Ala	Phe	Leu	Arg	Glu	Phe	Asn
	370					375				380					
Pro	Leu	Ile	Ala	Glu	Gly	Gly	Ala	Tyr	Ser	Lys	His	Pro	Val	Ser	Leu
385					390					395					400
Arg	Val	Asn	Lys	Gln	Asn	Phe	Tyr	Leu	Pro	Ile	Lys	Pro	Tyr	Ser	Phe
				405					410					415	
Glu	Asn	Phe	Arg	Ile	Gln	Ser	Ala	Ser	Leu	Asp	Phe	Gly	Lys	Ile	Glu
			420					425					430		
Ile	Ala	Asn	Thr	Gly	Thr	Met	Gln	Asp	Leu	Phe	Gln	Phe	Leu	Asp	Val
		435					440					445			
Glu	Ala	Glu	Gln	Gln	Arg	Val	Glu	Ser	Trp	Phe	Thr	Pro	Ile	Phe	Phe
	450					455					460				
Ser	Val	Gln	Lys	Gly	Gln	Ile	Ile	Cys	Lys	Arg	Phe	Asp	Ala	Leu	Ile
465					470					475					480
Asp	Gly	Arg	Ile	Arg	Leu	Ala	Leu	Trp	Gly	Lys	Thr	Asp	Ile	Val	Arg
				485					490					495	
Glu	Arg	Leu	Ala	Met	Thr	Leu	Gly	Ile	Asp	Pro	Glu	Leu	Ile	Lys	Lys
			500					505					510		
Leu	Phe	Arg	Asn	Thr	Met	Leu	Lys	Thr	Lys	Asn	Phe	Phe	Leu	Ile	Lys
		515					520					525			
Ile	Arg	Gly	Pro	Ile	Ser	Ser	Pro	Glu	Ile	Asp	Trp	Ser	Ser	Ala	Tyr
	530					535					540				
Ala	Arg	Ile	Ala	Leu	Leu	Lys	Ser	Tyr	Thr	Ile	Ala	Gly	Pro	Leu	Asn
545					550					555					560
Ser	Leu	Ala	Asp	Lys	Leu	Phe	Ser	Ser	Leu	Gly	Glu	Pro	Thr	Pro	Thr
				565					570					575	
Gln	Thr	Val	Ser	Pro	Leu	Pro	Trp	Glu	Val	Ser	Glu	Thr	Glu		
			580					585					590		

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 215 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(324977..325621)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 323:

Met	Thr	Val	Glu	Val	Lys	Asp	Leu	Thr	Val	Ala	Val	Lys	Gly	Lys	Glu
1				5					10					15	
Ile	Leu	Ser	Asn	Val	Ser	Phe	Ser	Leu	Val	Pro	Gly	Arg	Ile	Thr	Leu
			20					25					30		
Phe	Ile	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Ile	Leu	Arg	Ser	Leu
		35					40					45			
Val	Gly	Leu	Thr	Pro	Ile	Ser	Ser	Gly	Ser	Ile	Ser	Val	Val	Gly	Asp
	50					55					60				
Pro	Pro	Gly	Phe	Val	Phe	Gln	Gln	Pro	Glu	Leu	Phe	Pro	His	Met	Thr
65					70				75						80
Val	Leu	Asp	Asn	Cys	Ala	His	Pro	Gln	Met	Ile	Val	Lys	Lys	Arg	Gly
			85					90						95	
Glu	Arg	Glu	Ala	Lys	Asp	Lys	Ala	Leu	Asp	Leu	Leu	Gly	Met	Leu	Glu
			100					105					110		
Leu	Arg	Glu	Tyr	Ala	Ser	Ser	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	Gln
		115					120					125			
Arg	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Leu	Asp	Met	Arg	Ala
	130					135					140				
Ile	Leu	Phe	Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Phe	Ser	Ala	Ser
145					150				155						160
Lys	Phe	Leu	Gln	Ile	Val	Leu	Ser	Leu	Lys	Glu	Gln	Gly	Met	Thr	Ile
			165					170						175	
Ala	Ile	Ser	Thr	His	Asp	Met	Leu	Phe	Ile	Asn	Gln	Cys	Leu	Asp	Arg
			180					185					190		
Val	Tyr	Leu	Val	Asp	Lys	Gly	Gln	Ile	Ile	Asp	Ala	Tyr	Asp	Ser	Leu
		195				200						205			
His	Asp	Asp	Pro	Gln	Gly	Lys									
	210					215									

(2) INFORMATIONS POUR LA SEQ ID NO: 324:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(325621..326268)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 324:

Gly	Ile	Val	Glu	His	Tyr	Leu	Leu	Thr	Ala	Lys	Leu	Leu	Leu	Arg	Gly
1				5					10					15	

Cys	Gly	Tyr	Thr	Leu	Leu	Ile	Thr	Ala	Ile	Ser	Leu	Val	Cys	Gly	Phe
			20					25					30		
Val	Leu	Gly	Trp	Gly	Ile	Gly	Thr	Val	Asn	Ser	Arg	Tyr	Phe	Pro	Cys
		35					40					45			
Arg	Ile	Ser	Lys	Phe	Leu	Gly	Asn	Phe	Tyr	Val	Val	Ala	Val	Arg	Gly
	50					55					60				
Thr	Pro	Leu	Phe	Ile	Gln	Ile	Leu	Ile	Val	Tyr	Phe	Gly	Leu	Pro	Ser
	65				70					75				80	
Leu	Ile	Lys	Val	Asn	Leu	Ser	Pro	Leu	Val	Ala	Gly	Leu	Ile	Ala	Leu
			85						90					95	
Thr	Leu	Asn	Ser	Ala	Ala	Tyr	Leu	Ala	Glu	Asn	Val	Arg	Ala	Gly	Ile
			100					105					110		
Asn	Ala	Leu	Pro	Val	Gln	Gln	Trp	Glu	Ala	Ala	Lys	Val	Leu	Gly	Tyr
		115					120					125			
Thr	Gly	Pro	Gln	Ile	Phe	Leu	His	Ile	Leu	Tyr	Pro	Gln	Val	Phe	Lys
	130					135					140				
Asn	Ile	Leu	Pro	Ser	Leu	Ala	Asn	Glu	Phe	Val	Ser	Leu	Ile	Lys	Glu
	145				150					155				160	
Ser	Ser	Ile	Leu	Met	Val	Val	Gly	Val	Pro	Glu	Leu	Thr	Lys	Val	Thr
			165					170						175	
Lys	Asp	Ile	Val	Ala	Arg	Glu	Leu	Asn	Pro	Met	Glu	Met	Tyr	Leu	Ile
		180						185					190		
Cys	Ala	Gly	Leu	Tyr	Leu	Ile	Met	Thr	Ser	Ala	Phe	Ser	Tyr	Phe	Ala
		195					200					205			
Arg	Leu	Ser	Glu	Lys	Glu	Ser	Ala								
	210					215									

(2) INFORMATIONS POUR LA SEQ ID NO: 325:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 326469..327203

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 325:

Met	Asp	Arg	Ser	Pro	Leu	Phe	Leu	Ile	Ile	Met	Gly	Ala	Pro	Gly	Ser
1				5					10					15	
Gly	Lys	Gly	Thr	Gln	Ser	Lys	Leu	Leu	Ala	Ser	Gln	Leu	Ser	Leu	Leu
			20					25					30		
His	Ile	Ser	Ser	Gly	Asp	Leu	Leu	Arg	Gly	Ala	Val	Ser	Lys	Asp	Thr
		35					40					45			
Pro	Leu	Ser	Gln	Glu	Ile	Lys	Ser	Tyr	Leu	Asp	Gln	Gly	Lys	Leu	Leu
	50					55					60				
Pro	Asp	Thr	Leu	Val	Trp	Lys	Leu	Val	His	Glu	Lys	Leu	Asp	Glu	Phe
	65				70					75				80	
Gln	Gln	Asp	Thr	Leu	Leu	Arg	Arg	Leu	Ser	Phe	Leu	Ser	Arg	Ser	Glu
			85					90						95	
Asn	Ser	Ala	Ile	Leu	Asp	Gly	Phe	Pro	Arg	Thr	Val	Thr	Gln	Ala	Lys
		100						105					110		
Leu	Leu	His	Glu	Phe	Leu	Ser	Ser	Tyr	Phe	Pro	Asn	Tyr	Lys	Val	Ile
		115					120					125			
Leu	Leu	Asp	Ile	Ser	Asp	Glu	Glu	Val	Leu	Asn	Arg	Leu	Thr	Ser	Arg



(2) INFORMATIONN POUR LA SEQ ID NO: 326:

(A) LONGUEUR: 290 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 327281..328150

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 326:

Cys	Leu	Tyr	Arg	Gly	Ser	Pro	Met	Pro	His	Gln	Val	Leu	Leu	Ser	Pro
1				5					10					15	
Val	Cys	Asp	Leu	Leu	Ser	Asn	Ala	Glu	Gly	Ile	Glu	Thr	Gln	Val	Leu
			20					25					30		
Phe	Gly	Glu	Arg	Ile	Cys	Asn	His	Asn	His	Arg	His	Tyr	Ala	Tyr	Ser
	35					40						45			
Gln	Leu	Val	Phe	Ser	Ser	Ile	Trp	Lys	Pro	Tyr	Pro	Gly	Asp	Ser	Leu
	50					55					60				
Gln	Asn	Ile	Pro	Leu	Phe	Ser	Ser	Gln	Leu	Gln	Pro	Pro	Asn	Ala	Val
65					70					75					80
Val	Cys	Ser	Gln	Glu	Ala	Phe	Leu	Asp	Pro	Trp	His	Ile	Pro	Leu	Pro
				85				90						95	
Phe	Ala	Ala	Pro	Leu	His	Ile	Asp	Asn	Gln	Asn	Gln	Val	Ser	Leu	Ser
			100					105					110		
Pro	Ala	Ser	Ile	Ala	Leu	Leu	Asn	Ser	Asn	Ser	Arg	Ser	Asn	Tyr	Ala
	115						120					125			
Lys	Ala	Phe	Cys	Ser	Thr	Lys	Glu	Ile	Arg	Phe	Leu	Asn	Ser	Ser	Phe
	130					135					140				
Ser	Leu	Arg	Asp	Leu	Val	Ser	Phe	Ala	Glu	Gln	Leu	Ile	Asp	Thr	Pro
145					150					155					160
Tyr	Val	Trp	Gly	Gly	Arg	Cys	Ile	His	Lys	Gln	Leu	Pro	Arg	Asn	Gly
			165						170					175	
Val	Asp	Cys	Ser	Gly	Tyr	Ile	Gln	Leu	Leu	Tyr	Gln	Val	Thr	Gly	Arg
			180					185					190		
Asn	Ile	Pro	Arg	Asn	Ala	Arg	Asp	Gln	Tyr	Arg	Asp	Cys	Ser	Pro	Val
	195						200					205			
Lys	Asp	Phe	Ser	Ser	Leu	Pro	Ile	Gly	Gly	Leu	Ile	Phe	Leu	Lys	Lys
	210					215					220				

Ala	Ser	Thr	Gly	Gln	Ile	Asn	His	Val	Met	Met	Lys	Ile	Ser	Glu	His
225					230					235					240
Glu	Phe	Ile	His	Ala	Ala	Glu	Lys	Ile	Gly	Lys	Val	Glu	Lys	Val	Ile
			245						250					255	
Leu	Gly	Asn	Arg	Ala	Phe	Phe	Lys	Gly	Asn	Leu	Phe	Cys	Ser	Leu	Gly
		260						265					270		
Glu	Pro	Pro	Ile	Glu	Ala	Val	Phe	Gly	Val	Pro	Lys	Asn	Arg	Lys	Ala
		275					280					285			
Phe	Phe														
	290														

## (2) INFORMATIONS POUR LA SEQ ID NO: 327:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 134 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(328204..328605)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 327:

Phe	Val	Thr	Lys	Asn	Met	Ile	Gln	Glu	Ser	Val	Ala	Thr	Gly	Arg	Arg
1				5					10					15	
Lys	Gln	Ala	Val	Ser	Ser	Val	Arg	Leu	Arg	Ser	Gly	Asn	Gly	Lys	Ile
			20					25					30		
Asp	Val	Asn	Gly	Lys	Thr	Leu	Glu	Gln	Tyr	Phe	Pro	Leu	Glu	Val	Gln
		35					40					45			
Arg	Ala	Thr	Ile	Leu	Ala	Pro	Leu	Arg	Met	Leu	Gly	Asp	Val	Asn	Ser
		50				55					60				
Phe	Asp	Leu	Ile	Ile	Arg	Val	Ser	Gly	Gly	Gly	Val	Gln	Gly	Gln	Val
65					70				75						80
Ile	Ala	Thr	Arg	Leu	Gly	Leu	Ala	Arg	Ala	Val	Leu	Gln	Glu	Lys	Glu
			85					90					95		
Asp	Ile	Lys	Gln	Glu	Leu	Lys	Ala	Gln	Gly	Phe	Leu	Thr	Arg	Asp	Pro
		100					105					110			
Arg	Lys	Lys	Glu	Arg	Lys	Lys	Tyr	Gly	Arg	Lys	Lys	Ala	Arg	Lys	Ser
		115					120					125			
Phe	Gln	Phe	Ser	Lys	Arg										
	130														

## (2) INFORMATIONS POUR LA SEQ ID NO: 328:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 104 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(328734..329045)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 328:

```

Lys Thr Thr Leu Ala Lys Ala Ser Asp Asp Arg Asn Lys Ala Trp Tyr
1          5          10          15
Val Val Asn Ala Glu Gly Lys Thr Leu Gly Arg Leu Ser Ser Glu Val
          20          25          30
Ala Lys Ile Leu Arg Gly Lys His Lys Val Thr Phe Thr Pro His Val
          35          40          45
Ala Met Gly Asp Gly Val Ile Val Ile Asn Ala Glu Lys Val Arg Leu
          50          55          60
Thr Gly Ala Lys Arg Ala Gln Lys Val Tyr His Tyr Tyr Thr Gly Phe
65          70          75          80
Ile Ser Gly Met Arg Glu Val Pro Phe Glu Asn Met Ile Ala Arg Asn
          85          90          95
Cys Leu Cys Tyr Arg Ala Cys Cys
          100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 329:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 124 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(329292..329663)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 329:

```

Phe Asn Ala Glu Ser Met Gln Arg Ile Gln Val Ile Thr Phe Thr Pro
1          5          10          15
Ser Pro Gly Arg Leu Asp Tyr Tyr Leu Pro Pro Ala Gly Pro Ala Val
          20          25          30
Arg Val Asp Gly Ala Cys Tyr Ser Gly Tyr Ala Ile Pro Pro Tyr Tyr
          35          40          45
Asp Ser Met Ile Ala Lys Val Ile Thr Lys Gly Lys Asn Arg Glu Glu
          50          55          60
Ala Ile Ala Ile Met Lys Arg Ala Leu Lys Glu Phe His Ile Gly Gly
65          70          75          80
Val His Ser Thr Ile Pro Phe His Gln Phe Met Leu Asp Asn Pro Lys
          85          90          95
Phe Leu Leu Ser Asp Tyr Asp Ile Asn Tyr Val Asp Gln Leu Leu Ala
          100          105          110
Ser Gly Ser Thr Phe Leu Asn Leu Ala Asp Gly Ser
          115          120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 330:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 353 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(329608..330666)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 330:

Leu	Met	Lys	Glu	Val	Leu	Ile	Ala	Asn	Arg	Gly	Glu	Ile	Ala	Val	Arg	1	5	10	15
Ile	Ile	Arg	Ala	Cys	His	Asp	Leu	Gly	Leu	Ala	Thr	Val	Ala	Val	Tyr	20	25	30	
Ser	Met	Ala	Asp	Gln	Glu	Ala	Leu	His	Val	Leu	Leu	Ala	Asp	Glu	Ala	35	40	45	
Val	Cys	Ile	Gly	Glu	Ala	Gln	Ala	Ala	Lys	Ser	Tyr	Leu	Lys	Ile	Ala	50	55	60	
Asn	Ile	Leu	Ala	Ala	Cys	Glu	Ile	Thr	Gly	Ala	Asp	Ala	Val	His	Pro	65	70	75	80
Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	Asn	Phe	Ala	Ser	Ile	Cys	Glu	85	90	95	
Ser	Cys	Gly	Leu	Thr	Phe	Ile	Gly	Pro	Ser	Ala	Glu	Ser	Ile	Ala	Thr	100	105	110	
Met	Gly	Asp	Lys	Val	Ala	Ala	Lys	Gln	Leu	Ala	Lys	Lys	Ile	Lys	Cys	115	120	125	
Pro	Val	Ile	Pro	Gly	Ser	Glu	Gly	Val	Val	Lys	Asp	Glu	Val	Glu	Gly	130	135	140	
Ile	Arg	Ile	Ala	Glu	Lys	Ile	Gly	Phe	Pro	Ile	Val	Ile	Lys	Ala	Val	145	150	155	160
Ala	Gly	Gly	Gly	Gly	Arg	Gly	Ile	Arg	Ile	Val	Arg	Glu	Lys	Asp	Glu	165	170	175	
Phe	Tyr	Arg	Ala	Phe	Thr	Ala	Ala	Arg	Ala	Glu	Ala	Glu	Ala	Gly	Phe	180	185	190	
Asn	Asn	Pro	Asp	Val	Tyr	Ile	Glu	Lys	Phe	Ile	Glu	Asn	Pro	Arg	His	195	200	205	
Leu	Glu	Val	Gln	Val	Ile	Gly	Asp	Lys	His	Gly	Asn	Tyr	Val	Tyr	Leu	210	215	220	
Gly	Glu	Arg	Asp	Cys	Thr	Val	Gln	Arg	Arg	Arg	Gln	Lys	Leu	Ile	Glu	225	230	235	240
Glu	Thr	Pro	Ser	Pro	Ile	Leu	Thr	Pro	Glu	Met	Gln	Ala	Lys	Val	Gly	245	250	255	
Lys	Val	Ala	Val	Asp	Leu	Ala	Arg	Ser	Ala	Gly	Tyr	Phe	Ser	Val	Gly	260	265	270	
Thr	Val	Glu	Phe	Leu	Leu	Asp	Lys	Glu	Lys	Arg	Phe	Tyr	Phe	Met	Glu	275	280	285	
Met	Asn	Thr	Arg	Ile	Gln	Val	Glu	His	Thr	Ile	Thr	Glu	Glu	Val	Thr	290	295	300	
Gly	Ile	Asp	Leu	Leu	Lys	Ala	Gln	Ile	Ser	Val	Ala	Lys	Gly	Glu	Lys	305	310	315	320
Leu	Pro	Trp	Lys	Gln	Lys	Asn	Ile	Glu	Phe	Lys	Gly	His	Val	Ile	Gln	325	330	335	
Cys	Arg	Ile	Asn	Ala	Glu	Asp	Pro	Ser	Asn	Asn	Phe	Tyr	Ser	Phe	Pro	340	345	350	
Trp																			

(2) INFORMATIONS POUR LA SEQ ID NO: 331:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 164 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(330670..331161)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 331:

```

Met Asp Leu Lys Gln Ile Glu Lys Leu Met Ile Ala Met Gly Arg Asn
1      5      10      15
Lys Met Lys Arg Ile Val Ile Lys Arg Glu Gly Leu Glu Leu Glu Leu
20      25      30
Glu Arg Asp Thr Val Pro Ser Ile Gln Glu Pro Val Phe Tyr Asp Asn
35      40      45
Arg Leu Phe Ala Gly Phe Ser Gln Glu Arg Pro Ile Pro Thr Asp Gln
50      55      60
Asn Leu Gly Asn Pro Ile Val Lys Glu Ser Ile Glu Lys Lys Glu Ser
65      70      75      80
Glu Ala Pro Ala Gln Gly Asp Phe Ile Val Ser Pro Leu Val Gly Thr
85      90      95
Phe Tyr Gly Ser Pro Ser Pro Glu Ala Pro Ala Phe Ile Lys Pro Gly
100     105     110
Asp Thr Val Ser Glu Asp Thr Val Val Cys Ile Val Glu Ala Met Lys
115     120     125
Val Met Asn Glu Val Lys Ala Gly Met Ser Gly Arg Val Glu Glu Ile
130     135     140
Leu Ile Thr Asn Gly Asp Pro Val Gln Phe Gly Ser Lys Leu Phe Arg
145     150     155     160
Ile Val Lys Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 332:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 185 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(331177..331731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 332:

```

Met Val Leu Ser Ser Gln Leu Ser Val Gly Met Phe Ile Ser Thr Lys
1      5      10      15
Asp Gly Leu Tyr Lys Val Val Ser Val Ser Lys Val Ser Gly Asn Lys
20      25      30
Gly Asp Thr Phe Ile Lys Val Ser Leu Gln Ala Ala Gly Ser Asp Val
35      40      45
Ile Val Glu Arg Asn Phe Lys Ala Gly Gln Glu Val Lys Glu Ala Gln
50      55      60
Phe Glu Pro Arg Asn Leu Glu Tyr Leu Tyr Leu Glu Glu Asp Lys Tyr
65      70      75      80
Leu Phe Leu Asp Leu Gly Asn Tyr Asp Lys Ile Tyr Ile Pro Lys Glu
85      90      95
Ile Met Lys Asp Asn Ala Met Phe Leu Lys Ala Gly Val Thr Val Phe
100     105     110

```

Ala Leu Val His Glu Gly Thr Val Phe Ser Met Glu Leu Pro His Phe  
 115 120 125  
 Leu Glu Leu Met Val Ala Lys Thr Asp Phe Pro Gly Asp Ser Leu Ser  
 130 135 140  
 Leu Ser Gly Gly Ala Lys Lys Ala Leu Leu Glu Thr Gly Val Glu Val  
 145 150 155 160  
 Leu Val Pro Pro Phe Val Glu Ile Gly Asp Val Ile Lys Val Asp Thr  
 165 170 175  
 Arg Thr Cys Glu Tyr Ile Gln Arg Val  
 180 185

(2) INFORMATIONS POUR LA SEQ ID NO: 333:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 228 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(331721..332404)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 333:

Met Lys Lys Gln Gly Val Leu Val Ala Pro Ser Ile Met Gly Ala Asp  
 1 5 10 15  
 Leu Ala Cys Ile Gly Arg Glu Ala Arg Asn Ile Glu Glu Ser Gly Ala  
 20 25 30  
 Asp Leu Ile His Ile Asp Val Met Asp Gly His Phe Val Pro Asn Ile  
 35 40 45  
 Thr Phe Gly Pro Gly Val Val Ala Ala Ile Asn Arg Ser Thr Glu Leu  
 50 55 60  
 Phe Leu Glu Val His Ala Met Ile Tyr Thr Pro Phe Glu Phe Val Glu  
 65 70 75 80  
 Ala Phe Val Lys Ala Gly Ala Asp Arg Ile Ile Val His Phe Glu Ala  
 85 90 95  
 Ala Glu Asn Ile Lys Glu Ile Ile Ser Tyr Ile Gln Lys Cys Gly Val  
 100 105 110  
 Gln Ala Gly Val Ala Phe Ser Pro Glu Thr Ser Ile Glu Phe Val Thr  
 115 120 125  
 Ser Phe Ile Pro Leu Cys Asp Val Ile Leu Leu Met Ser Val His Pro  
 130 135 140  
 Gly Phe Cys Gly Gln Lys Phe Ile Pro Asp Thr Ile Glu Arg Ile Gln  
 145 150 155 160  
 Phe Val Lys Gln Ala Ile Gln Val Leu Gly Arg Glu Gly Ser Cys Leu  
 165 170 175  
 Ile Glu Val Asp Gly Gly Ile Asp Lys Glu Ser Ala Arg Ala Cys Arg  
 180 185 190  
 Glu Ala Gly Ala Asp Ile Leu Val Ala Ala Ser Tyr Phe Phe Glu Lys  
 195 200 205  
 Asp Ser Ile Asn Met Lys Glu Lys Val Leu Leu Leu Gln Gly Glu Glu  
 210 215 220  
 His Gly Ala Lys  
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 334:

- (i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 81 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 332779..333021

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 334:

Ser	Pro	Arg	Ile	Trp	Phe	Gln	Arg	Thr	Leu	Asn	Glu	Lys	Val	Pro	Met
1				5					10					15	
Thr	Thr	Pro	Thr	Leu	Ile	Val	Thr	Pro	Pro	Ser	Pro	Pro	Ala	Pro	Ser
			20				25						30		
Tyr	Ser	Ala	Asn	Arg	Val	Pro	Gln	Pro	Ser	Leu	Met	Asp	Lys	Ile	Lys
		35				40					45				
Lys	Ile	Ala	Ala	Ile	Ala	Ser	Leu	Ile	Leu	Ile	Gly	Thr	Ile	Gly	Phe
	50				55					60					
Leu	Ala	Leu	Leu	Gly	His	Leu	Val	Gly	Phe	Leu	Ile	Ala	Pro	Gln	Ile
65				70					75					80	
His															

(2) INFORMATIONS POUR LA SEQ ID NO: 335:

- (i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 195 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 333005..333589

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 335:

Ser	Leu	His	Lys	Phe	Thr	Asn	Val	Leu	Leu	Ala	Leu	Phe	Ile	Thr	Ser
1			5					10						15	
Leu	Ala	Gly	Asn	Ala	Leu	Tyr	Leu	Gln	Lys	Thr	Ala	Asn	Leu	His	Leu
		20					25					30			
Tyr	Gln	Asp	Leu	Gln	Arg	Glu	Val	Gly	Ser	Leu	Lys	Glu	Ile	Asn	Phe
		35				40					45				
Met	Leu	Ser	Val	Leu	Gln	Lys	Glu	Phe	Leu	His	Leu	Ser	Lys	Glu	Phe
	50				55					60					
Ala	Thr	Thr	Ser	Lys	Asp	Leu	Ser	Ala	Val	Ser	Gln	Asp	Phe	Tyr	Ser
65				70				75						80	
Cys	Leu	Gln	Xaa	Xaa	Arg	Asp	Asn	Tyr	Lys	Gly	Phe	Glu	Ser	Leu	Leu
			85					90					95		
Asp	Glu	Tyr	Lys	Asn	Ser	Thr	Glu	Glu	Met	Arg	Lys	Leu	Phe	Ser	Gln
		100					105					110			
Glu	Ile	Ile	Ala	Asp	Leu	Lys	Gly	Ser	Val	Ala	Ser	Leu	Arg	Glu	Glu
		115				120					125				
Ile	Arg	Phe	Leu	Thr	Pro	Leu	Ala	Glu	Glu	Val	Arg	Arg	Leu	Ala	His
130						135					140				

Asn Gln Glu Ser Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg  
 145 150 155 160  
 Asp Ser Leu Arg Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr  
 165 170 175  
 Leu Thr Ser Ala Lys Leu His Tyr Asn Glu Lys Arg Ala Gln Ile Cys  
 180 185 190  
 Val Pro Arg  
 195

(2) INFORMATIONS POUR LA SEQ ID NO: 336:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 184 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(333806..334357)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 336:

Gln Glu Thr Lys Phe Asp Lys Gly Ile Gly Gly Tyr Met Ile Cys Cys  
 1 5 10 15  
 Asp Lys Val Leu Ser Ser Val Gln Ser Met Pro Val Ile Asp Lys Cys  
 20 25 30  
 Ser Val Thr Lys Cys Leu Gln Thr Ala Lys Gln Ala Val Val Leu Ala  
 35 40 45  
 Leu Ser Leu Phe Ala Val Phe Ala Ser Gly Ser Leu Ser Ile Leu Ser  
 50 55 60  
 Ala Ala Val Leu Phe Ser Gly Thr Ala Ala Val Leu Pro Tyr Leu Leu  
 65 70 75 80  
 Ile Leu Thr Thr Ala Leu Leu Gly Cys Val Tyr Ala Val Ile Val Leu  
 85 90 95  
 Leu Arg Ser Leu Ser Ala Val Val Gln Ser Cys Lys Lys Arg Ser Pro  
 100 105 110  
 Glu Glu Ile Glu Gly Ala Ala Arg Pro Ser Asp Gln Gln Glu Ser Gly  
 115 120 125  
 Gly Arg Leu Ser Xaa Glu Ser Ala Ser Pro Gln Ala Ser Pro Thr Ser  
 130 135 140  
 Ser Thr Leu Arg Leu Glu Ser Ala Phe Arg Ser Ile Gly Asp Ser Val  
 145 150 155 160  
 Ser Gly Ala Phe Asp Asp Ile Asn Lys Asp Asn Ser Arg Ser Arg Phe  
 165 170 175  
 Thr Leu Leu Leu Arg Asp Asp Met  
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 337:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 91 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: 334089..334361

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 337:

Thr	His	Pro	Arg	Arg	Ala	Val	Val	Asn	Ile	Ser	Arg	Tyr	Gly	Arg	Thr
1				5					10					15	
Ala	Ala	Val	Pro	Leu	Asn	Ser	Thr	Ala	Ala	Asp	Asn	Met	Asp	Lys	Leu
			20					25					30		
Pro	Glu	Ala	Asn	Thr	Ala	Asn	Lys	Asp	Asn	Ala	Arg	Thr	Thr	Ala	Cys
		35					40					45			
Leu	Ala	Val	Cys	Lys	His	Phe	Val	Thr	Glu	His	Leu	Ser	Ile	Thr	Gly
	50					55					60				
Ile	Asp	Cys	Thr	Leu	Asp	Lys	Thr	Leu	Ser	Gln	Gln	Ile	Met	Tyr	Pro
65					70				75						80
Pro	Ile	Pro	Leu	Ser	Asn	Phe	Val	Ser	Cys	His					
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 338:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(334729..335142)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 338:

Glu	Phe	Leu	Gly	Gly	Ser	Met	Glu	Cys	Val	Lys	Gln	Leu	Cys	Arg	Asn
1				5					10					15	
His	Leu	Arg	Leu	Asp	Asn	Leu	Thr	Asp	Pro	Val	Arg	Ser	Val	Leu	Thr
			20					25					30		
Lys	Gly	Thr	Thr	Ala	Glu	Lys	Val	Gln	Leu	Ala	Ala	Cys	Cys	Leu	Gly
		35					40					45			
Val	Val	Cys	Ser	Ile	Ile	Cys	Leu	Ala	Leu	Gly	Ile	Ala	Ala	Ala	Ala
	50					55					60				
Val	Gly	Val	Ser	Cys	Gly	Gly	Phe	Ala	Leu	Gly	Leu	Gly	Ile	Ile	Ala
65					70				75						80
Ile	Leu	Leu	Gly	Ile	Val	Leu	Phe	Ala	Thr	Ser	Ala	Leu	Asp	Val	Leu
			85						90					95	
Glu	Asn	His	Gly	Leu	Val	Gly	Cys	Pro	Phe	Lys	Leu	Pro	Cys	Lys	Ser
			100					105					110		
Ser	Pro	Ala	Asn	Glu	Pro	Ala	Val	Gln	Phe	Phe	Lys	Gly	Lys	Asn	Gly
		115				120						125			
Ser	Ala	Asp	Gln	Val	Ile	Leu	Val	Thr	Gln						
			130				135								

(2) INFORMATIONS POUR LA SEQ ID NO: 339:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 335195..335602

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 339:

```

Leu Ala Pro Phe Leu Leu Thr Glu Phe Ser Ser Leu Ser Leu Leu Leu
1          5          10          15
Ala Phe Ala Leu Ala Leu Glu Ile Phe Cys Ser Thr Ser Ala Val Leu
20          25          30
Gln His Lys Leu Phe His Ile Lys Val Cys Asp Arg Cys Asn Arg Ser
35          40          45
Leu Val Thr Ala Ser Val Val Ser Thr Pro Pro Thr Lys Ala Pro Pro
50          55          60
Lys Arg Lys Ala Pro Thr Pro Lys Asn Lys Asp Ala Ala Thr Thr Glu
65          70          75          80
Thr Gly Leu Gln Ser Thr Pro Glu Asn Asn Lys Pro Ala Thr Thr Arg
85          90          95
Arg Ala Met Ala Asn Ile Val Ala Thr Ala Thr Ala Ala Asn Leu Phe
100          105          110
Ala Val Gly Asn Glu Leu Leu Arg Ser Lys His Leu Ser Lys Arg Ala
115          120          125
Ile Leu Ser Thr Thr Leu Ser Cys
130          135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 340:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(335194..335673)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 340:

```

Val Arg Asn Glu Ile Trp Leu Lys Ser Val Glu Val Arg Phe Met Thr
1          5          10          15
Lys Val Tyr Ala His Ser Ile Gln Gln Glu Arg Val Val Asp Arg Ile
20          25          30
Ala Leu Leu Glu Arg Cys Leu Asp Leu Ser Asn Ser Leu Pro Thr Ala
35          40          45
Lys Arg Leu Ala Ala Val Ala Val Ala Thr Ile Leu Ala Ile Ala Leu
50          55          60
Leu Val Val Ala Gly Leu Leu Phe Ser Gly Val Leu Cys Ser Pro Val
65          70          75          80
Ser Val Val Ala Ala Ser Leu Phe Phe Gly Val Gly Ala Phe Leu Leu
85          90          95
Gly Gly Ala Leu Val Gly Gly Val Leu Thr Thr Glu Ala Val Thr Arg
100          105          110
Glu Arg Leu His Arg Ser Gln Thr Leu Met Trp Asn Asn Leu Cys Cys
115          120          125
Lys Thr Ala Glu Val Glu Gln Lys Ile Ser Arg Ala Ser Ala Asn Ala

```

	130		135		140										
Lys	Ser	Asn	Asp	Lys	Leu	Glu	Asn	Ser	Val	Ser	Lys	Lys	Gly	Ala	Ser
145					150					155					160

(2) INFORMATIONS POUR LA SEQ ID NO: 341:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(335903..336334)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 341:

Lys	Ala	Ala	Gly	Glu	Ala	Leu	Leu	Lys	Lys	Ser	Ala	Glu	Lys	Thr	Arg
1			5					10					15		
Arg	Gly	Ser	Ser	Ile	Tyr	Asp	Tyr	Phe	Gln	Gly	Tyr	Ile	Ser	Pro	Glu
		20					25					30			
Ile	Leu	Gly	Val	Leu	Phe	Ala	Asp	Ser	Gly	Val	Thr	Tyr	Gln	Glu	Thr
	35					40					45				
Leu	Glu	Tyr	Arg	Lys	Lys	Leu	Val	Met	Leu	Ser	Lys	Lys	Tyr	Pro	Lys
	50					55				60					
Ser	Gly	Ser	Leu	Arg	Leu	Arg	Leu	Ala	Thr	Thr	Ala	Leu	Glu	Leu	Gly
65				70				75					80		
Leu	Val	Lys	Glu	Gly	Val	Gln	Leu	Leu	Glu	Glu	Ser	Val	Lys	Asp	Ala
		85					90					95			
Pro	Glu	Asp	Leu	Ser	Leu	Arg	Leu	Gln	Phe	Cys	Lys	Ile	Leu	Cys	Asn
		100					105					110			
Arg	His	Asp	Tyr	Val	Arg	Ala	Lys	Tyr	His	Phe	Asp	Gln	Ala	Gln	Val
	115					120					125				
Phe	Ser	Leu	Lys	Arg	Gly	Cys	Phe	Pro	Lys	Lys	Leu	Pro	Ile	Leu	Ser
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 342:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 347 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(336338..337378)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 342:

Leu	Cys	Leu	Lys	Leu	Lys	Gln	Ile	Gln	Leu	Cys	Arg	Thr	Phe	Val	Cys
1			5					10					15		
Leu	Arg	His	Trp	Met	Cys	Phe	Ile	Gly	Ile	Gly	Ser	Leu	Leu	Leu	Pro
		20					25					30			
Thr	Ala	Leu	Arg	Ala	Thr	Glu	Arg	Met	Arg	Lys	Glu	Pro	Ile	Pro	Leu
	35					40					45				

```

Leu Asp Lys Gln Gln Ser Phe Trp Asn Val Asp Pro Tyr Cys Leu Glu
 50      55      60
Ser Ile Cys Ala Cys Phe Val Ala His Arg Asp Pro Leu Ser Ala Lys
65      70      75      80
Arg Leu Met Tyr Leu Phe Pro Gln Leu Ser Glu Glu Asp Val Ser Val
      85      90      95
Phe Ala Arg Cys Ile Leu Ser Ser Lys Arg Pro Glu Tyr Leu Phe Ser
      100      105      110
Lys Ser Glu Glu Glu Leu Phe Ala Lys Leu Ile Leu Pro Arg Val Ser
      115      120      125
Leu Gly Val His Arg Asp Asp Asp Leu Ala Arg Val Leu Val Leu Ala
130      135      140
Glu Pro Ser Ala Glu Glu Gln Lys Ala Arg Tyr Tyr Ser Leu Tyr Leu
145      150      155      160
Asp Val Leu Ala Leu Arg Ala Tyr Val Glu Arg Glu Arg Leu Ala Ser
      165      170      175
Ala Ala His Gly Asp Pro Glu Arg Ile Asp Leu Ala Thr Ile Glu Ala
      180      185      190
Ile Asn Thr Ile Leu Phe Gln Glu Glu Arg Trp Arg Tyr Pro Ser Lys
      195      200      205
Gln Glu Met Phe Glu Ser Arg Phe Ser Glu Leu Ala Ala Val Thr Asp
210      215      220
Ser Lys Phe Gly Val Cys Leu Gly Thr Val Val Leu Tyr Gln Ala Val
225      230      235      240
Ala Gln Arg Leu Asp Leu Ser Leu Asp Pro Val Thr Pro Pro Gly His
      245      250      255
Ile Tyr Leu Arg Tyr Lys Asp Lys Val Asn Ile Glu Thr Thr Ser Gly
      260      265      270
Gly Arg His Leu Pro Thr Glu Arg Tyr Cys Glu Cys Ile Lys Glu Ser
      275      280      285
Gln Leu Lys Val Arg Ser Gln Met Glu Leu Ile Gly Leu Thr Phe Met
290      295      300
Asn Arg Gly Ala Phe Phe Leu Gln Lys Gly Glu Phe Leu Gln Ala Ser
305      310      315      320
Leu Ala Tyr Glu Gln Ala Gln Ser Tyr Leu Ser Asp Glu Gln Ile Ser
      325      330      335
Asp Leu Leu Gly Ile Thr Tyr Val Leu Leu Gly
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 343:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 867 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(337347..339947)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 343:

```

Met Glu Lys Phe Ser Asp Ala Val Ser Glu Ala Leu Glu Lys Ala Phe
 1      5      10      15
Glu Leu Ala Lys Asn Ser Lys His Ser Tyr Val Thr Glu Asn His Leu
      20      25      30
Leu Lys Ser Leu Leu Gln Asn Pro Gly Ser Leu Phe Cys Leu Val Ile

```

		35					40					45				
Lys	Asp	Val	His	Gly	Asn	Leu	Gly	Leu	Leu	Thr	Ser	Ala	Val	Asp	Asp	
	50					55					60					
Ala	Leu	Arg	Arg	Glu	Pro	Thr	Val	Val	Glu	Gly	Thr	Ala	Val	Ala	Ser	
65					70					75					80	
Pro	Ser	Pro	Ser	Leu	His	Gln	Leu	Leu	Leu	Asn	Ala	His	Gln	Glu	Ala	
				85					90					95		
Arg	Ser	Met	Gly	Asp	Glu	Tyr	Leu	Ser	Gly	Asp	His	Leu	Leu	Leu	Ala	
			100					105					110			
Phe	Trp	Arg	Ser	Thr	Lys	Glu	Pro	Phe	Ala	Ser	Trp	Arg	Lys	Thr	Val	
		115					120					125				
Lys	Thr	Thr	Ser	Glu	Ala	Leu	Lys	Glu	Leu	Ile	Thr	Lys	Leu	Arg	Gln	
	130					135					140					
Gly	Ser	Arg	Met	Asp	Ser	Pro	Ser	Ala	Glu	Glu	Asn	Leu	Lys	Gly	Leu	
145					150					155					160	
Glu	Lys	Tyr	Cys	Lys	Asn	Leu	Thr	Val	Leu	Ala	Arg	Glu	Gly	Lys	Leu	
			165						170					175		
Asp	Pro	Val	Ile	Gly	Arg	Asp	Glu	Glu	Ile	Arg	Arg	Thr	Ile	Gln	Val	
			180					185					190			
Leu	Ser	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Met	Leu	Ile	Gly	Glu	Pro	Gly	
		195					200					205				
Val	Gly	Lys	Thr	Ala	Ile	Ala	Glu	Gly	Leu	Ala	Leu	Arg	Ile	Val	Gln	
	210					215					220					
Gly	Asp	Val	Pro	Glu	Ser	Leu	Lys	Glu	Lys	His	Leu	Tyr	Val	Leu	Asp	
225					230					235					240	
Met	Gly	Ala	Leu	Ile	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe	Glu	Glu	
			245						250					255		
Arg	Leu	Lys	Ser	Val	Leu	Lys	Ser	Val	Glu	Ala	Ser	Glu	Gly	Glu	Cys	
			260					265					270			
Ile	Leu	Phe	Ile	Asp	Glu	Val	His	Thr	Leu	Val	Gly	Ala	Gly	Ala	Thr	
		275					280					285				
Asp	Gly	Ala	Met	Asp	Ala	Ala	Asn	Leu	Leu	Lys	Pro	Ala	Leu	Ala	Arg	
	290					295					300					
Gly	Thr	Leu	His	Cys	Ile	Gly	Ala	Thr	Thr	Leu	Asn	Glu	Tyr	Gln	Lys	
305					310					315					320	
Tyr	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln	Pro	Ile	Phe	
			325						330					335		
Val	Thr	Glu	Pro	Ser	Leu	Glu	Asp	Ala	Val	Phe	Ile	Leu	Arg	Gly	Leu	
			340					345					350			
Arg	Glu	Lys	Tyr	Glu	Ile	Phe	His	Gly	Val	Arg	Ile	Thr	Glu	Gly	Ala	
		355					360					365				
Leu	Asn	Ala	Ala	Val	Val	Leu	Ser	Tyr	Arg	Tyr	Ile	Thr	Asp	Arg	Phe	</

His	Leu	Ala	Glu	Glu	Ala	Leu	Asn	Gln	Arg	Asp	Gly	Arg	Leu	Leu	Gln
		515					520					525			
Glu	Glu	Val	Asp	Glu	Arg	Leu	Ile	Ala	Gln	Val	Val	Ala	Asn	Trp	Thr
		530				535					540				
Gly	Ile	Pro	Val	Gln	Lys	Met	Leu	Glu	Gly	Glu	Ser	Glu	Lys	Leu	Leu
545					550					555					560
Val	Leu	Glu	Glu	Ser	Leu	Glu	Glu	Arg	Val	Val	Gly	Gln	Pro	Phe	Ala
				565					570					575	
Ile	Ala	Ala	Val	Ser	Asp	Ser	Ile	Arg	Ala	Ala	Arg	Val	Gly	Leu	Ser
			580					585					590		
Asp	Pro	Gln	Arg	Pro	Leu	Gly	Val	Phe	Leu	Phe	Leu	Gly	Pro	Thr	Gly
		595					600					605			
Val	Gly	Lys	Thr	Glu	Leu	Ala	Lys	Ala	Leu	Ala	Glu	Leu	Leu	Phe	Asn
	610					615					620				
Lys	Glu	Glu	Ala	Met	Ile	Arg	Phe	Asp	Met	Thr	Glu	Tyr	Met	Glu	Lys
625					630					635					640
His	Ser	Val	Ser	Lys	Leu	Ile	Gly	Ser	Pro	Pro	Gly	Tyr	Val	Gly	Tyr
				645					650					655	
Glu	Glu	Gly	Gly	Ser	Leu	Ser	Glu	Ala	Leu	Arg	Arg	Arg	Pro	Tyr	Ser
			660					665					670		
Val	Val	Leu	Phe	Asp	Glu	Ile	Glu	Lys	Ala	Asp	Lys	Glu	Val	Phe	Asn
		675					680					685			
Ile	Leu	Leu	Gln	Ile	Phe	Asp	Gly	Ile	Leu	Thr	Asp	Ser	Lys	Lys	
	690					695				700					
Arg	Lys	Val	Asn	Cys	Lys	Asn	Ala	Leu	Phe	Ile	Met	Thr	Ser	Asn	Ile
705					710					715					720
Gly	Ser	Gln	Glu	Leu	Ala	Asp	Tyr	Cys	Thr	Lys	Lys	Gly	Thr	Ile	Val
				725					730					735	
Asp	Lys	Glu	Ala	Val	Leu	Ser	Val	Val	Ala	Pro	Ala	Leu	Lys	Asn	Tyr
			740					745					750		
Phe	Ser	Pro	Glu	Phe	Ile	Asn	Arg	Ile	Asp	Asp	Ile	Leu	Pro	Phe	Val
		755					760					765			
Pro	Leu	Thr	Thr	Glu	Asp	Ile	Val	Lys	Ile	Val	Gly	Ile	Gln	Met	Asn
	770					775					780				
Arg	Val	Ala	Leu	Arg	Leu	Leu	Glu	Arg	Lys	Ile	Ser	Leu	Thr	Trp	Asp
785					790					795					800
Asp	Ser	Leu	Val	Leu	Phe	Leu	Ser	Glu	Gln	Gly	Tyr	Asp	Ser	Ala	Phe
				805					810					815	
Gly	Ala	Arg	Pro	Leu	Lys	Arg	Leu	Ile	Gln	Gln	Lys	Val	Val	Thr	Met
			820					825					830		
Leu	Ser	Lys	Ala	Leu	Leu	Lys	Gly	Asp	Ile	Lys	Pro	Gly	Met	Ala	Val
		835					840					845			
Glu	Leu	Thr	Met	Ala	Lys	Asp	Val	Val	Val	Phe	Lys	Ile	Lys	Thr	Asn
	850					855					860				
Pro	Ala	Val													
865															

## (2) INFORMATIONS POUR LA SEQ ID NO: 344:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 447 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 340507..341847

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 344:

Ala	His	Leu	Thr	His	Asp	Glu	Asp	Ile	Ala	Asn	Gln	Glu	Thr	Ala	Ala	1	5	10	15
Asp	Leu	Lys	Ser	Ile	Thr	Phe	Leu	Leu	Thr	Ser	Phe	Val	Glu	Glu	Ile	20	25	30	
Ser	Trp	Ile	Gln	Pro	Ala	Leu	Ile	Ala	Leu	Pro	Gln	Gln	Val	Ala	Asn	35	40	45	
Met	Leu	Leu	Ala	Ser	Pro	Glu	Leu	Gln	Glu	Tyr	His	Phe	Tyr	Leu	Lys	50	55	60	
Lys	Leu	Phe	Arg	Leu	Ala	Pro	His	Thr	Gly	Thr	Ser	Arg	Glu	Glu	Lys	65	70	75	80
Ile	Leu	Ala	Ser	Ser	Phe	Pro	Ala	Leu	Glu	Val	Ala	Tyr	Lys	Thr	Phe	85	90	95	
Cys	Ser	Leu	Thr	Asp	Ser	Glu	Ile	Pro	Phe	Gly	Glu	Ala	Val	Asp	Ser	100	105	110	
Glu	Gly	Lys	Ser	His	Pro	Leu	Ser	His	Ala	Leu	Ala	Ser	Leu	Tyr	Met	115	120	125	
Gln	Ser	Thr	Asp	Arg	Glu	Leu	Arg	Lys	Asn	Thr	Tyr	Gln	Lys	Gln	Cys	130	135	140	
Gln	Arg	His	His	Gly	Tyr	Arg	Leu	Ser	Leu	Ala	Asn	Leu	Leu	Asn	Gly	145	150	155	160
Lys	Ile	Gln	Ala	His	Leu	Phe	Asn	Ala	Lys	Ala	Arg	Asp	Tyr	Asp	Ser	165	170	175	
Cys	Leu	Glu	Ala	Ala	Leu	Phe	Gln	Asn	Asp	Ile	Ser	Thr	Ser	Val	Val	180	185	190	
Thr	Thr	Leu	Ile	Asp	Thr	Val	Lys	Gln	His	Thr	His	Leu	Ile	Thr	Lys	195	200	205	
Tyr	Phe	Gln	Leu	Lys	Gln	Lys	Ala	Leu	Gly	Leu	Ser	Asp	Phe	His	Phe	210	215	220	
Tyr	Asp	Val	Tyr	Ala	Pro	Leu	Val	Ala	Ser	Glu	Ala	Ser	Arg	His	Tyr	225	230	235	240
Ser	Tyr	Gln	Glu	Ala	Val	Thr	Leu	Ile	Cys	Asp	Ser	Leu	Ser	Pro	Leu	245	250	255	
Gly	Asn	Asp	Tyr	Val	Glu	Thr	Leu	Arg	Lys	Gly	Leu	Thr	Ser	Asp	Gly	260	265	270	
Trp	Val	Asp	Lys	Tyr	Glu	Asn	Thr	Asn	Lys	Arg	Ser	Gly	Ala	Tyr	Ser	275	280	285	
Ser	Gly	Cys	Tyr	Asn	Ser	Lys	Pro	Tyr	Ile	Leu	Leu	Asn	Tyr	Thr	Gly	290	295	300	
Thr	Leu	Tyr	Asp	Val	Ser	Val	Val	Ala	His	Glu	Gly	Gly	His	Ser	Met	305	310	315	320
His	Ser	Phe	Leu	Ser	His	Lys	His	Gln	Ser	Tyr	His	Glu	Ala	Gln	Tyr	325	330	335	
Pro	Ile	Phe	Leu	Ala	Glu	Ile	Ala	Ser	Thr	Leu	Asn	Glu	Thr	Leu	Leu	340	345	350	
Met	Glu	Phe	Leu	Leu	Lys	Gln	Ala	Pro	Ser	Lys	Glu	Glu	Lys	Ile	Ala	355	360	365	
Ile	Leu	Ser	Arg	Ser	Leu	Asp	Thr	Val	Phe	Ala	Thr	Leu	Phe	Arg	Gln	370	375	380	
Thr	Leu	Phe	Ala	Ala	Phe	Glu	Leu	Glu	Met	His	Ser	Ala	Ala	Glu	Gln	385	390	395	400
Gly	Leu	Pro	Leu	Thr	Glu	Glu	Phe	Phe	Ser	Gln	Ser	Tyr	Glu	Lys	Leu	405	410	415	
Gln	Arg	Leu	Phe	Tyr	Gly	Asp	Cys	Ile	Thr	Phe	Asp	Glu	His	Ser	Cys	420	425	430	
Ile	Glu	Ser	Ala	Arg	Ile	Pro	His	Phe	Tyr	Tyr	Asn	Phe	Tyr	Val		435	440	445	

(2) INFORMATIONS POUR LA SEQ ID NO: 345:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 80 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 341783..342022

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 345:

Leu	Leu	Met	Asn	Ile	Ala	Val	Ser	Asn	Arg	Leu	Ala	Phe	Leu	Ile	Ser
1				5					10					15	
Thr	Thr	Thr	Ser	Met	Phe	Asn	Gln	Tyr	Ala	Thr	Gly	Ile	Ile	Ala	Ser
			20					25					30		
Leu	Cys	Phe	Ser	Glu	Arg	Ile	Leu	Ser	Gly	Glu	Glu	Gly	Ala	Gln	Glu
		35					40					45			
Ala	Tyr	Leu	Thr	Phe	Leu	Arg	Ser	Gly	Gly	Ser	Asp	Phe	Pro	Ile	Glu
	50					55					60				
Ile	Leu	Lys	Lys	Ser	Gly	Leu	Asp	Met	Thr	Ser	Ile	Ser	Ser	Tyr	Ala
65					70				75						80

(2) INFORMATIONS POUR LA SEQ ID NO: 346:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 74 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 342249..342470

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 346:

Met	Ser	Asp	Gln	Ala	Thr	Thr	Leu	Lys	Ile	Lys	Pro	Leu	Gly	Asp	Arg
1				5		-			10					15	
Ile	Leu	Val	Lys	Arg	Glu	Glu	Glu	Ala	Ser	Thr	Ala	Arg	Gly	Gly	Ile
			20					25					30		
Ile	Leu	Pro	Asp	Thr	Ala	Lys	Lys	Lys	Gln	Asp	Arg	Ala	Glu	Val	Val
			35				40					45			
Ala	Leu	Gly	Thr	Gly	Lys	Lys	Asp	Asp	Lys	Gly	Gln	Gln	Leu	Pro	Phe
	50					55					60				
Glu	Val	Gln	Val	Gly	Asp	Ile	Val	Leu	Ile						
65					70										

(2) INFORMATIONS POUR LA SEQ ID NO: 347:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 258 acides aminés

(B) TYPE: acide aminé



(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 342597..343370

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 347:

Met	Val	Ala	Lys	Asn	Ile	Lys	Tyr	Asn	Glu	Glu	Ala	Arg	Lys	Lys	Ile
1				5					10					15	
Gln	Lys	Gly	Val	Lys	Thr	Leu	Ala	Glu	Ala	Val	Lys	Val	Thr	Leu	Gly
			20					25					30		
Pro	Lys	Gly	Arg	His	Val	Val	Ile	Asp	Lys	Ser	Phe	Gly	Ser	Pro	Gln
		35					40					45			
Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Glu	Val	Glu	Leu	Ala	Asp
	50					55					60				
Lys	His	Glu	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys
65					70					75					80
Thr	Ala	Asp	Lys	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala
				85				90						95	
Glu	Ala	Ile	Tyr	Thr	Glu	Gly	Leu	Arg	Asn	Val	Thr	Ala	Gly	Ala	Asn
			100					105					110		
Pro	Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Lys	Val	Val	Val
		115					120					125			
Asp	Gln	Val	Lys	Lys	Ile	Ser	Lys	Pro	Val	Gln	His	His	Lys	Glu	Ile
	130					135					140				
Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Asn	Asp	Ala	Glu	Ile	Gly	Asn
145					150					155					160
Leu	Ile	Ala	Lys	Ala	Met	Glu	Lys	Val	Gly	Lys	Asn	Gly	Ser	Ile	Thr
				165					170					175	
Val	Glu	Glu	Ala	Lys	Gly	Phe	Glu	Thr	Val	Leu	Asp	Val	Val	Glu	Gly
			180					185					190		
Met	Asn	Phe	Asn	Arg	Gly	Tyr	Leu	Ser	Ser	Tyr	Phe	Ala	Thr	Asn	Pro
		195					200					205			
Glu	Thr	Gln	Glu	Cys	Val	Leu	Glu	Asp	Ala	Leu	Val	Leu	Ile	Tyr	Asp
	210					215					220				
Lys	Lys	Ile	Ser	Gly	Ile	Lys	Asp	Phe	Leu	Pro	Val	Leu	Gln	Gln	Val
225				230						235					240
Ala	Glu	Ser	Gly	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Ile	Glu	Gly
				245					250					255	

Glu Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 348:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 224 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 343361..344032

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 348:

```

Arg Arg Thr Leu Ala Thr Leu Val Val Asn Arg Ile Arg Gly Gly Phe
1      5      10
Arg Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala
20      25      30
Met Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Gln Leu Ile Ser Glu
35      40      45
Glu Leu Gly Met Lys Leu Glu Asn Ala Asn Leu Ala Met Leu Gly Lys
50      55      60
Ala Lys Lys Val Ile Val Ser Lys Glu Asp Thr Thr Ile Val Glu Gly
65      70      75      80
Met Gly Glu Lys Glu Ala Leu Glu Ala Arg Cys Glu Ser Ile Lys Lys
85      90      95
Gln Ile Glu Asp Ser Ser Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu
100     105     110
Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Arg Val Gly Ala
115     120     125
Ala Thr Glu Ile Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala
130     135     140
Gln His Ala Thr Ile Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly
145     150     155     160
Gly Thr Ala Leu Ile Arg Cys Ile Pro Thr Leu Glu Ala Phe Leu Pro
165     170     175
Met Leu Thr Asn Glu Asp Glu Gln Ile Gly Ala Arg Ile Val Leu Lys
180     185     190
Ala Leu Ser Ala Pro Leu Lys Gln Ile Ala Ala Asn Ala Gly Lys Glu
195     200     205
Gly Ala Ile Ile Phe Gln Gln Val Met Ser Phe Cys Glu Arg Arg Ile
210     215     220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 349:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 90 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 343956..344225

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 349:

```

Asn Lys Leu Leu Gln Thr Gln Glu Lys Lys Val Leu Ser Ser Ser Asn
1      5      10      15
Lys Leu Cys Pro Ser Ala Asn Glu Gly Tyr Asp Ala Leu Arg Asp Ala
20      25      30
Tyr Thr Asp Met Leu Glu Ala Gly Ile Leu Asp Pro Ala Lys Val Thr
35      40      45
Arg Ser Ala Leu Glu Ser Ala Ala Ser Val Ala Gly Leu Leu Leu Thr
50      55      60
Thr Glu Ala Leu Ile Ala Glu Ile Pro Glu Glu Lys Pro Ala Ala Ala
65      70      75      80
Pro Ala Met Pro Gly Ala Gly Met Asp Tyr
85      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 350:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 344357..345142

[illegible]

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui .

(viii) POSITION DANS LE GENOME: complement(345161..345913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 351:

Met	Asn	Val	Ser	Asp	Leu	Leu	Asn	Ile	Leu	Asn	Glu	Leu	Leu	His	Pro
1				5					10					15	
Glu	Tyr	Phe	Ser	Asp	Tyr	Gly	Pro	Asn	Gly	Leu	Gln	Val	Gly	Asn	Thr
			20					25					30		
Gln	Thr	Ala	Ile	Arg	Lys	Val	Ala	Val	Ala	Val	Thr	Ala	Asp	Leu	Ala
		35					40					45			
Thr	Ile	Glu	Lys	Ala	Ile	Ala	Cys	Glu	Ala	Asn	Val	Leu	Leu	Val	His
	50					55					60				
His	Gly	Ile	Phe	Trp	Lys	Gly	Met	Pro	Tyr	Pro	Ile	Thr	Gly	Ile	Leu
65				70						75					80
Tyr	Gln	Arg	Met	Gln	Arg	Leu	Met	Glu	Gly	Asn	Ile	Gln	Leu	Ile	Ala
			85						90					95	
Tyr	His	Leu	Pro	Leu	Asp	Ala	His	Thr	Thr	Ile	Gly	Asn	Asn	Trp	Lys
			100					105					110		
Val	Ala	Arg	Asp	Leu	Gly	Trp	Glu	Gln	Leu	Glu	Ser	Phe	Gly	Ser	Ser
		115					120					125			
Gln	Pro	Ser	Leu	Gly	Val	Lys	Gly	Val	Phe	Pro	Glu	Met	Glu	Val	His
	130					135					140				
Asp	Phe	Ile	Ser	Gln	Leu	Ser	Ala	Tyr	Tyr	Gln	Thr	Pro	Val	Leu	Ala
145				150						155					160
Lys	Ala	Leu	Gly	Gly	Lys	Lys	Arg	Val	Ser	Ser	Ala	Ala	Leu	Ile	Ser
			165						170					175	
Gly	Gly	Ala	Tyr	Arg	Glu	Ile	Ser	Glu	Ala	Lys	Asn	Gln	Gln	Val	Asp
		180						185					190		
Cys	Phe	Ile	Thr	Gly	Asn	Phe	Asp	Glu	Pro	Ala	Trp	Ser	Leu	Ala	His
	195					200						205			
Glu	Leu	Ala	Ile	His	Phe	Leu	Ala	Phe	Gly	His	Thr	Ala	Thr	Glu	Lys
	210					215					220				
Val	Gly	Pro	Lys	Ala	Leu	Ala	Gln	Tyr	Leu	Lys	Gly	Ala	Gly	Leu	Glu
225				230						235					240
Ser	Val	Val	Phe	Leu	Asp	Thr	Asp	Asn	Pro	Phe					
				245					250						

(2) INFORMATIONS POUR LA SEQ ID NO: 352:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 341 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(346080..347102)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 352:

Val	Cys	Trp	Tyr	Asp	Phe	Thr	Arg	Ile	Ser	Met	Ile	Arg	Thr	Ala	Phe
1				5					10					15	
Phe	Gln	Asp	Lys	Glu	Cys	Phe	Pro	Leu	Glu	Ala	Leu	Arg	Ser	Trp	Phe
		20						25					30		
Leu	Glu	Ser	Lys	Arg	Ser	Phe	Pro	Trp	Arg	Asp	Ser	Pro	Thr	Pro	Tyr
		35				40						45			
Arg	Val	Trp	Val	Ser	Glu	Val	Met	Leu	Gln	Gln	Thr	Arg	Ala	Glu	Val

50		55		60	
Val	Val	Pro	Tyr	Phe	Leu
65		70		75	
Asp	Leu	Ala	Gln	Ala	Arg
		85		90	
Leu	Gly	Tyr	Tyr	Ser	Arg
		100		105	
Ile	Thr	Glu	Ile	Phe	Gly
		115		120	
Ser	Ser	Ile	Lys	Gly	Ile
		130		135	
Phe	Ala	Phe	Lys	Gln	Lys
145				150	
Val	Met	Ser	Arg	Leu	Phe
				165	
Thr	Arg	Arg	Glu	Ile	Thr
				180	
Asp	Pro	Gln	Val	Ile	Ala
				195	
Cys	Lys	Lys	Gln	Pro	Leu
				210	
Thr	Ala	Tyr	Arg	Gln	Gly
225				230	
Arg	Ala	Ala	Ile	Ser	Arg
				245	
Lys	Asp	Gln	Val	Leu	Met
				260	
Gly	Leu	Tyr	Glu	Phe	Pro
				275	
Asp	Ile	Glu	Lys	Ile	Ile
				290	
Leu	His	Phe	Val	Ser	Ser
305					
Ile	Ala	Leu	His	Tyr	Ser
				325	
Arg	Ile	Ala	Thr	Arg	
				340	

(2) INFORMATIONS POUR LA SEQ ID NO: 353:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 347113..347940

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 353:

Trp	Ile	Met	Gln	Glu	Phe	Ile	Gly	Thr	Ala	Asp	Arg	His	Ile	Arg	Leu
1				5				10					15		
Ser	Ser	Phe	Leu	Arg	Thr	Ser	Leu	Pro	His	Leu	Pro	Lys	Lys	Thr	Ile
			20					25				30			
Leu	Glu	Ser	Val	Arg	Tyr	His	Gly	Cys	Arg	Val	Asn	Gly	Arg	Ile	Glu
			35				40					45			

Arg	Phe	Glu	Ser	Tyr	Lys	Leu	Gln	Pro	Gly	Asp	Arg	Val	Ser	Leu	Gln
50						55					60				
Ile	Ile	Glu	His	Ser	Ser	Pro	Gln	Leu	Leu	Trp	Glu	Asp	Glu	His	Leu
65					70					75					80
Cys	Ile	Tyr	Asn	Lys	Pro	Ala	Lys	Gln	Thr	Ser	Glu	Asp	Leu	Ala	His
				85					90					95	
Gln	Leu	Asn	Val	His	Leu	Val	His	Arg	Leu	Asp	Arg	Asp	Thr	Ser	Gly
			100					105					110		
Cys	Ile	Leu	Phe	Ala	Lys	His	Ala	Lys	Ala	Ser	Ser	Leu	Ile	Thr	Gln
		115					120					125			
Leu	Phe	Lys	Asn	Arg	Glu	Ile	Asp	Lys	Arg	Tyr	Ile	Ala	Leu	Val	Phe
	130						135				140				
Gly	Gln	Pro	Arg	Gln	Glu	Ser	Gly	Ile	Ile	Thr	Thr	Tyr	Thr	Ala	Pro
145					150					155					160
Cys	Tyr	Arg	Arg	Thr	Gly	Ala	Val	Leu	Phe	Gly	Asn	Thr	Asp	Gln	Asn
				165					170					175	
Ser	Gly	Lys	Ile	Thr	Ile	Thr	Lys	Trp	Glu	Ile	Leu	Thr	Arg	Tyr	Pro
			180					185					190		
Lys	Tyr	Thr	Leu	Leu	Leu	Cys	Arg	Pro	Val	Thr	Gly	Arg	Thr	His	Gln
		195					200					205			
Ile	Arg	Leu	His	Met	Lys	Thr	Ile	Gly	His	Pro	Ile	Val	Gly	Asp	Val
	210					215					220				
Asp	Tyr	Gly	Asn	Gln	Glu	Gln	Pro	Lys	Asn	Val	Val	Arg	Thr	Leu	Leu
225					230					235					240
His	Ala	Ala	Ser	Leu	Ala	Phe	Ile	Ser	Pro	Phe	Ser	Asn	Glu	Lys	Ile
				245					250					255	
Glu	Ile	Ser	Ser	Leu	Thr	Pro	Ser	Gln	Asp	Pro	Tyr	Pro	Phe	Tyr	Ala
			260					265					270		
Asp	Phe	Arg	Pro												
		275													

(2) INFORMATIONS POUR LA SEQ ID NO: 354:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 673 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(348146..350164)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 354:

Asn	Phe	Leu	Leu	Lys	Ile	Lys	Asn	Pro	Tyr	Lys	Asn	Pro	Gly	Val	Lys
1				5					10					15	
Gly	Met	Ser	Phe	Gly	Ile	Gly	Ser	Ala	Cys	Ser	Ser	Leu	Trp	Ser	Arg
			20					25					30		
Leu	Cys	Gly	Ser	Ser	Gly	Ser	Glu	Gly	Asn	Ser	Glu	Glu	Gly	Val	Thr
		35					40				45				
Ser	Ser	Gly	Ser	Asp	Ala	Ala	Ser	Gly	Ser	Gly	Ala	Ala	Ser	Ala	Val
	50					55					60				
Cys	Gln	Gln	Pro	Thr	Ser	Ser	Ala	Ser	Thr	Glu	Gly	Asn	Gly	Pro	Ser
65				70						75					80
Val	Gln	Ile	Pro	Met	Val	Gly	Thr	Tyr	Ser	Ala	Asn	Val	Gln	Ser	Leu
				85					90					95	
Val	Asn	Gln	Gly	His	Gly	Gly	Arg	Gly	Phe	Val	Asn	Arg	Cys	Tyr	Gln



Ile	Ser	Ile	Val	Gly	Gly	Pro	Ser	Asn	Gln	Ser	Ala	Glu	Tyr	Gln	Glu
			580					585				590			
Phe	Gln	Asn	Thr	Val	Met	Gln	Glu	Ser	Leu	Thr	His	Leu	Gln	Ser	Ser
		595					600					605			
Leu	Arg	Val	Ser	Lys	Arg	Thr	Asn	Asn	Arg	Thr	Arg	Ala	Glu	Val	Arg
	610					615					620				
Lys	Leu	Val	Val	Lys	Tyr	Glu	Ala	Gln	Ser	Ser	Phe	Leu	Ser	Leu	Leu
625					630					635					640
Glu	Gly	Leu	Arg	Asp	Pro	Asn	Ser	Lys	Glu	Ser	Lys	Asp	Leu	Met	Arg
			645						650				655		
Glu	Cys	Phe	Ala	Ser	Trp	Ala	Gln	Lys	Ala	Gly	Val	Gln	Ser	Ser	Ser
			660					665					670		
Ile															

(2) INFORMATIONS POUR LA SEQ ID NO: 355:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 287 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 350423..351283

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 355:

Leu	Met	Leu	Lys	Ile	Asp	Leu	Thr	Gly	Lys	Ile	Ala	Phe	Ile	Ala	Gly
1			5					10					15		
Ile	Gly	Asp	Asp	Asn	Gly	Tyr	Gly	Trp	Gly	Ile	Ala	Lys	Met	Leu	Ala
		20					25					30			
Glu	Ala	Gly	Ala	Thr	Ile	Leu	Val	Gly	Thr	Trp	Val	Pro	Ile	Tyr	Lys
		35				40					45				
Ile	Phe	Ser	Gln	Ser	Trp	Glu	Leu	Gly	Lys	Phe	Asn	Ala	Ser	Arg	Glu
	50				55					60					
Leu	Ser	Asn	Gly	Glu	Leu	Leu	Thr	Phe	Ala	Lys	Ile	Tyr	Pro	Met	Asp
65				70				75							80
Ala	Ser	Phe	Asp	Thr	Pro	Glu	Asp	Ile	Pro	Gln	Glu	Ile	Leu	Glu	Asn
			85					90					95		
Lys	Arg	Tyr	Lys	Asp	Leu	Ser	Gly	Tyr	Thr	Val	Ser	Glu	Val	Val	Glu
			100					105					110		
Gln	Val	Lys	Lys	Asp	Phe	Gly	His	Ile	Asp	Ile	Leu	Val	His	Ser	Leu
		115				120						125			
Ala	Asn	Ser	Pro	Glu	Ile	Ala	Lys	Pro	Leu	Leu	Asp	Thr	Ser	Arg	Lys
	130					135					140				
Gly	Tyr	Leu	Ala	Ala	Leu	Ser	Thr	Ser	Ser	Tyr	Ser	Phe	Ile	Ser	Leu
145				150						155					160
Leu	Ser	His	Phe	Gly	Pro	Ile	Met	Asn	Ala	Gly	Ala	Ser	Thr	Ile	Ser
			165					170					175		
Leu	Thr	Tyr	Leu	Ala	Ser	Met	Arg	Ala	Val	Pro	Gly	Tyr	Gly	Gly	Gly
		180						185					190		
Met	Lys	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ser	Asp	Thr	Lys	Val	Leu	Ala
		195					200					205			
Trp	Glu	Ala	Gly	Arg	Arg	Trp	Gly	Val	Arg	Val	Asn	Thr	Ile	Ser	Ala
	210					215					220				
Gly	Pro	Leu	Ala	Ser	Arg	Ala	Gly	Lys	Ala	Ile	Gly	Phe	Ile	Glu	Arg



225				230					235					240
Met	Val	Asp	Tyr	Tyr	Gln	Asp	Trp	Ala	Pro	Leu	Pro	Ser	Pro	Met
				245					250					255
Ala	Glu	Gln	Val	Gly	Ala	Ala	Ala	Ala	Phe	Leu	Val	Ser	Pro	Leu
			260					265					270	
Ala	Gln	Leu	Arg	Glu	Lys	Leu	Ser	Met	Trp	Ile	Thr	Glu	Pro	Met
		275					280					285		

(2) INFORMATIONS POUR LA SEQ ID NO: 356:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(351314..352207)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 356:

Met	Ser	Leu	Gln	Lys	Leu	Leu	Val	Thr	Asp	Ile	Asp	Gly	Thr	Ile	Thr
1				5					10					15	
His	Gln	Ser	His	Leu	Leu	His	Asp	Arg	Val	Val	Lys	Ala	Leu	His	Gln
			20					25					30		
Tyr	Tyr	Asp	Ser	Gly	Trp	Gln	Leu	Phe	Phe	Leu	Thr	Gly	Arg	Tyr	Phe
		35				40						45			
Ser	Tyr	Ala	Tyr	Pro	Leu	Phe	Gln	Asn	Phe	Ser	Val	Pro	Phe	Leu	Leu
	50					55					60				
Gly	Ser	Gln	Asn	Gly	Ser	Ser	Val	Trp	Ser	Ser	Thr	Asp	Lys	Glu	Phe
65					70					75				80	
Ile	Tyr	Phe	Arg	Ser	Leu	Ser	Arg	Asp	Phe	Leu	Cys	Val	Leu	Glu	Lys
			85						90					95	
Tyr	Phe	Glu	Asp	Leu	Asp	Leu	Ile	Ala	Cys	Ile	Glu	Ser	Gly	Ala	Ser
			100					105					110		
Asn	Arg	Asp	Val	Tyr	Phe	Arg	Lys	Gly	Leu	Gly	Lys	Thr	Ser	Gln	Glu
		115					120					125			
Leu	Lys	Ala	Ile	Leu	Asp	Ala	Val	Tyr	Phe	Pro	Thr	Pro	Glu	Ala	Ala
	130					135					140				
Arg	Leu	Leu	Val	Asp	Val	Gln	Gly	His	Leu	Ser	Glu	Glu	Phe	Ser	Tyr
145					150					155					160
Glu	Asp	Phe	Ala	Ile	Ala	Lys	Phe	Phe	Gly	Glu	Arg	Glu	Glu	Val	Lys
			165						170					175	
Lys	Ile	Met	Asp	Arg	Phe	Ile	Gln	Ser	Pro	Glu	Val	Ser	Ser	Gln	Val
		180						185					190		
Thr	Met	Asn	Tyr	Met	Arg	Trp	Pro	Phe	Asp	Phe	Lys	Tyr	Ala	Val	Leu
	195					200						205			
Leu	Leu	Thr	Leu	Lys	Asp	Val	Ser	Lys	Gly	Phe	Ala	Val	Asp	Gln	Val
	210					215					220				
Val	Gln	Thr	Phe	Tyr	Lys	Glu	Asn	Lys	Pro	Phe	Ile	Met	Ala	Ser	Gly
225					230					235					240
Asp	Asp	Val	Asn	Asp	Ile	Asp	Leu	Leu	Ser	Arg	Gly	Asp	Phe	Lys	Ile
			245						250					255	
Val	Ile	Gln	Thr	Ala	Pro	Glu	Glu	Met	His	Gly	Leu	Ala	Asp	Phe	Leu
			260					265					270		
Ala	Pro	Pro	Ala	Lys	Asp	Leu	Gly	Ile	Leu	Ser	Ala	Trp	Glu	Ala	Gly
		275					280						285		

Glu Leu Arg Tyr Lys Gln Leu Val Asn Pro  
290 295

(2) INFORMATIONS POUR LA SEQ ID NO: 357:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 161 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(352245..352727)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 357:

```

Asp Pro Ala Arg Lys Arg Ser Phe Met Leu Arg Leu Phe Gln His Ile
1      5      10      15
Leu Cys Phe Leu Glu Glu Val Pro Ser Phe Val Asp Val Leu Gln Glu
20      25      30
Leu Ser Phe Val Asn Glu Ala Phe Ser Gly Ser Met Arg Trp Glu Val
35      40      45
Gly Lys Met Leu Gly Ser Leu Leu Leu Leu Gly Ile Phe Gly Gly
50      55      60
Gly Cys Leu Leu Phe Arg Arg Phe Leu Arg Ser Arg Gly His Leu Pro
65      70      75      80
Ser Gly Asn Ser Ser Ile Lys Ile Leu Asp Gln Arg Val Leu Ala Ser
85      90      95
Lys Thr Ser Ile Tyr Val Ile Lys Val Ala Asn Lys Thr Leu Val Val
100     105     110
Ala Glu Arg Gly Glu Arg Val Thr Leu Leu Ser Glu Phe Pro Pro Asn
115     120     125
Thr Asp Leu Asn Glu Leu Ile Gln Lys Asp Gln Lys Lys Pro Ser Thr
130     135     140
Ser Arg Gly Glu Met Leu Ser Gly Phe Leu Lys Gln Phe Lys Glu Lys
145     150     155     160
Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 358:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(353305..353661)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 358:

```

Met Phe Gly Val Gly Ile Asp Ile Ile Glu Ile Asp Arg Ile Arg Lys
1      5      10      15
Ser Tyr Gln Thr Tyr Gly Asp Arg Phe Leu Lys Lys Ile Phe Thr Glu

```

			20					25					30				
Gly	Glu	Arg	Val	Tyr	Cys	Phe	Ser	Lys	Ser	Asn	Pro	Tyr	Ala	Ser	Leu		
		35					40					45					
Ala	Ala	Arg	Phe	Ala	Ala	Lys	Glu	Ala	Val	Ala	Lys	Ala	Leu	Gly	Thr		
	50					55					60						
Gly	Ile	Gly	Lys	Leu	Leu	Lys	Trp	Lys	Glu	Ile	Glu	Met	Arg	Arg	Asp		
65				70					75						80		
Ser	Arg	Gln	Pro	Gln	Val	Val	Val	Pro	Glu	Ala	Leu	Leu	Cys	Ser	Leu		
			85					90					95				
Gly	Val	Lys	Arg	Val	Leu	Leu	Ser	Val	Ser	His	Ser	Arg	Glu	Tyr	Ala		
		100					105						110				
Thr	Ala	Val	Ala	Ile	Ala	Glu											
		115															

(2) INFORMATIONS POUR LA SEQ ID NO: 359:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(353670..354218)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 359:

Val	Leu	Ala	Lys	Gly	Arg	Asn	Thr	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ser		
1			5					10					15				
Pro	Ile	Phe	Arg	Asp	Lys	Asp	Leu	Phe	Val	Val	Gly	Gly	Gly	Asp	Ser		
		20					25					30					
Ala	Leu	Glu	Ala	Met	Phe	Leu	Thr	Arg	Tyr	Gly	Lys	Arg	Val	Phe			
	35				40					45							
Val	Val	His	Arg	Arg	Asp	Thr	Leu	Arg	Ala	Ser	Lys	Val	Met	Val	Asn		
	50				55					60							
Lys	Ala	Gln	Ala	Asn	Glu	Lys	Ile	Phe	Phe	Leu	Trp	Asn	Ser	Glu	Ile		
65				70					75					80			
Val	Lys	Ile	Ser	Gly	Asp	Thr	Leu	Val	Arg	Ser	Ile	Asp	Ile	Tyr	Asn		
		85					90					95					
Asn	Val	Asp	Lys	Thr	Thr	Thr	Thr	Met	Glu	Ala	Ala	Gly	Val	Phe	Phe		
		100					105					110					
Ala	Ile	Gly	His	Gln	Pro	Asn	Thr	Ala	Phe	Leu	Gly	Gly	Gln	Val	Ala		
	115					120					125						
Leu	Asp	Glu	Asn	Gly	Tyr	Ile	Ile	Thr	Glu	Lys	Gly	Ser	Ser	Arg	Thr		
	130			135					140								
Ser	Val	Pro	Gly	Val	Phe	Ala	Ala	Gly	Asp	Val	Gln	Asp	Lys	Tyr	Tyr		
145				150					155					160			
Arg	Gln	Ala	Ile	Thr	Ser	Ala	Gly	Ser	Gly	Cys	Met	Ala	Ala	Leu	Asp		
		165					170							175			
Val	Glu	Arg	Phe	Leu	Glu	Asn											
		180															

(2) INFORMATIONS POUR LA SEQ ID NO: 360:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 155 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(354140..354604)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 360:

```

Met Thr His Ala Lys Leu Val Ile Ile Gly Ser Gly Pro Ala Gly Tyr
1      5      10      15
Thr Ala Ala Ile Tyr Ala Ser Arg Ala Leu Leu Thr Pro Val Leu Phe
      20      25      30
Glu Gly Phe Phe Ser Gly Ile Ala Gly Gly Gln Leu Met Thr Thr Thr
      35      40      45
Glu Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Val Leu Gly His Gln
      50      55      60
Leu Met Asp Leu Met Lys Thr Gln Ala Gln Arg Phe Gly Thr Gln Val
      65      70      75      80
Leu Ser Lys Asp Ile Thr Ala Val Asp Phe Ser Val Arg Pro Phe Val
      85      90      95
Leu Lys Ser Gly Glu Glu Thr Phe Thr Cys Asp Ala Cys Ile Ile Ala
      100     105     110
Thr Gly Ala Ser Ala Lys Arg Leu Ser Ile Pro Gly Ala Gly Asp Asn
      115     120     125
Glu Phe Trp Gln Lys Gly Val Thr Leu Ala Leu Phe Val Thr Glu Pro
      130     135     140
Leu Pro Phe Phe Val Thr Lys Ile Cys Leu Leu
145      150      155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 361:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 538 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 355059..356672

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 361:

```

Leu Tyr Ala Ile His Gly Phe Thr Ala Thr Glu Glu Glu Pro Thr Ser
1      5      10      15
Glu Val His Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Ser
      20      25      30
Lys Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile
      35      40      45
Pro Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Thr Val Gly Ala
      50      55      60
Glu Val Glu Val Tyr Leu Asp Gln Thr Glu Asp Asp Glu Gly Lys Val
      65      70      75      80
Val Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile
      85      90      95
Leu Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg

```

(2) INFORMATION POUR LA SEQ ID NO: 362:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 195 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 356793..357377

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 362:

```

Met Asn Lys Asp Leu Val Ala Ile Phe Asp Tyr Met Glu Arg Glu Lys
1      5      10      15
Gly Ile Gln Arg Ser Thr Ile Val Gly Ala Ile Glu Ser Ala Leu Lys
      20      25      30
Ile Ala Ala Lys Lys Thr Leu Arg Asp Asp Ala Asn Val Ser Val Ser
      35      40      45
Ile Asn Pro Arg Thr Gly Asp Ile Glu Val Phe Cys Glu Lys Gln Ile
50      55      60
Val Glu Lys Cys Gln Asn Pro Ser Lys Glu Ile Pro Leu Asp Lys Ala
65      70      75      80
Arg Glu Tyr Asp Pro Asp Cys Gln Ile Gly Gln Tyr Met Asp Val Pro
      85      90      95
Phe Ile Ser Asp Gln Phe Gly Arg Ile Ala Ala His Ala Ala Arg Gln
      100     105     110
Ile Ile Gly Gln Lys Leu Arg His Ala Glu Arg Asp Val Ile Tyr Glu
      115     120     125
Glu Tyr Arg His Arg Lys Asn Glu Ile Ile Ser Gly Val Val Lys Ser
      130     135     140
Phe Ala Arg Gly Ala Asn Leu Val Val Asp Leu Gly Lys Val Glu Gly
145     150     155     160
Leu Leu Pro Ala Arg Phe Tyr Pro Lys Thr Glu Lys His Lys Val Gly
      165     170     175
Asp Lys Ile Tyr Ala Leu Leu Tyr Glu Tyr Arg Asn Leu Lys Met Val
      180     185     190
Glu Leu Lys
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 363:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 256 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 357326..358093

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 363:

```

Asp Leu Cys Ala Ser Leu Arg Val Gln Glu Ser Glu Asn Gly Gly Ala
1      5      10      15
Glu Val Ile Leu Ser Arg Ser His Pro Glu Phe Val Lys Gln Leu Phe
      20      25      30
Val Gln Glu Val Pro Glu Leu Glu Glu Gly Ser Val Glu Ile Val Lys

```

(2) INFORMATION POUR LA SEQ ID NO: 364:

(A) LONGUEUR: 897 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 358053..360743

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 364:

Met	Glu	Lys	Ala	Lys	Leu	Thr	Lys	Asn	Leu	Lys	Xaa	Lys	Ile	Lys	Asn
1				5					10					15	
Ala	Gln	Leu	Thr	Lys	Ala	Xaa	Gly	Leu	Asp	Lys	Leu	Lys	Gln	Lys	Leu
			20					25					30		
Ala	Gln	Ala	Gly	Ser	Ser	Asp	Thr	Lys	Asn	Ser	Pro	Ala	Ser	Lys	Ala
		35					40					45			
Gln	Thr	Lys	Glu	Lys	Ser	Ser	Lys	Lys	Thr	Ala	Gly	Thr	Pro	Ala	Pro
	50						55				60				
Ala	Pro	Glu	Val	Asp	Leu	Gly	Ala	Thr	Glu	Ser	Thr	Ala	Arg	Arg	Ile
65					70					75					80
Arg	Ala	Lys	Asp	Arg	Ser	Ser	Phe	Ala	Ala	Glu	Pro	Thr	Val	Thr	Thr
			85						90					95	
Ala	Leu	Pro	Gly	Asp	Ala	Ser	His	Leu	Thr	Leu	Asp	Ala	Ile	Pro	Ala
			100					105					110		
Ile	Lys	Ala	Pro	Glu	Ile	Thr	Ser	Val	Thr	Gln	Lys	Glu	Gln	Thr	Leu
		115					120					125			

Arg	Glu	Cys	Thr	Asp	Thr	Ser	Ser	Val	Gln	Gln	Glu	Glu	Lys	Lys	Glu
130						135					140				
Ser	Ser	Glu	Glu	Thr	Ser	Pro	Glu	Thr	Pro	Glu	Arg	Ile	Glu	Glu	Thr
145					150					155					160
Pro	Ile	Ile	Arg	Thr	Arg	Thr	Glu	Pro	Lys	Ser	Val	Val	Ser	Ile	Lys
				165					170					175	
Pro	Lys	Phe	Gly	Pro	Thr	Gly	Lys	His	Ile	Asn	His	Leu	Leu	Ala	Lys
			180					185					190		
Thr	Phe	Lys	Ala	Pro	Ala	Lys	Glu	Thr	Lys	Ala	Ala	Ser	Thr	Glu	Glu
		195					200					205			
Thr	Thr	Gln	Gln	Gln	Pro	Arg	Gln	Asn	Asp	Ala	Ala	Ser	His	Asn	Asn
	210					215					220				
Lys	Gln	Gln	Pro	Ser	Gly	Thr	Ser	Ser	Arg	Pro	Ala	Ser	Ser	Ala	Pro
225					230					235					240
Ser	Tyr	Arg	Arg	Glu	Ser	Thr	Ser	Asn	Asn	Asn	Asn	Asn	Ala	Lys	Arg
				245					250					255	
Gly	Ser	Glu	Arg	Asp	Arg	Ser	Lys	Arg	Ser	Asp	Glu	Ser	Val	Lys	Ala
			260					265					270		
Phe	Thr	Gly	Arg	Asp	Arg	Tyr	Gly	Leu	Asn	Glu	Gly	Ser	Ser	Glu	Glu
		275					280					285			
Asp	Lys	Trp	Arg	Lys	Lys	Arg	Val	His	Lys	Thr	Lys	Lys	Gln	Ala	Glu
	290					295					300				
Glu	His	Val	Val	Gln	Cys	Pro	Ala	His	Ile	Lys	Ile	Ala	Leu	Pro	Ile
305					310					315					320
Thr	Val	Lys	Asp	Leu	Ala	Ala	Glu	Met	Lys	Leu	Lys	Ala	Ser	Glu	Leu
				325					330					335	
Ile	Gln	Lys	Leu	Phe	Ile	His	Gly	Met	Thr	Tyr	Val	Val	Asn	Asp	Val
			340					345					350		
Leu	Asp	Ser	Gln	Thr	Val	Val	Glu	Tyr	Ile	Gly	Leu	Glu	Phe	Gly	Cys
	355						360					365			
Thr	Ile	Glu	Ile	Asp	Ser	Ser	Ala	Lys	Glu	Lys	Leu	Cys	Leu	Val	Glu
	370					375					380				
Asn	Thr	Val	Arg	Asp	Glu	Val	Asn	Ala	Thr	Asp	Pro	Glu	Lys	Leu	Ile
385					390					395					400
Ile	Arg	Ser	Pro	Ile	Val	Ala	Phe	Met	Gly	His	Val	Asp	His	Gly	Lys
			405						410					415	
Thr	Thr	Ile	Ile	Asp	Ala	Leu	Arg	Gln	Ser	Asn	Met	Ala	Ala	Ser	Glu
			420					425					430		
Ala	Gly	Ala	Ile	Thr	Gln	His	Thr	Gly	Ala	Phe	Lys	Cys	Thr	Thr	Pro
		435					440					445			
Val	Gly	Glu	Ile	Thr	Val	Leu	Asp	Thr	Pro	Gly	His	Glu	Ala	Phe	Ser
	450					455					460				
Ala	Met	Arg	Ala	Arg	Gly	Ala	Glu	Val	Cys	Asp	Ile	Val	Val	Leu	Val
465					470	-				475					480
Val	Ala	Gly	Asp	Glu	Gly	Ile	Lys	Glu	Gln	Thr	Ile	Glu	Ala	Ile	Glu
			485					490						495	
His	Ala	Lys	Gly	Ala	Asn	Ile	Thr	Ile	Val	Val	Ala	Ile	Asn	Lys	Cys
			500					505					510		
Asp	Lys	Pro	Lys	Leu	Gln	Cys	Arg	Asn	Ser	Val	Pro	Ser	Val	Ser	Arg
		515					520					525			
Ile	Arg	Ser	Leu	Leu	Pro	Glu	Ala	Trp	Gly	Gly	Ser	Ile	Ala	Thr	Ile
	530					535					540				
Asn	Thr	Ser	Ala	Lys	Thr	Gly	Glu	Gly	Leu	Gln	Asp	Leu	Leu	Glu	Met
545					550					555					560
Leu	Ala	Leu	Gln	Ala	Glu	Val	Leu	Glu	Leu	Lys	Ala	Asp	Pro	Ser	Ala
			565					570						575	
Arg	Ala	Arg	Gly	Leu	Val	Ile	Glu	Ser	Glu	Leu	His	Lys	Gly	Leu	Gly
			580					585					590		
Ala	Val	Ala	Thr	Val	Leu	Val	Gln	Asn	Gly	Thr	Leu	His	Leu	Gly	Glu



(2) INFORMATION POUR LA SEQ ID NO: 365:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 360753..361121

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 365:

Met Ala Glu Asn Arg Arg Met Lys Lys Val Asn Ala Met Leu Arg Glu  
1 5 10 15  
Ala Ile Ala Lys Val Ile Leu Lys Asp Val Lys His Pro Lys Ile Ser  
20 25 30



Phe 1	Glu	Gly	Val	Leu 5	Leu	Val	Asp	Lys	Pro 10	Gln	Gly	Arg	Thr	Ser 15	Phe
Ser	Leu	Ile	Arg 20	Ser	Leu	Val	Arg	Leu 25	Ile	Gly	Val	Lys	Lys 30	Ile	Gly
His	Ala	Gly 35	Thr	Leu	Asp	Pro	Phe 40	Ala	Thr	Gly	Val	Met 45	Val	Met	Leu
Ile	Gly 50	Arg	Lys	Phe	Thr	Arg 55	Leu	Ser	Asp	Ile	Met 60	Leu	Phe	Glu	Asp
Lys 65	Glu	Tyr	Ala	Ala	Val 70	Ala	His	Leu	Gly	Thr 75	Thr	Thr	Asp	Thr	Tyr 80
Asp	Cys	Asp	Gly 85	Lys	Ile	Val	Gly	Arg	Ser 90	Lys	Lys	Val	Pro	Thr 95	Met
Asp	Glu	Val	Leu 100	Thr	Cys	Thr	Ser	Tyr 105	Phe	Gln	Gly	Glu	Ile 110	Gln	Gln
Val	Pro	Pro 115	Met	Phe	Ser	Ala	Lys 120	Lys	Val	Gln	Gly	Lys 125	Lys	Leu	Tyr
Glu	Tyr 130	Ala	Arg	Gln	Gly	Leu 135	Ser	Ile	Glu	Arg	Arg 140	Phe	Ala	Thr	Val
Thr 145	Val	Asn	Leu	Arg	Leu 150	Val	Lys	Tyr	Glu	Tyr 155	Pro	Arg	Leu	His	Phe 160
Val	Val	Gln	Cys 165	Ser	Lys	Gly	Thr	Tyr 170	Ile	Arg	Ser	Ile	Ala	His 175	Glu
Leu	Gly 180	Asn	Met	Leu	Gly	Cys	Gly 185	Ala	Tyr	Leu	Glu	Glu	Leu 190	Arg	Arg
Leu	Arg 195	Ser	Gly	Ser	Phe	Ser	Ile 200	Asp	Gln	Cys	Ile	Asp 205	Gly	Asn	Leu
Leu	Asp 210	Glu	Pro	Glu	Phe	Asn 215	Val	Ser	Pro	Tyr	Leu 220	Arg	Asp	Ala	Asn
Gly 225	Leu	Ile	Leu	Gln	Pro 230	Ala	Pro	Val	Leu						

## (2) INFORMATIONS POUR LA SEQ ID NO: 367:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 307 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 361826..362746

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 367:

```

Met Tyr Leu Leu Ile Tyr Val Met Gln Met Asp Leu Phe Tyr Ser Leu
1          5          10          15
Leu Pro Ser Ser Asn Pro Ile Glu Ser Val Thr Ile Xaa Phe Phe Asp
          20          25          30
Gly Cys Xaa Leu Xaa His Gln Ala Leu Leu Ser Phe Leu Thr Lys Phe
          35          40          45
Pro Gly Lys Ser Gly Val Ile Thr Phe Ser Gln His Pro Glu His Thr
          50          55          60
Leu Ser Asn Ser Pro Pro Glu Thr Ile Thr Ser Leu Glu Glu Arg Ile
65          70          75          80
Gln Leu Leu Ala Gly Cys Gly Ile Asp Tyr Leu Ala Val Leu Pro Phe
          85          90          95
Asn Gln Glu Ile Ala Asn Gln Glu Ala Glu Leu Phe Ile Gln Ser Ile
          100          105          110
Tyr Lys Thr Leu His Pro Ser Arg Ile Val Leu Gly Tyr Asp Ser Arg
          115          120          125
Leu Gly Lys Gly Gly Leu Gly Thr Ala Gln Thr Leu Arg Pro Phe Ala
          130          135          140
Ala Ser Leu Gly Ile Ser Leu Glu Glu Val Pro Pro Leu Gln Ile Glu
145          150          155          160
Gly Thr Ile Val Ser Ser Arg Lys Ile Arg Gln Phe Leu Arg Glu Lys
          165          170          175
Asp Leu Cys Ser Ala Glu Lys Phe Leu Gly Arg Pro Phe Ala Tyr Thr
          180          185          190
Gly Lys Val Ala His Gly Arg Gly Ile Gly Thr Ser Phe Gly Tyr Ala
          195          200          205
Thr Ile Asn Leu Pro Leu Thr His Ser Leu Leu Pro Leu Gly Val Tyr
          210          215          220
Thr Cys Thr Ile Val Ile Glu Gly Phe Ser Tyr Ala Gly Val Met Asn
225          230          235          240
Leu Gly Met Ala Pro Thr Met Gln Arg His Gln Leu Cys Leu Glu Ala
          245          250          255
His Ile Leu Asp Phe Ser Glu Asp Leu Tyr Asp Lys Ser Ile Thr Val
          260          265          270
Ile Leu Glu Gln Phe Leu Arg Glu Glu Lys Leu Phe Ser Ser Lys Asp
          275          280          285
Glu Leu Val Leu Ala Ile Gln Glu Asp Ile Arg Gln Ala Arg Leu Asn
          290          295          300
Lys Asn Arg
305

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 368:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(362816..363853)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 368:

Met	Gly	Gln	Thr	Glu	Cys	Gly	Ile	Val	Gly	Leu	Pro	Asn	Val	Gly	Lys	1	5	10	15
Ser	Gly	Leu	Phe	Asn	Ala	Leu	Thr	Gly	Ala	Gln	Val	Ala	Ser	Cys	Asn	20	25	30	
Tyr	Pro	Phe	Cys	Thr	Ile	Asp	Pro	Asn	Val	Gly	Ile	Val	Pro	Val	Ile	35	40	45	
Asp	Pro	Arg	Leu	Glu	Thr	Leu	Ala	Arg	Ile	Ser	Gln	Ser	Gln	Lys	Ile	50	55	60	
Ile	Tyr	Ala	Asp	Met	Lys	Phe	Val	Asp	Ile	Ala	Gly	Leu	Val	Lys	Gly	65	70	75	80
Ala	Ala	Ser	Gly	Ala	Gly	Leu	Gly	Asn	Arg	Phe	Leu	Ser	His	Ile	Arg	85	90	95	
Glu	Thr	His	Ala	Ile	Ala	His	Val	Val	Arg	Cys	Phe	Asp	Asn	Asp	Asp	100	105	110	
Ile	Thr	His	Val	Ser	Gly	Lys	Ile	Asp	Pro	Glu	Glu	Asp	Ile	Ala	Val	115	120	125	
Ile	Asn	Leu	Glu	Leu	Val	Leu	Ala	Asp	Phe	Ser	Ser	Ala	Thr	Ser	Val	130	135	140	
Arg	Glu	Lys	Leu	Gly	Lys	Gln	Ala	Lys	Gly	Lys	Lys	Asp	Ile	Gly	Gln	145	150	155	160
Leu	Leu	Pro	Leu	Leu	Asp	Arg	Val	Val	Asp	His	Leu	Glu	Ser	Gly	Asn	165	170	175	
Pro	Val	Arg	Thr	Leu	Ser	Leu	Ser	Leu	Glu	Glu	Lys	Val	Leu	Leu	Lys	180	185	190	
Pro	Tyr	Pro	Phe	Leu	Thr	Gly	Lys	Pro	Met	Leu	Tyr	Ile	Ala	Asn	Ile	195	200	205	
Asp	Glu	Asp	Ser	Leu	Thr	Asp	Leu	Asp	Asn	Pro	Tyr	Val	Gln	Lys	Val	210	215	220	
Arg	Glu	Ile	Ala	Lys	Arg	Glu	Glu	Ala	Asn	Val	Val	Pro	Ile	Cys	Val	225	230	235	240
Lys	Leu	Glu	Glu	Glu	Ile	Leu	Ser	Leu	Pro	Leu	Glu	Glu	Arg	Gln	Asp	245	250	255	
Phe	Leu	His	Ser	Leu	Gly	Leu	Gln	Glu	Ser	Gly	Leu	Asn	Arg	Leu	Val	260	265	270	
Ala	Ser	Ala	Tyr	His	Thr	Leu	Gly	Leu	Ile	Ser	Tyr	Phe	Thr	Thr	Gly	275	280	285	
Pro	Gln	Glu	Thr	Arg	Ala	Trp	Thr	Ile	Ser	Lys	Gly	Val	Thr	Ala	Ala	290	295	300	
Glu	Ala	Ala	Gly	Glu	Ile	His	Ser	Asp	Ile	Gln	Arg	Gly	Phe	Ile	Arg	305	310	315	320
Ala	Glu	Val	Val	Thr	Met	Glu	Asp	Ile	Val	Ala	Tyr	Asp	Gly	Arg	Ala	325	330	335	
Gly	Ala	Arg	Glu	Ala	Gly	Lys	Leu	Arg	Ala							340	345		

(2) INFORMATIONS POUR LA SEQ ID NO: 369:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 360 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 364116..365195

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 369:

Met	Gly	Glu	Lys	Thr	Glu	Lys	Ala	Thr	Pro	Lys	Arg	Leu	Arg	Asp	Ala	1	5	10	15
Arg	Lys	Lys	Gly	Gln	Val	Ala	Lys	Ser	Gln	Asp	Phe	Pro	Ser	Ala	Ile	20	25	30	
Thr	Phe	Ile	Val	Ser	Met	Phe	Leu	Thr	Phe	Ser	Leu	Ala	Ser	Phe	Phe	35	40	45	
Ala	Glu	His	Leu	Gly	Ser	Phe	Leu	Val	Ser	Ile	Phe	Lys	Thr	Ala	Pro	50	55	60	
Gln	Asn	His	Asp	Pro	His	Leu	Ala	Ile	Tyr	Tyr	Leu	Lys	Asn	Cys	Leu	65	70	75	80
Ile	Leu	Ile	Leu	Thr	Val	Ser	Leu	Pro	Leu	Leu	Gly	Ala	Val	Gly	Phe	85	90	95	
Val	Gly	Leu	Leu	Ile	Gly	Phe	Leu	Ile	Val	Gly	Pro	Thr	Phe	Ser	Thr	100	105	110	
Glu	Val	Phe	Lys	Pro	Asp	Leu	Lys	Lys	Phe	Asn	Pro	Ile	Asp	Asn	Leu	115	120	125	
Lys	Gln	Lys	Phe	Lys	Val	Lys	Thr	Phe	Ile	Glu	Leu	Leu	Lys	Ser	Ile	130	135	140	
Phe	Lys	Ile	Ser	Gly	Ala	Ala	Leu	Ile	Leu	Tyr	Ile	Val	Leu	Lys	Asn	145	150	155	160
Arg	Val	Glu	Leu	Val	Ile	Glu	Thr	Ala	Gly	Val	Pro	Pro	Leu	Val	Thr	165	170	175	
Ala	Gln	Val	Phe	Lys	Glu	Ile	Leu	Tyr	Lys	Ala	Val	Thr	Ser	Ile	Gly	180	185	190	
Leu	Phe	Phe	Leu	Val	Val	Ala	Val	Ile	Asp	Leu	Val	Tyr	Gln	Arg	His	195	200	205	
Ser	Phe	Ala	Lys	Glu	Leu	Lys	Met	Glu	Lys	Phe	Glu	Val	Lys	Gln	Glu	210	215	220	
Phe	Lys	Asp	Thr	Glu	Gly	Asn	Pro	Glu	Ile	Lys	Gly	Arg	Arg	Arg	Gln	225	230	235	240
Ile	Ala	Gln	Glu	Ile	Ala	Tyr	Glu	Asp	Thr	Ser	Ser	Gln	Ile	Lys	His	245	250	255	
Ala	Ser	Ala	Val	Val	Ser	Asn	Pro	Lys	Asp	Ile	Ala	Val	Ala	Ile	Gly	260	265	270	
Tyr	Met	Pro	Glu	Lys	Tyr	Lys	Ala	Pro	Trp	Ile	Ile	Ala	Met	Gly	Val	275	280	285	
Asn	Leu	Arg	Ala	Lys	Arg	Ile	Ile	Ala	Glu	Ala	Glu	Lys	Tyr	Gly	Val	290	295	300	
Pro	Ile	Met	Arg	Asn	Val	Pro	Leu	Ala	His	Gln	Leu	Leu	Asp	Glu	Gly	305	310	315	320
Lys	Glu	Leu	Lys	Phe	Ile	Pro	Glu	Thr	Thr	Tyr	Glu	Ala	Val	Gly	Glu	325	330	335	
Ile	Leu	Leu	Tyr	Ile	Thr	Ser	Leu	Asn	Ala	Gln	Asn	Leu	Glu	Asn	Lys	340	345	350	
Asn	Ile	Asn	Gln	Phe	Asp	Asn	Leu									355	360		

(2) INFORMATIONS POUR LA SEQ ID NO: 370:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 365198..365587

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 370:

Met	Asn	Lys	Leu	Leu	Asn	Phe	Val	Ser	Arg	Thr	Phe	Gly	Gly	Asp	Ala
1				5					10					15	
Ala	Leu	Asn	Met	Ile	Asn	Lys	Ser	Ser	Asp	Leu	Ile	Leu	Ala	Met	Trp
		20					25						30		
Met	Leu	Gly	Val	Val	Leu	Met	Ile	Ile	Leu	Pro	Leu	Pro	Pro	Ala	Met
		35					40					45			
Val	Asp	Phe	Met	Ile	Thr	Ile	Asn	Leu	Ala	Ile	Ser	Val	Phe	Leu	Leu
	50					55				60					
Met	Val	Ala	Leu	Tyr	Ile	Pro	Ser	Ala	Leu	Gln	Leu	Ser	Val	Phe	Pro
65					70				75						80
Ser	Leu	Leu	Leu	Ile	Thr	Thr	Met	Phe	Arg	Leu	Gly	Ile	Asn	Ile	Ser
				85				90						95	
Ser	Ser	Arg	Gln	Ile	Leu	Leu	His	Ala	Tyr	Ala	Gly	His	Val	Ile	Gln
		100						105					110		
Ala	Ser	Glu	Thr	Ser	Ser	Leu	Glu	Glu	Thr	Met	Ser	Leu	Asp	Leu	Leu
		115					120					125			
Ser	Ser														
	130														

(2) INFORMATIONS POUR LA SEQ ID NO: 371:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 614 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 365479..367320

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 371:

His	Phe	Phe	Leu	Pro	Thr	Asn	Ser	Pro	Ser	Cys	Leu	Cys	Trp	Ser	Arg
1				5					10					15	
Asp	Pro	Ser	Phe	Gly	Asp	Phe	Val	Val	Gly	Gly	Asn	Tyr	Val	Val	Gly
			20					25					30		
Phe	Ile	Ile	Phe	Leu	Ile	Ile	Thr	Ile	Ile	Gln	Phe	Ile	Val	Val	Thr
		35					40					45			
Lys	Gly	Ala	Glu	Arg	Val	Ala	Glu	Val	Ala	Ala	Arg	Phe	Arg	Leu	Asp
	50					55					60				
Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Arg	Ala	Gly

65					70					75					80
Met	Ile	Asp	Ala	Thr	Gln	Ala	Arg	Asp	Lys	Arg	Ser	Gln	Ile	Gln	Lys
				85					90					95	
Glu	Ser	Glu	Leu	Tyr	Gly	Ala	Met	Asp	Gly	Ala	Met	Lys	Phe	Ile	Lys
			100					105					110		
Gly	Asp	Val	Ile	Ala	Gly	Ile	Val	Ile	Ser	Leu	Ile	Asn	Ile	Val	Gly
		115					120					125			
Gly	Leu	Val	Ile	Gly	Val	Thr	Met	Lys	Gly	Met	Thr	Met	Ala	Gln	Ala
	130					135					140				
Ala	His	Ile	Tyr	Thr	Leu	Ile	Thr	Ile	Gly	Asp	Gly	Leu	Val	Ser	Gln
145					150					155					160
Ile	Pro	Ser	Leu	Leu	Ile	Ser	Leu	Thr	Ala	Gly	Ile	Val	Thr	Thr	Arg
			165						170					175	
Val	Ser	Ser	Asp	Lys	Asp	Thr	Asn	Leu	Gly	Lys	Glu	Ile	Ser	Ser	Gln
			180					185					190		
Leu	Val	Lys	Glu	Pro	Arg	Ala	Leu	Leu	Leu	Ser	Ala	Gly	Ala	Thr	Leu
		195					200					205			
Gly	Ile	Gly	Phe	Phe	Lys	Gly	Phe	Pro	Leu	Trp	Ser	Phe	Ala	Leu	Met
	210					215					220				
Ala	Val	Leu	Phe	Ala	Val	Leu	Gly	Ile	Leu	Leu	Ile	Thr	Lys	Lys	Asn
225					230					235					240
Ser	Pro	Gly	Lys	Lys	Gly	Gly	Ala	Ser	Ser	Thr	Thr	Thr	Val	Gly	Ala
			245						250					255	
Ala	Asp	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Asn	Ser	Asp	Asp	Tyr	Ala	Leu
		260						265					270		
Thr	Leu	Pro	Val	Ile	Leu	Glu	Leu	Gly	Lys	Asp	Leu	Ser	Lys	Leu	Ile
		275					280						285		
Gln	Gln	Arg	Thr	Lys	Ser	Gly	Gln	Ser	Phe	Val	Asp	Asp	Met	Ile	Pro
	290					295					300				
Lys	Met	Arg	Gln	Ala	Leu	Tyr	Gln	Asp	Ile	Gly	Ile	Arg	Tyr	Pro	Gly
305					310					315					320
Ile	His	Val	Arg	Thr	Asp	Ser	Pro	Ser	Leu	Glu	Gly	Asn	Asp	Tyr	Met
			325						330					335	
Ile	Leu	Leu	Asn	Glu	Val	Pro	Tyr	Val	Arg	Gly	Lys	Ile	Pro	Pro	Asn
		340						345					350		
His	Val	Leu	Thr	Asn	Glu	Val	Glu	Glu	Asn	Leu	Ser	Arg	Tyr	Asn	Leu
	355						360					365			
Pro	Phe	Ile	Thr	Tyr	Lys	Asn	Ala	Ala	Gly	Leu	Pro	Ser	Thr	Trp	Val
	370					375					380				
Ser	Thr	Asp	Ala	Leu	Thr	Ile	Leu	Glu	Lys	Ala	Ala	Ile	Lys	Tyr	Trp
385					390					395					400
Ser	Pro	Leu	Glu	Val	Ile	Ile	Leu	His	Leu	Ser	Tyr	Phe	Phe	His	Arg
			405						410					415	
Asn	Ser	Gln	Glu	Phe	Leu	Gly	Ile	Gln	Glu	Val	Arg	Ser	Met	Ile	Glu
		420						425					430		
Phe	Met	Glu	Arg	Ser	Phe	Pro	Asp	Leu	Val	Lys	Glu	Val	Thr	Arg	Leu
	435						440					445			
Ile	Pro	Leu	Gln	Lys	Leu	Thr	Glu	Ile	Phe	Lys	Arg	Leu	Val	Gln	Glu
	450					455					460				
Gln	Ile	Ser	Ile	Lys	Asp	Leu	Arg	Thr	Ile	Leu	Glu	Ser	Leu	Ser	Glu
465					470					475					480
Trp	Ala	Gln	Thr	Glu	Lys	Asp	Thr	Val	Leu	Leu	Thr	Glu	Tyr	Val	Arg
			485						490					495	
Ser	Ser	Leu	Lys	Leu	Tyr	Ile	Ser	Phe	Lys	Phe	Ser	Gln	Gly	Gln	Ser
		500						505					510		
Ala	Ile	Ser	Val	Tyr	Leu	Leu	Asp	Pro	Glu	Ile	Glu	Glu	Met	Ile	Arg
	515						520					525			
Gly	Ala	Ile	Lys	Gln	Thr	Ser	Ala	Gly	Ser	Tyr	Leu	Ala	Leu	Asp	Pro
	530					535					540				

Asp Ser Val Asn Leu Ile Leu Lys Ser Met Arg Met Thr Ile Thr Pro  
 545 550 555 560  
 Thr Pro Pro Gly Gly Gln Pro Pro Val Leu Leu Thr Ala Ile Asp Val  
 565 570 575  
 Arg Arg Tyr Val Arg Lys Leu Ile Glu Thr Glu Phe Pro Asp Ile Ala  
 580 585 590  
 Val Ile Ser Tyr Gln Glu Val Leu Pro Glu Ile Arg Ile Gln Pro Leu  
 595 600 605  
 Gly Arg Ile Gln Ile Phe  
 610

(2) INFORMATIONS POUR LA SEQ ID NO: 372:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 421 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 367341..368603

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 372:

Met Thr Ala Ser Gly Gly Ala Gly Gly Leu Gly Ser Thr Gln Thr Val  
 1 5 10 15  
 Asp Val Ala Arg Ala Gln Ala Ala Ala Thr Gln Asp Ala Gln Glu  
 20 25 30  
 Val Ile Gly Ser Gln Glu Ala Ser Glu Ala Ser Met Leu Lys Glu Cys  
 35 40 45  
 Glu Asp Leu Ile Asn Pro Ala Ala Thr Arg Ile Xaa Lys Lys Glu  
 50 55 60  
 Glu Lys Phe Glu Ser Leu Glu Ala Arg Arg Lys Xaa Thr Ala Asp Lys  
 65 70 75 80  
 Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Gly Asp Thr Pro Leu  
 85 90 95  
 Glu Asp Arg Phe Thr Glu Asp Leu Ser Glu Val Ser Gly Glu Asp Phe  
 100 105 110  
 Arg Gly Leu Lys Asn Ser Phe Asp Asp Asp Ser Ser Ser Asp Glu Ile  
 115 120 125  
 Leu Asp Ala Leu Thr Ser Lys Phe Ser Asp Pro Thr Ile Lys Asp Leu  
 130 135 140  
 Ala Leu Asp Tyr Leu Ile Gln Ile Ala Pro Ser Asp Gly Lys Leu Lys  
 145 150 155 160  
 Ser Ala Leu Ile Gln Ala Lys His Gln Leu Met Ser Gln Asn Pro Gln  
 165 170 175  
 Ala Ile Val Gly Gly Arg Asn Val Leu Leu Ala Ser Glu Thr Phe Ala  
 180 185 190  
 Ser Arg Ala Asn Thr Ser Pro Ser Ser Leu Arg Ser Leu Tyr Phe Gln  
 195 200 205  
 Val Thr Ser Ser Pro Ser Asn Cys Ala Asn Leu His Gln Met Leu Ala  
 210 215 220  
 Ser Tyr Ser Pro Ser Glu Lys Thr Ala Val Met Glu Phe Leu Val Asn  
 225 230 235 240  
 Gly Met Val Ala Asp Leu Lys Ser Glu Gly Pro Ser Ile Pro Pro Ala  
 245 250 255  
 Lys Leu Gln Val Tyr Met Thr Glu Leu Ser Asn Leu Gln Ala Leu His





(2) INFORMATIONS POUR LA SEQ ID NO: 374:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 388 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 369088..370251

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 374:

Met	Pro	Ser	Leu	Ser	Gln	Ser	Arg	Arg	Ile	Ile	Gln	Gln	Ser	Ser	Ile	1	5	10	15
Arg	Lys	Ile	Trp	Asn	Gln	Ile	Asp	Thr	Ser	Pro	Lys	His	Gly	Val	Cys	20	25	30	
Val	Pro	Leu	Phe	Ser	Leu	His	Thr	Gln	Glu	Ser	Cys	Gly	Ile	Gly	Glu	35	40	45	
Phe	Leu	Asp	Leu	Ile	Pro	Met	Ile	Asp	Trp	Cys	Ile	Ser	Cys	Gly	Phe	50	55	60	
Gln	Ile	Leu	Gln	Ile	Leu	Pro	Ile	Asn	Asp	Thr	Gly	Ser	Cys	Ser	Ser	65	70	75	80
Pro	Tyr	Asn	Ser	Ile	Ser	Ser	Ile	Ala	Leu	Asn	Pro	Leu	His	Leu	Ser	85	90	95	
Ile	Ser	Ala	Leu	Pro	Tyr	Lys	Glu	Glu	Val	Pro	Ala	Ala	Glu	Thr	Arg	100	105	110	
Ile	Arg	Glu	Met	Gln	Gln	Leu	Ser	Gln	Leu	Pro	Gln	Val	His	Tyr	Glu	115	120	125	
Lys	Val	Arg	Ser	Met	Lys	Arg	Asp	Phe	Phe	Gln	Glu	Tyr	Tyr	Arg	Val	130	135	140	
Cys	Lys	Gln	Lys	Lys	Leu	Thr	Asp	His	Pro	Asp	Phe	Tyr	Ala	Phe	Cys	145	150	155	160
Glu	Gln	Glu	Lys	Tyr	Trp	Leu	His	Pro	Tyr	Ala	Leu	Phe	Arg	Ser	Ile	165	170	175	
Arg	Glu	His	Leu	Asp	Asn	Leu	Pro	Ile	Asn	His	Trp	Pro	Thr	Thr	Tyr	180	185	190	
Thr	Asp	Leu	Ser	Gln	Ile	Thr	Glu	His	Glu	Arg	Thr	Phe	Ala	Glu	Asp	195	200	205	
Ile	Gln	Phe	His	Ser	Tyr	Leu	Gln	Tyr	Leu	Cys	Phe	Gln	Gln	Met	Thr	210	215	220	
Gln	Val	Arg	Glu	His	Ala	Asn	Cys	Lys	Ser	Cys	Leu	Ile	Lys	Gly	Asp	225	230	235	240
Ile	Pro	Ile	Leu	Ile	Ser	Lys	Asp	Ser	Cys	Asp	Val	Trp	Phe	Tyr	Arg	245	250	255	
His	Tyr	Phe	Ser	Ser	Ser	Glu	Ser	Val	Gly	Ala	Pro	Pro	Asp	Leu	Tyr	260	265	270	
Asn	Ala	Glu	Gly	Gln	Asn	Trp	His	Leu	Pro	Ile	Tyr	Asn	Met	Lys	Thr	275	280	285	
Leu	Gln	Gln	Asp	Asn	Tyr	Leu	Trp	Trp	Lys	Glu	Arg	Leu	Arg	Tyr	Ala	290	295	300	
Glu	Asn	Phe	Tyr	Ser	Leu	Tyr	Arg	Leu	Asp	His	Ile	Val	Gly	Leu	Phe	305	310	315	320
Arg	Phe	Trp	Val	Trp	Asp	Glu	Ser	Gly	Cys	Gly	Arg	Phe	Glu	Pro	His	325	330	335	
Asp	Pro	Lys	Asp	Tyr	Leu	Ala	Gln	Gly	Gln	Asp	Ile	Leu	Ser	His	Leu	340	345	350	
Leu	Thr	Ser	Ser	Ser	Met	Leu	Pro	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Ile				

Tyr	Asp	Val	Phe	Ser	Leu	Arg	Ser	Leu	Val	Asp	Tyr	Leu	Arg	Ser	Gln
1				5					10					15	
His	Glu	Leu	Ile	Asp	Ile	His	Val	Pro	Val	Asp	Pro	His	Leu	Glu	Ile
			20					25					30		
Ala	Glu	Ile	His	Arg	Arg	Val	Val	Glu	Arg	Glu	Gly	Pro	Ala	Leu	Leu
			35				40					45			
Phe	His	Gln	Val	Lys	Gly	Ser	Pro	Phe	Pro	Val	Leu	Thr	Asn	Leu	Phe
	50					55					60				
Gly	Thr	Arg	Arg	Arg	Val	Asp	Leu	Leu	Phe	Pro	Asp	Leu	Ser	Ser	Asp
65					70					75					80



## (2) INFORMATIONS POUR LA SEQ ID NO: 377:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 137 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 373119..373529

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 377:

Asn	Glu	Lys	Asn	Lys	Thr	Leu	Ile	Ser	Lys	Ile	Met	Phe	Ser	Leu	Val
1				5					10					15	
Ser	Leu	Phe	Val	Gly	Gly	Phe	Leu	Leu	Lys	Ala	Pro	Ala	Pro	Thr	Gln
			20					25					30		
Ser	Ala	Asp	Thr	Phe	Gln	Thr	Leu	Ile	Glu	Ser	Lys	Glu	Pro	Val	Ile
		35					40					45			
Phe	Thr	Lys	Gln	Cys	Gly	Asp	Asn	Val	Thr	Gln	Ile	Leu	Cys	Asp	Ala
	50					55					60				
Ile	Asp	Ser	Ala	Lys	Lys	Asp	Ile	Phe	Leu	Xaa	Ile	Tyr	Asp	Leu	Ser
65					70					75				80	
Ala	Pro	Ala	Ile	Thr	Thr	Ser	Leu	Lys	Lys	Gln	Val	Ser	Ala	Arg	Ile
				85					90					95	
Pro	Val	Cys	Ile	His	Tyr	Gln	Arg	Ile	Ser	Lys	Asn	Ala	Glu	Phe	Ser
			100					105					110		
Gln	Ser	Pro	Tyr	Leu	Thr	Pro	Trp	Glu	Asn	Ile	Leu	Pro	Cys	Thr	Glu
		115					120					125			
Asn	Ser	Cys	Ile	Lys	Lys	Leu	Trp	Gln							
		130					135								

## (2) INFORMATIONS POUR LA SEQ ID NO: 378:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 197 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 373614..374204

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 378:

Lys	Ala	Gln	Lys	Phe	Val	Ile	Leu	Leu	Lys	Arg	Lys	Pro	Leu	Val	Gly
1				5					10					15	
Ala	Leu	Leu	Thr	Ile	Asn	Ser	Ser	Ser	Ile	Val	Ser	Phe	Asp	Gly	Gly
			20					25					30		
Ser	Ser	Ala	Ala	Leu	Glu	Thr	Val	Leu	His	His	Ile	Arg	Ser	Ala	Lys
		35					40					45			
Glu	Ser	Ile	Gln	Val	Gly	Met	Phe	Ala	Leu	Thr	Leu	Pro	Gln	Ile	Ile
	50					55					60				
Ala	Glu	Leu	Asn	Ala	Ala	Gln	Asn	Cys	Gly	Val	Asp	Val	Val	Ile	Leu
65					70					75				80	

Val	Asp	Lys	Gly	Tyr	Lys	Ser	Phe	Thr	Val	Gln	Gln	Ile	Lys	Gln	Leu
				85					90					95	
Glu	His	Pro	Ser	Leu	Ser	Ile	Tyr	Glu	Lys	Val	Thr	Pro	Tyr	Gln	Leu
			100					105					110		
His	His	Lys	Phe	Gly	Ile	Phe	Asp	Lys	Lys	Thr	Leu	Ile	Thr	Gly	Ser
		115					120					125			
Val	Asn	Trp	Ser	Glu	Asn	Gly	Phe	Leu	Ile	Asn	Thr	Glu	Asp	Met	Ile
	130					135					140				
Val	Ile	Glu	Asn	Leu	Thr	Glu	Lys	Gln	Gln	Ser	Lys	Ile	Gln	Ala	Ile
145					150					155					160
Trp	Glu	Gly	Leu	Val	Arg	Glu	Cys	Ala	Leu	Tyr	Tyr	Ser	Pro	Asp	Gln
			165						170					175	
Glu	Glu	Lys	Glu	Lys	Asp	Pro	Leu	Ile	Ile	Pro	Phe	Pro	Pro	Ser	Glu
			180					185					190		
Lys	Lys	Gln	Ala	Ala											
			195												

(2) INFORMATIONS POUR LA SEQ ID NO: 379:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(374224..374736)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 379:

Asn	Glu	Arg	Asn	Arg	Gly	Cys	Arg	Arg	Arg	Phe	Met	Arg	Ile	Ile	Pro
1			5						10					15	
Phe	Asp	Pro	Tyr	Gly	Ser	Met	Ala	Phe	Gln	Ala	Ile	Ala	Lys	Asp	Pro
			20					25					30		
Gln	Glu	Arg	Lys	Asn	Gly	Ser	Ile	Ser	Glu	Lys	Ile	Ser	Glu	Glu	Ile
		35				40						45			
Ala	Arg	Asn	Glu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Ala	Ile	Ala	Asp	Gln
	50					55					60				
Glu	Asp	Lys	Glu	Lys	Lys	Gln	Lys	His	Arg	Phe	Lys	Ile	Leu	Thr	Lys
65					70					75					80
Lys	Gln	Thr	Arg	Met	Leu	Gly	Gln	Leu	Arg	His	Phe	Arg	Leu	Asp	
			85					90					95		
Phe	Gln	Lys	Leu	Gln	Ala	Gly	Val	Val	Ile	Glu	Trp	Ser	Trp	Asp	Asp
			100					105					110		
Lys	Ser	Lys	Arg	Ser	Lys	Ser	Leu	Gly	Ser	Arg	Ile	Thr	Arg	Lys	Ser
		115				120						125			
Lys	Lys	Thr	Ile	Cys	Ile	Ser	Ala	Ala	Ala	Ala	Gln	Ala	Ile	Ala	His
	130					135					140				
Ala	Ala	Glu	Ala	Trp	Val	Ile	Ala	Arg	Asn	Glu	Gly	Ile	Leu	Glu	Met
145				150						155					160
Thr	Leu	Ser	Leu	Phe	Gln	His	Lys	Asp	Asn	Glu					
			165						170						

(2) INFORMATIONS POUR LA SEQ ID NO: 380:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 563 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(374703..376391)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 380:

Glu	Lys	Ile	Met	Ser	Ile	Ser	Gly	Ser	Gly	Asn	Val	Ser	Pro	Ala	Thr	1	5	10	15
Pro	Asp	Phe	Asp	Pro	Ser	Ile	Leu	Met	Gly	Arg	Gln	Ala	Ala	Ser	Ala	20	25	30	
His	Ala	Ala	Lys	Glu	Ala	Ser	Gly	Ala	Ser	Lys	Ala	Thr	Glu	Thr	Ser	35	40	45	
Ala	Ala	Glu	Gln	Gln	Ala	Leu	Ile	Ser	Ser	Gly	Thr	Glu	Leu	Asp	Tyr	50	55	60	
Val	Thr	Asp	Leu	Gln	Gln	Ser	Glu	Gly	Lys	Tyr	Lys	Lys	Thr	Leu	Asp	65	70	75	80
Lys	Thr	Ser	Lys	Ser	Pro	Lys	Thr	Lys	Leu	Lys	Gly	Asn	Phe	Ser	Lys	85	90	95	
Val	Arg	Ala	Gly	Thr	Lys	Gly	Phe	Leu	Thr	Gly	Phe	Gly	Thr	Arg	Ala	100	105	110	
Ser	Arg	Ile	Ser	Ala	Arg	Lys	Ala	Glu	Asn	Asn	Gly	Glu	Gly	Met	Ser	115	120	125	
Met	Ile	Pro	Ser	Gln	Met	Glu	Tyr	Val	Lys	Lys	Lys	Gly	Asn	Arg	Val	130	135	140	
Ser	Pro	Glu	Met	Gln	Asn	Phe	Tyr	Leu	Gly	Ala	Ser	Gly	Leu	Trp	Ser	145	150	155	160
Pro	Thr	Ser	Asp	Val	Ser	Ser	Lys	Thr	Glu	Asn	Arg	Leu	Gly	Ala	Thr	165	170	175	
Ala	Leu	Ser	Thr	Thr	Pro	Ser	Leu	Thr	Thr	Met	Gln	Asp	Pro	Val	Ser	180	185	190	
Ile	Glu	His	Leu	Ser	Ser	Gly	Glu	Ile	Thr	Ala	Leu	Ala	Ser	Phe	Asn	195	200	205	
Pro	Asn	Val	Arg	Ala	Ala	Ser	Leu	Asn	Glu	Gln	Thr	Ile	Asn	Ala	Trp	210	215	220	
Thr	Glu	Ala	Arg	Leu	Gly	Gly	Glu	Met	Val	Ser	Thr	Leu	Leu	Asp	Pro	225	230	235	240
Asn	Ile	Glu	Thr	Ser	Ser	Leu	Leu	Arg	Arg	Ala	Pro	Thr	Val	Ser	Asn	245	250	255	
Glu	Gly	Met	Val	Asp	Val	Ser	Asp	Met	Gly	Asn	Gln	Thr	Thr	Ser	Leu	260	265	270	
Ser	Met	Glu	Gly	Leu	Val	Asn	Thr	Val	Val	Asp	Asp	Pro	Ala	Ser	Ala	275	280	285	
Glu	Glu	Glu	Lys	Lys	Thr	Gly	Glu	Leu	Ser	Leu	Glu	Glu	Met	Ala	Ala	290	295	300	
Met	Ala	Lys	Met	Met	Ala	Ala	Leu	Leu	Ser	Ser	Gly	Gln	Gly	Met	Ala	305	310	315	320
Val	Phe	Ile	Ala	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ser	Thr	Gln	Phe	Pro	325	330	335	
Glu	Pro	Lys	Phe	Ser	Gly	Thr	Ile	Pro	His	His	Phe	Ser	Lys	Lys	Glu	340	345	350	
Asp	Asn	Glu	Thr	Ile	Trp	Gly	Leu	Asp	Ser	Gln	Ile	Gly	Ser	Ile	Ala	355	360	365	
Phe	Asp	Thr	Arg	Arg	Glu	Asn	Asn	Ala	Ser	Pro	Leu	Pro	Thr	Thr	Ser	370	375	380	

```

Leu His Glu Glu Ala Ser Tyr Arg Phe Pro Val Gly Glu Ala Pro Leu
385                               390                               395                               400
Asp Val Asn Glu Ile Pro Phe Ala Val Gln His Ser Thr Val Phe Ser
                               405                               410                               415
Glu Glu Thr Ala Asn Thr Glu Gln Ala Leu Ile Gln Asn Glu Ser Leu
                               420                               425                               430
Gly Glu Ile Pro Val Ser Ala Glu Val Val Gly Gln Asp Thr Val Ser
                               435                               440                               445
Ser Ala Tyr Gln Phe Pro Ser His Leu Gly Met Ala Val Leu Ala Ser
                               450                               455                               460
Val Pro Leu Ser Thr Glu Asp Tyr Lys Thr Ala Val Glu His Arg Lys
465                               470                               475                               480
Gly Pro Gly Gly Pro Asp Pro Leu Ile Tyr Gln Tyr Arg Asn Val
                               485                               490                               495
Ala Val Asp Pro Ala Ile Ile Phe Gln Ser Pro Ser Pro Phe Ser Val
                               500                               505                               510
Ser Ser Arg Phe Ser Val Gln Gly Lys Pro Glu Ala Val Ala Val Tyr
                               515                               520                               525
Asn Asp Asp Gln Glu Glu Ala Gly Gly Asn Arg Asp Ser Asp Glu
                               530                               535                               540
Gly Lys Asp Gln Glu Gln Asp Lys Thr Arg Glu Thr Glu Asp Ala Gly
545                               550                               555                               560
Gly Asp Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 381:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(376748..377038)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 381:

```

Met Lys Lys Arg Ser Ser Arg Lys Leu Ala Gln Val Ile Gly Arg Lys
1                               5                               10                               15
Thr Gly Asn Tyr Phe Pro Ala Ser Ile Glu Gly Glu Thr Lys Lys Glu
                               20                               25                               30
His Lys Arg Tyr Tyr Ser Thr Ala Ser Lys Glu Lys Glu Ser Leu Arg
                               35                               40                               45
Lys Arg Ala Lys Glu Phe Asp Val Leu Val His Ser Leu Leu Asp Lys
50                               55                               60
His Val Pro Gln Asn Ser Asp Gln Val Leu Ile Phe Thr Tyr Gln Asn
65                               70                               75                               80
Gly Phe Val Glu Thr Asp Phe His Asn Phe Gly Arg Tyr Ser Val Lys
                               85                               90                               95
Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 382:

(i) CARACTERISTIQUES DE LA SEQUENCE:



(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 377853..378737

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 382:

Asn	His	Leu	Thr	Lys	Tyr	Leu	Cys	Met	Leu	Leu	Lys	Gly	Ala	Pro	Ala
1				5					10					15	
Ala	Asp	His	Ile	Leu	Ala	Thr	Ile	Lys	Glu	Asn	Ile	Arg	Ala	Cys	Ser
			20					25					30		
Lys	Ala	Pro	Gly	Leu	Ala	Val	Val	Leu	Ile	Gly	Asn	Asn	Pro	Ala	Ser
		35					40					45			
Glu	Ile	Tyr	Val	Asn	Met	Lys	Ile	Lys	Arg	Ala	Thr	Asp	Leu	Gly	Met
	50				55						60				
Val	Ser	Lys	Ser	Tyr	Arg	Lys	Pro	Ser	Asp	Ala	Thr	Leu	Ser	Asp	Ile
65					70					75					80
Leu	Ala	Leu	Ile	His	Gln	Leu	Asn	Asn	Asp	Glu	Asn	Ile	His	Gly	Ile
				85					90					95	
Leu	Val	Gln	Leu	Pro	Leu	Pro	Lys	His	Leu	Asp	Ala	Gln	Ala	Ile	Leu
		100						105					110		
Ser	Thr	Ile	Thr	Pro	Asp	Lys	Asp	Val	Asp	Gly	Leu	His	Pro	Val	Asn
	115						120					125			
Val	Gly	Lys	Leu	Leu	Leu	Gly	Glu	Thr	Asp	Gly	Phe	Ile	Pro	Cys	Thr
	130					135					140				
Pro	Ala	Gly	Ile	Val	Glu	Leu	Cys	Lys	Tyr	Tyr	Glu	Ile	Pro	Leu	His
145					150					155					160
Gly	Lys	His	Val	Val	Ile	Leu	Gly	Arg	Ser	Asn	Ile	Val	Gly	Lys	Pro
				165					170					175	
Leu	Ala	Ala	Leu	Leu	Met	Gln	Arg	His	Ala	Asp	Thr	Asn	Ala	Ser	Val
			180					185					190		
Thr	Leu	Leu	His	Ser	Gln	Ser	Glu	His	Leu	Thr	Glu	Ile	Thr	Arg	Thr
	195						200					205			
Ala	Asp	Ile	Leu	Ile	Ser	Ala	Ile	Gly	Val	Pro	Leu	Phe	Val	Asn	Lys
	210					215					220				
Glu	Met	Ile	Ala	Glu	Lys	Thr	Val	Ile	Met	Asp	Val	Gly	Thr	Ser	Arg
225					230					235					240
Ile	Pro	Ala	Ala	Asn	Pro	Lys	Gly	Tyr	Ile	Leu	Val	Gly	Asp	Val	Asp
				245					250					255	
Phe	Asn	Asn	Val	Val	Pro	Val	Cys	Arg	Ala	Ile	Thr	Pro	Val	Pro	Gly
			260					265					270		
Gly	Val	Gly	Pro	Met	Thr	Val	Ala	Met	Leu	Met	Arg	Asn	Thr	Trp	Glu
		275					280					285			
Ser	Phe	Leu	Arg	His	Thr	Ser									
	290					295									

(2) INFORMATION POUR LA SEQ ID NO: 383:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 141 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 383:

(2) INFORMATION POUR LA SEQ ID NO: 384:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 379017..379403

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 384:

[illegible]

## (2) INFORMATIONS POUR LA SEQ ID NO: 385:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 123 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(379641..380009)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 385:

Gln	Glu	Gln	Lys	Leu	Asn	Ser	Leu	Arg	Asp	His	Gly	Gly	Asn	Leu	Gly
1				5					10					15	
Asp	Ala	Tyr	Val	Thr	Ile	Ser	Lys	Gly	Glu	Ala	Trp	Leu	Leu	Gln	Ser
			20					25					30		
Ser	Ile	Ala	Pro	Tyr	Arg	Phe	Gly	Asn	Ile	Asn	Asn	His	Glu	Glu	Arg
		35					40					45			
Arg	Lys	Arg	Lys	Leu	Leu	Leu	His	Lys	Tyr	Glu	Ile	His	Lys	Leu	Asp
	50					55				60					
Ala	Arg	Ile	Ser	Gln	Lys	Gly	Leu	Thr	Val	Val	Pro	Leu	Ser	Phe	Phe
65				70					75					80	
Phe	Ser	Lys	Gly	Phe	Val	Lys	Val	Arg	Ile	Gly	Cys	Cys	Arg	Gly	Lys
			85					90					95		
Lys	Ala	His	Asp	Lys	Arg	Gln	Ser	Ile	Ile	Glu	Arg	Glu	Lys	Asn	Arg
			100				105						110		
Glu	Leu	Ala	Ala	Ala	Met	Lys	Arg	Ser	Cys	Arg					
		115					120								

## (2) INFORMATIONS POUR LA SEQ ID NO: 386:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 366 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 380373..381470

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 386:

Met	Lys	Phe	Val	Ile	Ser	Arg	Asn	Glu	Leu	Gly	Asn	Leu	Ile	Lys	Lys
1				5					10					15	
Val	Gln	Asn	Val	Val	Pro	Gln	Ser	Thr	Pro	Ile	Pro	Val	Leu	Thr	His
			20					25					30		
Val	Leu	Ile	Glu	Ser	Cys	Asn	Asp	Glu	Leu	Val	Phe	Thr	Ala	Thr	Asp
		35					40					45			
Leu	Thr	Val	Ser	Thr	Arg	Cys	Val	Val	Lys	Ala	Lys	Val	Tyr	Glu	Ser
	50					55			60						
Gly	Ser	Val	Thr	Ile	Pro	Ser	Arg	Arg	Phe	Phe	Gln	Leu	Ile	Arg	Glu
65				70					75					80	
Leu	Thr	Glu	Ala	Asn	Ile	Glu	Val	Ala	Ala	His	Ser	Gly	Glu	Met	Ala
			85					90						95	

```

Thr Ile Thr Ser Gly Ser Ser Cys Phe Arg Leu Leu Ser Met Gly Lys
      100      105      110
Glu Asp Phe Pro Met Leu Pro Asp Met Gln Asn Ala Leu Arg Phe Thr
      115      120      125
Leu Asp Ser Glu Arg Leu Lys Asp Met Phe Gln Arg Thr Ser Phe Ala
      130      135      140
Val Ser Arg Glu Glu Ser Arg Tyr Val Leu Thr Gly Val Leu Leu Ser
145      150      155      160
Ile Ala Asn Gly Thr Met Thr Val Val Gly Thr Asp Gly Lys Arg Leu
      165      170      175
Ala Lys Ile Asp Thr Glu Ile Ser Leu Asp Pro Ser Phe Ser Gly Asp
      180      185      190
Tyr Ile Ile Pro Ile Lys Ala Val Glu Glu Ile Ile Arg Met Ser Ser
195      200      205
Glu Asp Val Gln Ser Thr Ile Phe Leu Asp Gln Thr Lys Ile Ala Val
210      215      220
Glu Cys Gly Asn Thr Leu Leu Val Thr Lys Leu Leu Ser Gly Glu Phe
225      230      235      240
Pro Asp Phe Ser Pro Val Ile Ser Thr His Ser Ser Val Gln Leu Asp
      245      250      255
Leu His Arg Glu Glu Leu Ile Ser Leu Leu Lys Gln Val Ala Leu Phe
260      265      270
Thr Asn Glu Ser Ser His Ser Val Lys Phe Ser Phe Ser Pro Gly Glu
275      280      285
Leu Thr Leu Thr Ala Asn Cys Thr Lys Val Gly Glu Gly Lys Val Ser
290      295      300
Met Ala Val Asn Tyr Thr Gly Glu Thr Leu Glu Ile Ala Phe Asn Pro
305      310      315      320
Phe Phe Phe Leu Asp Ile Leu Lys His Ser Arg Asp Glu Leu Val Gln
      325      330      335
Leu Gly Ile Ser Asp Ser Tyr Asn Pro Gly Ile Ile Thr Asp Ser Thr
340      345      350
Arg Ser Leu Phe Val Ile Met Pro Met Arg Leu His Asp Asp
355      360      365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 387:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: 381473..382567

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 387:

```

Met Arg Val Leu Ser Leu Phe Leu Lys Asp Phe Arg Asn Tyr Thr Asp
1      5      10      15
Leu Arg Leu Glu Leu Gly Pro Glu Met Asn Ser Ile Phe Gly Leu Asn
20      25      30
Ala Gln Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Ile Leu Ser Leu
35      40      45
Gly Arg Ser Phe Arg Thr Ser Arg Leu Thr Asp Ala Ile Arg Phe Gly
50      55      60
Ala Ser His Phe Phe Ile Glu Ala Val Phe Ser His Lys Glu Val Phe

```

65					70					75					80
His	Thr	Leu	Ser	Ile	Gln	Val	Asp	Lys	Lys	Gly	Lys	Lys	Ile	Leu	Phe
				85					90					95	
Asp	Gly	Ala	Pro	Ile	Thr	Lys	Leu	Ser	Glu	Leu	Val	Gly	Leu	Phe	Pro
			100					105					110		
Val	Ile	Leu	Phe	Ser	Ile	Lys	Asp	Ile	Ala	Ile	Ile	Glu	Gly	Ser	Pro
		115					120					125			
Ser	Glu	Arg	Arg	Arg	Phe	Leu	Asp	Leu	Leu	Leu	Ala	Gln	Ala	Ser	Asp
	130					135					140				
Lys	Tyr	Thr	Glu	His	Ile	Ser	Leu	Tyr	His	Lys	Ala	Leu	Asp	Gln	Arg
145					150					155					160
Asn	Ala	Ser	Ile	Lys	Ala	Gln	Asn	Gln	Lys	Ala	Ile	Ser	Ala	Trp	Asn
			165						170					175	
Ser	Pro	Leu	Ile	Ala	Tyr	Gly	Ser	Leu	Val	Ala	Phe	Leu	Arg	Asn	Glu
			180					185					190		
Cys	Thr	Lys	Lys	Leu	Asn	Thr	Ile	Phe	Gln	Thr	Leu	Trp	Asp	Asn	Thr
	195						200					205			
Leu	Lys	Glu	Thr	Leu	Ser	Leu	Arg	Tyr	Glu	Ser	Ser	Leu	Ile	Thr	Glu
	210					215					220				
Glu	Ser	Pro	Thr	Leu	Asn	Asp	Ile	Ala	Ser	Asn	Tyr	Tyr	Glu	Gln	Leu
225					230					235					240
Arg	Ile	Ala	Asn	Thr	Lys	Asp	Leu	Asp	Leu	Gly	Tyr	Thr	Met	Val	Gly
			245						250					255	
Pro	His	Arg	Asp	Glu	Leu	Leu	Leu	Thr	Ile	Asn	Asp	Leu	Pro	Val	Ala
			260					265					270		
Lys	Phe	Ser	Ser	Glu	Gly	Gln	Lys	His	Ser	Leu	Leu	Ala	Val	Leu	Arg
	275						280					285			
Phe	Ala	Glu	Cys	Val	Tyr	Leu	Gln	Glu	Glu	Phe	Cys	Ile	His	Pro	Leu
	290					295				300					
Leu	Cys	Met	Asp	Asp	Ile	His	Ala	Cys	Leu	Asp	Gln	Gln	Arg	Leu	Asp
305					310					315					320
Gln	Leu	Leu	Gln	Leu	Ser	Asn	Ser	Leu	Gly	Gln	Val	Val	Thr	Thr	Ser
			325						330					335	
Thr	Ile	Cys	Pro	Asp	His	Arg	Ser	Thr	Thr	Ser	Cys	Ile	Phe	His	Val
			340				345					350			
Thr	Gln	Ala	Gln	Val	Ser	Leu	Val	Ala	Pro	Gln	Ser	Leu			
	355					360						365			

(2) INFORMATIONS POUR LA SEQ ID NO: 388:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 333 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 382704..383702

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 388:

Asn	Asn	Ile	Asn	Arg	Cys	Cys	Glu	Met	Lys	Asn	Phe	Leu	Leu	Thr	Ile
1			5				10					15			
Leu	Phe	Leu	Leu	Met	Gly	Thr	Ser	Leu	Leu	Ala	Asp	Pro	Ser	Val	Ile
		20					25					30			
Gln	Thr	Leu	Thr	Ser	Gly	Val	Ala	Gly	Val	Asn	Ser	Ile	Arg	Glu	Glu
	35					40						45			

```

Lys Glu Ser Val Val Cys Val His Ala Phe Leu Arg Ser Tyr Gly Ser
 50          55          60
Leu Lys Pro Ile Gly Arg Val Leu Glu Lys Glu Asn Tyr Asp Val Phe
65          70          75          80
Ile Trp Asn Tyr Glu Thr Arg Lys Phe Thr Leu Glu Lys His Ala Glu
          85          90          95
His Leu Val Arg Leu Leu Asn Lys Ile Ala Glu Leu Lys Pro Gly Ile
          100          105          110
Pro Ile Asn Phe Val Thr His Ser Val Gly Gly Val Ile Val Arg Val
          115          120          125
Ala Leu Ala His Pro Asp Cys Pro Glu Glu Ala Lys Lys Gly Lys Ala
130          135          140
Val Leu Met Ala Pro Pro Asn Ala Gly Ser Thr Leu Ala Arg Arg Tyr
145          150          155          160
Ser Arg Ser Ser Leu Val Gln Phe Val Phe Gly Arg Lys Leu Gly Met
          165          170          175
Gln Leu Leu Thr Tyr Ser Pro Glu His Met Leu Asn Ile Ala Lys Met
          180          185          190
Pro Ser Ser Val Asp Val Leu Val Leu Ser Gly Thr Lys Lys Ser Lys
          195          200          205
Phe Leu Leu Phe Gln Leu Glu Asp Asn Asp Gly Lys Val Cys Val
210          215          220
Thr Glu Thr Arg Leu Asp Thr Pro His Gln Asn Tyr Ile Ile Asp Ala
225          230          235          240
Asn His Thr Tyr Ile Ile Thr Asn Lys Thr Ser Leu Phe Leu Met Arg
          245          250          255
Glu Phe Leu Arg Asn Gly Ser Arg Ser Ser Ala Leu Thr Gln Val Pro
          260          265          270
Glu Glu Ile Glu Ala Ser Ile Gln Gln Ser Pro Lys Ala Lys Val Asn
          275          280          285
Lys Glu Lys Ser Lys Asp Ile Tyr Val Ile His Cys Leu Gly Ala His
290          295          300
Pro Tyr Ser Leu Tyr Gly Phe Pro Lys Ser Arg Thr Ser Pro Asn Glu
305          310          315          320
Asn Ser Arg Lys Val Leu Glu Gly Gln Glu Tyr Lys Lys
          325          330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 389:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(383655..383945)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 389:

```

Trp Leu Ser Gly Pro Val Gly Ile Val Arg Ile Leu His Thr Gly Trp
1          5          10          15
Ser Val Gly Ile Pro Glu Ala Leu Ala Trp Ile Gly Leu Ile Ser Val
          20          25          30
Asn Leu Ala Val Leu Asn Leu Leu Pro Ile Pro Val Leu Asp Gly Gly
          35          40          45
Tyr Ile Leu Leu Cys Leu Trp Glu Ile Leu Ser Arg Arg Arg Leu Asn

```

50					55					60				
Met	Arg	Leu	Val	Glu	Lys	Ala	Leu	Val	Pro	Phe	Met	Ile	Leu	Leu
65					70					75				80
Leu	Phe	Phe	Val	Phe	Leu	Thr	Leu	Gln	Asp	Leu	Ser	Arg	Val	Phe
				85					90					95
Gly														

(2) INFORMATIONS POUR LA SEQ ID NO: 390:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(383949..385217)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 390:

Val	Ala	Leu	Glu	Ala	Asp	Phe	Cys	Phe	Ser	Arg	Arg	Pro	Leu	Ala	Asn
1				5					10					15	
Leu	Leu	Val	Ala	Ile	Phe	Val	Phe	Gly	Ile	Leu	Tyr	Phe	Ser	Gly	Gly
			20					25					30		
Arg	Thr	Lys	Ser	Phe	Ser	Glu	His	Thr	Ser	Ile	Val	Gly	Trp	Val	His
		35					40					45			
Pro	Ser	Leu	Glu	Gln	Gln	Gly	Leu	His	Ala	Gly	Asp	Gln	Ile	Phe	Phe
	50					55					60				
Cys	Asn	Gly	Gln	Pro	Tyr	Ser	Gly	His	Lys	Met	Ala	Phe	Ser	Ser	Ser
65					70					75					80
Leu	Leu	Glu	Arg	Lys	Leu	Ser	Leu	Gln	Gly	Gln	His	Pro	Ala	Tyr	Phe
				85					90					95	
Ser	Glu	Ser	Glu	Ala	Phe	Ser	Leu	Glu	Ala	Pro	Phe	Asn	Pro	Asp	Met
			100					105					110		
Glu	Gly	Val	Pro	Cys	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	Tyr	Arg	Gly	Ser
		115				120						125			
Asp	Pro	Leu	Pro	Glu	Lys	Ser	Pro	Leu	Val	Asp	Ala	Gly	Leu	Ser	Glu
	130					135					140				
Gly	Asp	Arg	Leu	Val	Trp	Met	Asp	Gly	Leu	Leu	Val	Phe	Ser	Gly	Ala
145					150					155					160
Gln	Val	Ser	Gln	Met	Leu	Asn	Glu	Lys	Gln	Ser	Phe	Leu	Arg	Val	Glu
			165						170					175	
Arg	Gln	Gly	Lys	Val	Val	Phe	Val	Arg	Gln	Ala	Arg	Val	Leu	Ala	Gly
			180					185					190		
Asp	Leu	Thr	Leu	Thr	Pro	Tyr	Phe	Lys	Asn	Glu	Leu	Ile	Asp	Cys	Gln
	195					200						205			
Tyr	Glu	Ala	Gly	Leu	Lys	Gly	Lys	Trp	Ala	Ser	Leu	Tyr	Met	Leu	Pro
	210					215					220				
Tyr	Ile	Ile	Asn	Gly	Asp	Gly	Phe	Val	Glu	Ser	Lys	Val	Lys	Leu	Leu
225					230					235					240
Asn	Asn	Glu	Arg	Val	Ser	Leu	Asp	Tyr	Asn	Leu	Glu	Leu	Gly	Asp	Lys
				245					250					255	
Ile	Val	Ala	Val	Asp	Gly	Ile	Pro	Val	Met	Ser	Asn	Ala	Asp	Ile	Leu
		260						265					270		
Arg	Leu	Val	Gln	Asp	His	Arg	Val	Ser	Leu	Ile	Phe	Gln	Arg	Met	Ser
		275					280						285		

```

Pro Glu Gln Leu Thr Val Leu Glu Gln Lys Ala Ala Asp Gln Ala Phe
  290                295                300
Ile Asn Ser Tyr Asp Met Asp Asp Leu Leu Arg Val Ala Glu Ser Val
305                310                315                320
Gly Glu Glu Arg Glu Val Ser Arg Leu Gly Asp Tyr Arg Leu Val Thr
                325                330                335
Arg Val Gln Pro Arg Pro Trp Ala His Ile Tyr Ser Glu Ala Leu Leu
                340                345                350
Asp Lys Gln Arg Ala Leu Ala Ser Lys Phe Arg Asp Glu Gln Glu Arg
                355                360                365
Arg Tyr Tyr Leu Glu Arg Ile Glu Ala Glu Asn Gln Arg Ile Ser Leu
                370                375                380
Gly Ile Pro Leu Arg Ser Ser Arg Ser Val Gln Ser Gly Ser Leu Gly
385                390                395                400
Ile Asp Gly Gly Ile Arg Phe Arg Gln Leu Lys Asp Cys Glu Ser Leu
                405                410                415
Gly Asp Gly Ala Gly Glu Pro
                420

```

(2) INFORMATIONS POUR LA SEQ ID NO: 391:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(385178..385507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 391:

```

Met Thr Ile Ile Tyr Phe Val Leu Ala Ala Leu Ala Leu Gly Phe Leu
  1                5                10                15
Ile Leu Ile His Glu Leu Gly His Leu Leu Ala Ala Lys Ala Val Gly
                20                25                30
Met Ser Val Glu Ser Phe Ser Ile Gly Phe Gly Pro Ala Leu Val Arg
                35                40                45
Lys Lys Ile Gly Ser Val Glu Tyr Arg Ile Gly Ala Ile Pro Phe Gly
  50                55                60
Gly Tyr Val Arg Ile Lys Gly Met Asp Arg Asn Asp Lys Asp Asn Ser
65                70                75                80
Gly Asp Lys Glu Lys Thr Val Tyr Asp Ile Pro Glu Gly Phe Phe Ser
                85                90                95
Lys Ser Pro Trp Lys Arg Ile Phe Val Leu Ala Ala Gly Leu
                100                105                110

```

(2) INFORMATIONS POUR LA SEQ ID NO: 392:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 380 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: complement(385706..386845)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 392:

Leu	Leu	Lys	His	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Arg	1	5	10	15
Gln	Val	Leu	Gln	Val	Val	Arg	Ser	Ile	Pro	Asp	Thr	Phe	Ile	Ile	Glu	20	25	30	
Thr	Leu	Ala	Ala	Tyr	Gly	Arg	Asn	Gln	Glu	Ala	Leu	Ile	Ser	Gln	Ile	35	40	45	
Arg	Glu	Phe	Asn	Pro	Arg	Val	Val	Ala	Val	Arg	Glu	Glu	Thr	Thr	Tyr	50	55	60	
Lys	Glu	Leu	Arg	Lys	Leu	Phe	Pro	His	Ile	Glu	Ile	Leu	Leu	Gly	Glu	65	70	75	80
Glu	Gly	Leu	Val	Ser	Val	Ala	Thr	Glu	Pro	Ser	Val	Thr	Ile	Thr	Ile	85	90	95	
Val	Ala	Ser	Ser	Gly	Ile	Asp	Ala	Leu	Pro	Ala	Val	Ile	Ala	Ala	Ile	100	105	110	
Arg	Gln	Lys	Lys	Thr	Ile	Ala	Leu	Ala	Asn	Lys	Glu	Ser	Leu	Val	Ala	115	120	125	
Ala	Gly	Glu	Leu	Val	Thr	Thr	Leu	Ala	Arg	Glu	Asn	Gly	Val	Gln	Ile	130	135	140	
Leu	Pro	Ile	Asp	Ser	Glu	His	Asn	Ala	Leu	Phe	Gln	Cys	Leu	Glu	Gly	145	150	155	160
Arg	Asp	Ser	Ser	Thr	Ile	Lys	Lys	Leu	Leu	Leu	Thr	Ala	Ser	Gly	Gly	165	170	175	
Pro	Leu	Arg	Asn	Lys	Ser	Lys	Glu	Glu	Leu	Gln	Lys	Val	Ser	Leu	Gln	180	185	190	
Glu	Val	Leu	Arg	His	Pro	Val	Trp	Asn	Met	Gly	Pro	Lys	Ile	Thr	Val	195	200	205	
Asp	Ser	Ser	Thr	Leu	Val	Asn	Lys	Gly	Leu	Glu	Ile	Glu	Ala	Phe		210	215	220	
Trp	Leu	Phe	Gly	Leu	Glu	Ala	Val	Glu	Ile	Glu	Ala	Val	Ile	His	Pro	225	230	235	240
Gln	Ser	Leu	Val	His	Gly	Met	Val	Glu	Phe	Cys	Asp	Gly	Thr	Ile	Leu	245	250	255	
Ser	Val	Met	Lys	Pro	Pro	Ser	Met	Leu	Phe	Pro	Ile	Gln	His	Val	Leu	260	265	270	
Thr	Phe	Pro	Glu	Arg	Ser	Pro	Ala	Ile	Gly	Pro	Gly	Phe	Asp	Phe	Leu	275	280	285	
Ser	Asn	Arg	Thr	Leu	Glu	Phe	Pro	Ile	Asp	Glu	Asp	Arg	Phe	Pro		290	295	300	
Ser	Val	His	Leu	Ala	Lys	Arg	Val	Leu	Leu	Glu	Lys	Gly	Ser	Met	Gly	305	310	315	320
Cys	Phe	Phe	Asn	Gly	Ala	Asn	Glu	Ala	Leu	Val	His	Arg	Phe	Leu	Ala	325	330	335	
Gly	Glu	Ile	Ser	Trp	His	Gln	Ile	Val	Pro	Lys	Leu	Gln	Ala	Leu	Val	340	345	350	
Asp	Gln	His	Arg	Val	Gln	Ser	Cys	Leu	Ser	Leu	Glu	Glu	Ile	Leu	Ser	355	360	365	
Val	Asp	Ala	Glu	Ala	Arg	Ala	Arg	Ala	Gln	Glu	Cys					370	375	380	

(2) INFORMATIONS POUR LA SEQ ID NO: 393:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 167 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 386127..386627

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 393:

Gly	Trp	Ile	Thr	Ala	Ser	Ile	Ser	Thr	Ala	Ser	Ser	Pro	Asn	Ser	Gln
1				5					10					15	
Lys	Ala	Ser	Ile	Ile	Ser	Lys	Pro	Leu	Phe	Thr	Lys	Val	Glu	Glu	Ser
			20					25					30		
Thr	Val	Ile	Leu	Gly	Pro	Ile	Phe	Gln	Thr	Gly	Cys	Arg	Lys	Thr	Ser
			35				40					45			
Cys	Lys	Glu	Thr	Phe	Cys	Asn	Ser	Ser	Phe	Asp	Leu	Phe	Leu	Asn	Gly
	50					55					60				
Pro	Pro	Glu	Ala	Val	Asn	Asn	Asn	Phe	Leu	Met	Val	Glu	Glu	Ser	Leu
65					70					75					80
Pro	Ser	Lys	His	Trp	Lys	Ser	Ala	Leu	Cys	Ser	Leu	Ser	Met	Gly	Arg
				85					90					95	
Ile	Cys	Thr	Pro	Phe	Ser	Leu	Ala	Lys	Val	Val	Thr	Asn	Ser	Pro	Ala
			100					105					110		
Ala	Thr	Asn	Asp	Ser	Leu	Leu	Ala	Lys	Ala	Ile	Val	Phe	Phe	Cys	Arg
			115				120					125			
Ile	Ala	Ala	Met	Thr	Ala	Gly	Lys	Ala	Ser	Ile	Pro	Asp	Glu	Ala	Thr
	130					135					140				
Met	Val	Ile	Val	Thr	Glu	Gly	Ser	Val	Ala	Thr	Glu	Thr	Asn	Pro	Ser
145					150					155					160
Ser	Pro	Lys	Arg	Ile	Ser	Ile									
				165											

(2) INFORMATIONS POUR LA SEQ ID NO: 394:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 167 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(386872..387372)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 394:

Gly	Pro	Ser	Leu	Ser	Leu	Val	Met	Arg	Xaa	Phe	Thr	Lys	Thr	Asp	Ile
1				5					10					15	
Leu	Pro	Ile	Phe	Leu	Val	Leu	Leu	Ile	Asn	Leu	Gly	Ile	Ser	Tyr	Cys
			20					25					30		
Phe	Phe	Ser	Ser	Phe	Val	Cys	Val	Ser	Phe	Asp	Thr	Ile	Phe	Ala	Phe
			35				40					45			
Ser	Leu	Gly	Ile	Arg	Val	Arg	Leu	Val	Asp	Tyr	Leu	Val	Met	Leu	Leu
	50					55					60				
Leu	Ser	Ala	Ser	Ile	Val	Gly	Ala	Phe	Lys	Ala	Val	Gly	Val	Leu	Met
65				70						75					80
Ser	Leu	Ala	Phe	Leu	Leu	Ile	Pro	Gly	Leu	Ile	Ala	Lys	Leu	Ile	Ala

				85					90					95					
Ser	Ser	Val	Gln	Glu	Met	Met	Val	Tyr	Ser	Met	Val	Phe	Gly	Gly	Leu				
			100					105					110						
Ala	Ala	Leu	Ile	Ala	Pro	Ala	Leu	Ser	Arg	Ser	Ile	Leu	Ser	Val	Tyr				
		115					120					125							
Gly	Ile	Gly	Leu	Ser	Thr	Ser	Gly	Leu	Ala	Val	Gly	Leu	Leu	Leu	Val				
	130					135					140								
Phe	Tyr	Val	Val	Met	Leu	Val	Phe	Val	Cys	Ser	Lys	Arg	Ala	Ile	Met				
145					150				155						160				
Leu	Arg	Gln	Lys	Leu	Asp	Lys													
				165															

(2) INFORMATIONS POUR LA SEQ ID NO: 395:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(387338..387724)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 395:

Leu	Tyr	Ile	Asp	Asp	Ile	Gln	Val	Ile	Val	Phe	Phe	Ala	Ile	Ala	Val				
1				5					10					15					
Ser	Cys	Ser	Val	Val	Gly	Thr	Phe	Leu	Val	Leu	Lys	Lys	Met	Ala	Met				
		20						25					30						
Tyr	Ala	Asn	Val	Val	Ser	His	Thr	Ile	Leu	Phe	Gly	Leu	Val	Cys	Val				
		35					40					45							
Cys	Leu	Phe	Thr	His	Gln	Leu	Ile	His	Leu	Ser	Met	Gln	Ala	Leu	Thr				
	50					55				60									
Ile	Ala	Ala	Val	Ser	Thr	Thr	Leu	Leu	Thr	Gly	Ala	Ser	Ile	His	Phe				
65					70					75				80					
Leu	Arg	Asn	Val	Phe	Lys	Val	Ala	Glu	Glu	Ala	Ser	Thr	Ala	Leu	Val				
				85				90					95						
Phe	Ser	Leu	Leu	Phe	Ser	Ala	Ser	Leu	Leu	Leu	Val	Phe	Leu	Thr					
		100						105					110						
Arg	Asn	Ala	His	Val	Gly	Thr	Glu	Leu	Val	Ile	Gly	Asn	Ala	Asp	Xaa				
		115					120					125							
Tyr																			

(2) INFORMATIONS POUR LA SEQ ID NO: 396:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(387816..388250)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 396:

Leu	Phe	Ser	Arg	Asp	Glu	Glu	His	Leu	Leu	Lys	Ile	Phe	Trp	Tyr	Leu
1				5					10					15	
Arg	Glu	Gln	Asn	Thr	Tyr	Gln	Val	Gly	Val	Arg	Asp	Phe	Val	Arg	Ser
			20					25					30		
Arg	Lys	Tyr	Gln	Glu	Tyr	Phe	Gly	Asp	Lys	Val	Phe	Pro	Arg	Phe	Arg
		35					40					45			
Met	Phe	Leu	Leu	Cys	Lys	Lys	Gly	Leu	Val	Ser	Cys	Ser	Glu	His	Gln
	50					55					60				
Trp	Ser	Leu	Thr	Asp	Lys	Gly	Leu	Ala	Arg	Ala	Lys	Leu	Val	Arg	
65					70					75				80	
Ala	His	Arg	Leu	Trp	Glu	Ser	Tyr	Leu	Val	Ser	Gln	Leu	Gly	Phe	Asn
				85					90					95	
Lys	Asn	Glu	Val	His	His	Phe	Ala	Glu	Glu	Met	Glu	His	Val	Leu	Thr
			100					105					110		
Asp	Glu	Leu	Asp	Ser	Thr	Leu	Ser	Gln	Met	Leu	Gln	Asp	Pro	Asp	Tyr
		115					120					125			
Asp	Pro	His	Gln	Arg	Glu	Ile	Pro	Lys	Arg	Thr	Arg	Lys	Ser	Asp	Gly
	130					135					140				
Cys															
145															

## (2) INFORMATIONS POUR LA SEQ ID NO: 397:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 311 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(388237..389169)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 397:

Met	Leu	Ser	Cys	Ile	Phe	Gln	Asp	Thr	Ile	Phe	Leu	Ser	Ser	Phe	Leu
1				5					10					15	
Ala	Val	Ser	Leu	Ile	Cys	Met	Thr	Thr	Ala	Leu	Trp	Gly	Thr	Ile	Leu
			20					25					30		
Leu	Val	Glu	Arg	Gln	Pro	Leu	Leu	Ser	Glu	Ser	Leu	Ser	His	Ala	Cys
		35					40					45			
Tyr	Pro	Gly	Leu	Leu	Ile	Gly	Ala	Leu	Leu	Ser	Tyr	Lys	Val	Pro	Ala
	50					55					60				
Phe	Ser	Asp	Ser	Leu	Trp	Val	Ile	Ile	Phe	Phe	Gly	Cys	Leu	Ala	Ser
65					70					75				80	
Val	Leu	Gly	Cys	Leu	Gly	Ile	Ser	Phe	Leu	Glu	Lys	Lys	Leu	Ala	Met
			85						90					95	
His	Lys	Asp	Ser	Ala	Leu	Cys	Leu	Val	Leu	Val	Ser	Phe	Phe	Gly	Val
			100					105					110		
Gly	Val	Ile	Leu	Val	Ser	Tyr	Val	Lys	Asp	Cys	Cys	Pro	Leu	Leu	Tyr
		115					120					125			
Asn	Lys	Ile	Asn	Ala	Tyr	Leu	Tyr	Gly	Gln	Ala	Ala	Thr	Leu	Gly	Tyr
	130					135					140				
Thr	Glu	Ala	Lys	Leu	Ala	Leu	Ile	Ile	Phe	Cys	Leu	Ser	Ala	Val	Val
145					150					155				160	
Leu	Trp	Trp	Trp	Tyr	Arg	Gln	Ile	Ser	Val	Ala	Ile	Phe	Asp	Arg	Glu

				165				170					175				
Phe	Ala	Tyr	Ser	Cys	Gly	Leu	Arg	Thr	Arg	Thr	Ala	Glu	Leu	Val	Val		
			180					185					190				
Leu	Val	Phe	Ile	Ser	Leu	Val	Ile	Val	Ser	Gly	Val	Arg	Ser	Val	Gly		
		195					200					205					
Ile	Leu	Leu	Ile	Ser	Ala	Met	Phe	Val	Ala	Pro	Pro	Leu	Ser	Ala	Arg		
	210					215					220						
Gln	Leu	Ser	Asp	Arg	Leu	Ser	Thr	Ile	Leu	Ile	Leu	Ser	Ser	Ile	Phe		
225					230					235					240		
Gly	Gly	Ile	Cys	Gly	Ala	Leu	Gly	Cys	Tyr	Phe	Ser	Val	Ala	Phe	Thr		
			245					250						255			
Cys	Gln	Thr	Val	Val	Glu	Gly	Lys	Pro	Ile	Ser	Ile	Ile	Leu	Pro	Thr		
		260					265						270				
Gly	Pro	Leu	Val	Val	Phe	Phe	Ala	Gly	Val	Leu	Val	Phe	Leu	Cys	Leu		
	275					280						285					
Ile	Phe	Ser	Trp	Lys	Thr	Gly	Trp	Ile	Thr	Arg	Tyr	Phe	Arg	Arg	Lys		
	290					295				300							
Met	Val	Leu	Ile	Phe	Ser	Arg											
305					310												

(2) INFORMATIONS POUR LA SEQ ID NO: 398:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(389173..389955)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 398:

Leu	Phe	Leu	Asn	Arg	Asp	Asn	Ala	Ile	Ala	Trp	Ser	Val	Glu	Asp	Leu		
1			5					10					15				
Cys	Val	Asn	Tyr	Asp	His	Ser	Asp	Val	Leu	Cys	His	Ile	Thr	Phe	Ser		
		20					25					30					
Leu	Pro	Ala	Gly	Asp	Leu	Ala	Ala	Ile	Ile	Gly	Pro	Asn	Gly	Ala	Gly		
	35					40					45						
Lys	Ser	Thr	Leu	Leu	Lys	Ala	Ser	Leu	Gly	Leu	Ile	Arg	Ala	Ser	Ser		
	50				55					60							
Gly	Gln	Ser	Leu	Phe	Phe	Gly	Gln	Arg	Phe	Ser	Lys	Ala	His	His	Arg		
65				70				75					80				
Ile	Ala	Tyr	Met	Pro	Gln	Arg	Ala	Ser	Val	Asp	Trp	Asp	Phe	Pro	Met		
			85					90					95				
Thr	Val	Leu	Asp	Leu	Val	Leu	Met	Gly	Cys	Tyr	Gly	Tyr	Lys	Gly	Ile		
		100					105					110					
Trp	Asn	Arg	Ile	Ser	Thr	Asp	Asp	Arg	Gln	Glu	Ala	Met	Arg	Ile	Leu		
	115					120					125						
Glu	Arg	Val	Gly	Leu	Glu	Ala	Phe	Ala	Asn	Arg	Gln	Ile	Gly	Lys	Leu		
	130				135					140							
Ser	Gly	Gly	Gln	Gln	Gln	Arg	Ala	Phe	Leu	Ala	Arg	Ser	Leu	Met	Gln		
145			150					155					160				
Lys	Ala	Asp	Leu	Tyr	Leu	Met	Asp	Glu	Leu	Phe	Ser	Ala	Ile	Asp	Met		
		165					170						175				
Ala	Ser	Tyr	Gln	Met	Val	Val	Asp	Val	Leu	Gln	Glu	Leu	Lys	Ser	Glu		
		180					185					190					

Gly	Lys	Thr	Ile	Val	Val	Ile	His	His	Asp	Leu	Ser	Asn	Val	Arg	Lys
		195					200					205			
Leu	Phe	Asp	His	Val	Ile	Leu	Leu	Asn	Lys	His	Leu	Val	Cys	Ser	Gly
	210					215					220				
Ser	Val	Glu	Glu	Cys	Leu	Thr	Lys	Glu	Ala	Ile	Phe	Gln	Ala	Tyr	Gly
225					230					235					240
Cys	Glu	Leu	Glu	Leu	Leu	Asp	Tyr	Thr	Leu	Lys	Leu	Ser	Arg	Gly	Lys
				245					250					255	
Tyr	Gln	Gly	Ser	Cys											
			260												

(2) INFORMATIONS POUR LA SEQ ID NO: 399:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 317 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(389945..390895)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 399:

Lys	Leu	Ile	Leu	Arg	Gly	Leu	Leu	Cys	Leu	Ala	Gly	Cys	Phe	Leu	Met
1				5					10				15		
Asn	Ser	Cys	Ser	Ser	Ser	Arg	Gly	Asn	Gln	Pro	Ala	Asp	Glu	Ser	Ile
			20					25					30		
Tyr	Val	Leu	Ser	Met	Asn	Arg	Met	Ile	Cys	Asp	Cys	Val	Ser	Arg	Ile
		35					40					45			
Thr	Gly	Asp	Arg	Val	Lys	Asn	Ile	Val	Leu	Ile	Asp	Gly	Ala	Ile	Asp
	50					55					60				
Pro	His	Ser	Tyr	Glu	Met	Val	Lys	Gly	Asp	Glu	Asp	Arg	Met	Ala	Met
65					70					75					80
Ser	Gln	Leu	Ile	Phe	Cys	Asn	Gly	Leu	Gly	Leu	Glu	His	Ser	Ala	Ser
				85					90					95	
Leu	Arg	Lys	His	Leu	Glu	Gly	Asn	Pro	Lys	Val	Phe	Asp	Phe	Gly	Gln
			100					105					110		
Arg	Leu	Leu	Asn	Lys	Asn	Cys	Phe	Asp	Leu	Leu	Ser	Glu	Gly	Gly	Phe
		115					120					125			
Pro	Asp	Pro	His	Ile	Trp	Thr	Asp	Met	Arg	Val	Trp	Gly	Ala	Ala	Val
		130				135						140			
Lys	Glu	Val	Ala	Ala	Ala	Leu	Ile	Gln	Gln	Phe	Pro	Gln	Tyr	Glu	Glu
145					150					155					160
Asp	Phe	Gln	Lys	Asn	Ala	Asp	Gln	Ile	Leu	Ser	Glu	Met	Glu	Glu	Leu
			165						170					175	
Asp	Arg	Trp	Ala	Val	Arg	Ser	Leu	Ser	Thr	Ile	Pro	Glu	Lys	Asn	Arg
		180						185					190		
Tyr	Leu	Val	Thr	Gly	His	Asn	Ala	Phe	Ser	Tyr	Phe	Thr	Arg	Arg	Tyr
		195					200						205		
Leu	Ser	Ser	Asp	Ala	Glu	Arg	Val	Ser	Gly	Glu	Trp	Arg	Ser	Arg	Cys
	210					215					220				
Ile	Ser	Pro	Glu	Gly	Leu	Ser	Pro	Glu	Ala	Gln	Ile	Ser	Ile	Arg	Asp
225					230					235					240
Ile	Met	Arg	Val	Val	Glu	Tyr	Ile	Ser	Ala	Asn	Asp	Val	Glu	Val	Val
				245					250					255	
Phe	Leu	Glu	Asp	Thr	Leu	Asn	Gln	Asp	Ala	Leu	Arg	Lys	Ile	Val	Ser

(2) INFORMATION POUR LA SEQ ID NO: 400:

(A) LONGUEUR: 99 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 391514..391810

[illegible]

(A) LONGUEUR: 529 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 392410..393996

Asn	Met	Thr	Gln	Thr	Ala	Glu	Lys	Pro	Phe	Gly	Lys	Leu	Arg	Ser	Phe
1				5					10					15	
Leu	Trp	Pro	Ile	His	Met	His	Glu	Leu	Lys	Lys	Val	Leu	Pro	Met	Phe
			20					25					30		
Leu	Met	Phe	Cys	Ile	Ser	Phe	Asn	Tyr	Thr	Ile	Leu	Arg	Asp	Thr	
		35				40					45				

Lys	Asp	Thr	Leu	Ile	Val	Thr	Ala	Pro	Gly	Ser	Gly	Ala	Glu	Ala	Ile
50						55					60				
Pro	Phe	Ile	Lys	Leu	Trp	Leu	Val	Val	Pro	Ser	Ala	Val	Val	Phe	Met
65					70					75					80
Leu	Ile	Tyr	Ala	Lys	Leu	Ser	Asn	Ile	Leu	Asn	Lys	Gln	Ala	Leu	Phe
				85					90					95	
Phe	Ala	Val	Leu	Ser	Pro	Phe	Val	Val	Phe	Phe	Ala	Leu	Phe	Pro	Val
			100					105					110		
Val	Ile	Tyr	Pro	Cys	Arg	His	Ile	Leu	His	Pro	Thr	Ala	Phe	Ala	Asp
		115					120					125			
Thr	Leu	Gln	Ser	Ile	Leu	Pro	Ser	Gly	Phe	Met	Gly	Phe	Ile	Ala	Met
	130					135					140				
Leu	Arg	Asn	Trp	Thr	Phe	Ala	Val	Phe	Tyr	Val	Leu	Ser	Glu	Leu	Trp
145					150					155					160
Gly	Ser	Val	Met	Leu	Ser	Leu	Met	Phe	Trp	Gly	Phe	Ala	Asn	Glu	Ile
			165						170					175	
Thr	Lys	Ile	Ser	Glu	Ala	Lys	Arg	Phe	Tyr	Ala	Leu	Phe	Gly	Val	Gly
			180					185					190		
Ala	Asn	Val	Ala	Leu	Leu	Ile	Ser	Gly	Pro	Ala	Ile	Ile	Trp	Ser	Ser
		195					200					205			
Lys	Leu	Arg	Ala	Ser	Leu	Gly	Glu	Gly	Val	Asp	Pro	Trp	Gly	Val	Ser
	210					215					220				
Leu	Tyr	Phe	Leu	Met	Ala	Met	Phe	Leu	Cys	Ser	Cys	Ala	Ile	Ile	Ala
225					230					235					240
Ala	Cys	Tyr	Trp	Trp	Met	Asn	Arg	Tyr	Val	Leu	Thr	Asp	Pro	Arg	Phe
			245						250					255	
Tyr	Asn	Pro	Ala	Glu	Leu	Lys	Ala	Lys	Lys	Ser	Lys	Pro	Lys	Met	Ser
			260					265					270		
Met	Gly	Glu	Ser	Phe	Ser	Tyr	Leu	Leu	Arg	Ser	Pro	Tyr	Met	Leu	Leu
		275					280					285			
Leu	Ala	Leu	Leu	Val	Ile	Cys	Tyr	Gly	Ile	Cys	Ile	Asn	Leu	Val	Glu
	290					295					300				
Val	Thr	Trp	Lys	Ser	Gln	Leu	Lys	Met	Gln	Phe	Pro	Asn	Pro	Asn	Asp
305					310					315					320
Tyr	Ser	Ala	Phe	Met	Gly	Asn	Phe	Ser	Phe	Trp	Thr	Gly	Val	Val	Ser
			325						330					335	
Val	Phe	Val	Met	Leu	Phe	Ile	Gly	Gly	Asn	Val	Ile	Arg	Arg	Phe	Gly
			340					345					350		
Trp	Leu	Thr	Gly	Ala	Leu	Val	Thr	Pro	Ile	Met	Val	Leu	Val	Thr	Gly
		355					360					365			
Ala	Val	Phe	Phe	Ala	Leu	Val	Ile	Phe	Arg	Asp	His	Ala	Thr	Gly	Leu
	370					375					380				
Val	Ala	Ala	Leu	Gly	Thr	Thr	Pro	Leu	Met	Leu	Ala	Val	Val	Val	Gly
385					390					395					400
Ala	Ile	Gln	Asn	Ile	Leu	Ser	Lys	Ser	Thr	Lys	Tyr	Ala	Leu	Phe	Asp
			405						410					415	
Ala	Thr	Lys	Glu	Leu	Ala	Tyr	Ile	Pro	Leu	Asp	Gln	Glu	Gln	Lys	Val
			420					425					430		
Lys	Gly	Lys	Ala	Ala	Ile	Asp	Val	Val	Ala	Ala	Arg	Phe	Gly	Lys	Ser
		435					440					445			
Gly	Gly	Ser	Leu	Ile	Gln	Gln	Gly	Leu	Leu	Val	Val	Cys	Gly	Ser	Ile
	450					455					460				
Gly	Ala	Met	Thr	Pro	Phe	Leu	Ala	Val	Ala	Leu	Phe	Ala	Ile	Ile	Met
465					470					475					480
Val	Trp	Leu	Thr	Ser	Ala	Thr	Lys	Leu	Asn	Lys	Leu	Phe	Leu	Ala	Ala
			485						490					495	
Ser	Ala	Ala	Lys	Glu	Gln	Glu	Leu	Xaa	Glu	Ala	Ala	Ala	Ala	Glu	Lys
			500					505					510		
Glu	Ala	Ser	Ser	Ala	Ala	Lys	Glu	Ser	Ala	Pro	Ala	Ile	Glu	Gly	Val



Ser

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi). DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 402:

Thr 1	Arg	Leu	Lys	Thr 5	Leu	Lys	Pro	Tyr	Lys 10	Ile	Glu	Asn	Ile	Arg 15	Asn
Phe	Ser	Ile	Ile 20	Ala	His	Ile	Asp	His 25	Gly	Lys	Ser	Thr	Ile 30	Ala	Asp
Arg	Leu 35	Leu	Glu	Ser	Thr	Ser	Thr 40	Ile	Glu	Gln	Arg	Glu 45	Met	Arg	Glu
Gln 50	Leu	Leu	Asp	Ser	Met	Asp 55	Leu	Glu	Arg	Glu	Arg 60	Gly	Ile	Thr	Ile
Lys 65	Ala	His	Pro	Val 70	Thr	Met	Thr	Tyr	Glu	Tyr 75	Glu	Gly	Glu	Thr	Tyr 80
Glu	Leu	Asn	Leu	Ile 85	Asp	Thr	Pro	Gly	His 90	Val	Asp	Phe	Ser	Tyr 95	Glu
Val	Ser	Arg	Ser 100	Leu	Ala	Ala	Cys	Glu 105	Gly	Ala	Leu	Leu	Ile 110	Val	Asp
Ala	Ala 115	Gln	Gly	Val	Gln	Ala	Gln 120	Ser	Leu	Ala	Asn	Val 125	Tyr	Leu	Ala
Leu 130	Glu	Arg	Asp	Leu	Glu	Ile 135	Ile	Pro	Val	Leu	Asn 140	Lys	Ile	Asp	Leu
Pro 145	Ala	Ala	Gln	Pro	Glu 150	Ala	Ile	Lys	Lys	Gln 155	Ile	Glu	Glu	Phe	Ile 160
Gly	Leu	Asp	Thr	Ser 165	Asn	Thr	Ile	Ala	Cys 170	Ser	Ala	Lys	Thr	Gly 175	Gln
Gly	Ile	Pro	Glu 180	Ile	Leu	Glu	Ser 185	Ile	Ile	Arg	Leu	Val 190	Pro	Pro	Pro
Lys	Pro 195	Pro	Gln	Glu	Thr	Glu	Leu 200	Lys	Ala	Leu	Ile 205	Phe	Asp	Ser	His
Tyr 210	Asp	Pro	Tyr	Val	Gly	Ile 215	Met	Val	Tyr	Val	Arg 220	Val	Ile	Ser	Gly
Glu 225	Ile	Lys	Lys	Gly 230	Asp	Arg	Ile	Thr	Phe	Met 235	Ala	Thr	Lys	Gly	Ser 240
Ser	Phe	Glu	Val 245	Leu	Gly	Ile	Gly	Ala	Phe 250	Leu	Pro	Glu	Ala	Thr 255	Leu
Met	Glu	Gly	Ser 260	Leu	Arg	Ala	Gly	Gln 265	Val	Gly	Tyr	Phe 270	Ile	Ala	Asn
Leu	Lys 275	Lys	Val	Lys	Asp	Val	Lys 280	Ile	Gly	Asp	Thr	Val 285	Thr	Thr	Val
Lys 290	His	Pro	Ala	Lys	Glu	Pro 295	Leu	Glu	Gly	Phe	Lys 300	Glu	Ile	Lys	Pro
Val 305	Val	Phe	Ala	Gly 310	Ile	Tyr	Pro	Ile	Asp	Ser 315	Ser	Asp	Phe	Asp	Thr 320

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Leu Lys Asp Ala Leu Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr
      325                      330                      335
Ile Glu Gln Glu Ser Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly
      340                      345                      350
Phe Leu Gly Leu Leu His Leu Glu Ile Ile Phe Glu Arg Ile Ser Arg
      355                      360                      365
Glu Phe Asp Leu Asp Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys
      370                      375                      380
Val Val Leu Lys Asn Gly Lys Thr Leu Phe Ile
385                      390                      395

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(2) INFORMATIONS POUR LA SEQ ID NO: 403:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 228 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 395309..395992

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 403:

```

Arg Tyr Leu Gln Ser Arg Leu Lys Lys Trp Gln Asn Pro Phe Tyr Leu
1      5      10      15
Ile Thr Gln Gln His Ile Leu Thr Gln Leu Leu Leu Asn Thr Trp Lys
      20      25      30
Ser Leu Gly Ser Ile Val Asn Ile Ile Thr Pro Gln Glu Tyr Leu Ser
      35      40      45
Asn Ile Met Ser Leu Cys Met Asp Lys Arg Gly Ile Cys Leu Lys Thr
      50      55      60
Asp Met Leu Asp Gln His Arg Leu Val Leu Ser Tyr Glu Leu Pro Leu
      65      70      75      80
Asn Glu Ile Val Ser Asp Phe Asn Asp Lys Leu Lys Ser Val Thr Lys
      85      90      95
Gly Tyr Gly Ser Phe Asp Tyr Arg Leu Gly Asp Tyr Lys Lys Gly Ala
      100     105     110
Ile Ile Lys Leu Glu Ile Leu Ile Asn Asp Glu Ala Val Asp Ala Phe
      115     120     125
Ser Cys Leu Val His Arg Asp Lys Ala Glu Ser Lys Gly Arg Ser Ile
      130     135     140
Cys Glu Lys Leu Val Asp Val Ile Pro Pro Gln Leu Phe Lys Ile Pro
      145     150     155     160
Ile Gln Ala Ala Ile Asn Lys Lys Ile Ile Ala Arg Glu Thr Ile Arg
      165     170     175
Ala Leu Ala Lys Asn Val Thr Ala Lys Cys Tyr Gly Gly Asp Ile Thr
      180     185     190
Arg Lys Arg Lys Leu Trp Asp Lys Gln Lys Lys Gly Lys Lys Arg Met
      195     200     205
Lys Glu Phe Gly Lys Val Ser Ile Pro Asn Thr Ala Phe Val Glu Val
      210     215     220
Leu Lys Met Glu
225

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(2) INFORMATIONS POUR LA SEQ ID NO: 404:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(396059..396538)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 404:

Phe	Glu	Asp	Val	Arg	Glu	Ala	Leu	Tyr	Ala	Ala	Lys	Ile	Ile	Ser	Tyr
1				5					10					15	
Ala	Gln	Gly	Phe	Met	Leu	Leu	Lys	Gln	Val	Ser	Gln	Asp	Lys	Gly	Trp
			20					25					30		
Asp	Leu	Asn	Leu	Gly	Glu	Leu	Ala	Leu	Ile	Trp	Arg	Gly	Gly	Cys	Ile
		35					40					45			
Ile	Gln	Ser	Ala	Phe	Leu	Asp	Lys	Ile	His	Gln	Gly	Phe	Glu	Asn	Ser
	50					55					60				
Pro	Glu	Ala	His	Ser	Leu	Ile	Leu	Gln	Asp	Tyr	Phe	Lys	Lys	Val	Leu
65					70					75				80	
Phe	Asp	Ser	Glu	Thr	Gly	Phe	Arg	Arg	Ala	Val	Leu	His	Ala	Ile	Gly
				85				90						95	
Ser	Gly	Val	Ala	Ile	Pro	Cys	Leu	Ser	Ser	Ala	Leu	Ser	Phe	Tyr	Asp
			100					105					110		
Gly	Tyr	Arg	Thr	Val	Asp	Ser	Pro	Leu	Phe	Leu	Val	Gln	Gly	Leu	Arg
		115					120					125			
Asp	Tyr	Phe	Gly	Ala	His	Gly	Tyr	Glu	Arg	Arg	Asp	Cys	Pro	Arg	Gly
	130					135					140				
Glu	Phe	Tyr	His	Thr	Asp	Trp	Leu	Glu	Thr	Lys	Lys	Thr	Phe	Arg	Ala
145					150					155					160

(2) INFORMATIONS POUR LA SEQ ID NO: 405:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 322 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(396542..397507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 405:

Glu	Gly	Ser	Val	Ala	Pro	Asn	Thr	Asp	Ile	Gly	Leu	Ile	Gly	Leu	Ala
1				5					10					15	
Val	Met	Gly	Lys	Asn	Leu	Val	Leu	Asn	Met	Val	Asp	His	Gly	Phe	Ser
			20					25					30		
Val	Ser	Val	Tyr	Asn	Arg	Ser	Pro	Ala	Lys	Thr	Glu	Glu	Phe	Leu	Lys
		35					40					45			
Asp	His	Gly	Glu	Ser	Gly	Ala	Leu	Gln	Gly	Phe	Thr	Thr	Ile	Gln	Glu
	50					55					60				
Phe	Val	Gln	Ser	Leu	Lys	Arg	Pro	Arg	Lys	Ile	Met	Ile	Met	Ile	Lys
65					70					75					80

Ala	Gly	Ala	Pro	Val	Asp	Glu	Met	Ile	Ala	Ser	Leu	Leu	Pro	Phe	Leu
				85					90					95	
Glu	Glu	Gly	Asp	Ile	Leu	Ile	Asp	Gly	Gly	Asn	Ser	Tyr	Tyr	Leu	Asp
			100					105					110		
Ser	Glu	Arg	Arg	Tyr	Val	Asp	Leu	Lys	Lys	Glu	Gly	Ile	Leu	Phe	Val
			115				120					125			
Gly	Met	Gly	Val	Ser	Gly	Gly	Glu	Glu	Gly	Ala	Arg	Lys	Gly	Pro	Ser
	130					135				140					
Ile	Met	Pro	Gly	Gly	Asn	Ile	Asp	Ala	Trp	Pro	Ala	Ile	Ala	Pro	Ile
145					150					155					160
Phe	Gln	Ser	Ile	Ala	Ala	Gln	Val	Gly	Gly	Arg	Pro	Cys	Cys	Ser	Trp
				165					170					175	
Ile	Gly	Thr	Gly	Gly	Ala	Gly	His	Phe	Val	Lys	Ala	Val	His	Asn	Gly
			180					185					190		
Ile	Glu	Tyr	Gly	Asp	Ile	Gln	Leu	Ile	Cys	Glu	Thr	Tyr	Glu	Ile	Leu
	195						200					205			
Lys	Thr	Arg	Leu	Asn	Leu	Ser	Leu	Glu	Gln	Ile	Gly	Asn	Ile	Phe	Phe
	210					215					220				
Glu	Trp	Asn	Gln	Thr	Asp	Leu	Asn	Ser	Tyr	Leu	Leu	Gly	Ala	Ala	Ala
225					230					235					240
Ala	Val	Leu	Ile	Ala	Lys	Asp	Glu	Asn	Gly	Asn	Ala	Ile	Ala	Ser	Thr
				245					250					255	
Ile	Leu	Asp	Val	Ala	Gly	Gln	Lys	Gly	Thr	Gly	Arg	Trp	Val	Ala	Glu
			260					265					270		
Asp	Ala	Ile	Lys	Ala	Gly	Val	Pro	Met	Ser	Leu	Ile	Ile	Glu	Ser	Val
		275					280					285			
Leu	Ala	Arg	Tyr	Leu	Ser	Thr	Trp	Lys	Glu	Val	Arg	Thr	Lys	Ala	Ala
	290					295					300				
Gln	Glu	Phe	Pro	Gly	Phe	Leu	Phe	Xaa	Val	Asn	Leu	His	Lys	Lys	Leu
305					310					315					320
Leu	Pro														

(2) INFORMATIONS POUR LA SEQ ID NO: 406:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 451 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(397401..398753)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 406:

Ile	Phe	Met	Gln	Gln	Leu	Ile	Asp	Asn	Leu	Lys	Lys	Arg	Gly	Ile	Leu
1				5					10					15	
Asp	Asn	Ser	Ser	Ala	Gly	Leu	Glu	Ser	Leu	Thr	Val	Pro	Val	Ser	Ala
			20					25					30		
Tyr	Leu	Gly	Phe	Asp	Pro	Thr	Ala	Pro	Ser	Leu	His	Ile	Gly	His	Trp
		35					40					45			
Ile	Gly	Ile	Cys	Phe	Leu	Arg	Arg	Leu	Ala	Ala	Tyr	Gly	Ile	Thr	Pro
	50					55					60				
Val	Ala	Leu	Val	Gly	Gly	Ala	Thr	Gly	Met	Ile	Gly	Asp	Pro	Ser	Gly
65					70				75						80
Lys	Ser	Val	Glu	Arg	Ser	Leu	Leu	Asp	Gln	Ala	Gln	Val	Leu	Asp	Asn

				85					90					95	
Ser	Lys	Lys	Ile	Ala	Ala	Ala	Leu	Ala	Ser	Tyr	Leu	Pro	Gly	Ile	Arg
			100					105					110		
Ile	Val	Asn	Asn	Ala	Asp	Trp	Leu	Gly	Ser	Leu	Ser	Met	Val	Asp	Phe
		115					120					125			
Leu	Arg	Asp	Val	Gly	Lys	His	Phe	Arg	Leu	Gly	Ser	Met	Leu	Ala	Lys
	130					135					140				
Asp	Val	Val	Lys	Gln	Arg	Val	Tyr	Ser	Glu	Glu	Gly	Ile	Ser	Tyr	Thr
145					150				155						160
Glu	Phe	Ser	Tyr	Leu	Leu	Leu	Gln	Ser	Tyr	Asp	Phe	Ala	His	Leu	Phe
				165					170					175	
Lys	Glu	His	Asn	Val	Val	Leu	Gln	Cys	Gly	Gly	Ser	Asp	Gln	Trp	Gly
			180					185					190		
Asn	Ile	Thr	Ser	Gly	Ile	Asp	Tyr	Ile	Arg	Arg	Arg	Gly	Leu	Gly	Gln
	195					200						205			
Ala	Tyr	Gly	Leu	Thr	Tyr	Pro	Leu	Leu	Thr	Asp	Ser	Lys	Gly	Lys	Lys
	210					215					220				
Ile	Gly	Lys	Thr	Glu	Ser	Gly	Thr	Ile	Trp	Leu	Asp	Pro	Ala	Leu	Thr
225					230					235					240
Pro	Pro	Tyr	Glu	Leu	Phe	Gln	Tyr	Phe	Leu	Arg	Leu	Pro	Asp	Gln	Glu
				245					250					255	
Ile	Ser	Lys	Val	Met	Arg	Thr	Leu	Thr	Leu	Leu	Asp	Asn	Glu	Glu	Val
			260					265					270		
Phe	Ala	Leu	Asp	Glu	Arg	Leu	Thr	Ser	Asp	Pro	Gln	Ala	Val	Lys	Xaa
	275						280					285			
Tyr	Ile	Ala	Glu	Val	Ile	Val	Lys	Asp	Val	His	Gly	Ser	Glu	Gly	Leu
	290					295					300				
Ala	Gln	Ala	Gln	Ala	Ala	Thr	Glu	Ser	Phe	Phe	Ala	Ser	Lys	Gly	Lys
305					310					315					320
Ser	Ile	Thr	Glu	Ala	Glu	Leu	Val	Ala	Leu	Val	Glu	Ser	Gly	Val	Gly
				325					330					335	
Val	Lys	Val	Ala	Arg	Ala	Asp	Leu	Ile	Gly	Lys	Arg	Trp	Leu	Asp	Ile
			340					345					350		
Val	Val	Glu	Leu	Gly	Phe	Cys	Ser	Ser	Arg	Gly	Gln	Ala	Arg	Arg	Leu
	355						360					365			
Ile	Gln	Gln	Arg	Gly	Leu	Tyr	Ile	Asn	Gln	Glu	Pro	Leu	Ala	Asp	Glu
	370					375					380				
Gln	Ser	Ile	Leu	Asp	Gly	Thr	Gln	Leu	Cys	Phe	Asp	Arg	Tyr	Val	Leu
385					390					395					400
Leu	Ser	Gln	Gly	Lys	Arg	Lys	Lys	Gln	Val	Ile	Asp	Leu	Lys	Leu	Gly
				405					410					415	
Gly	Val	Cys	Gly	Ser	Lys	Tyr	Arg	Tyr	Trp	Val	Asp	Trp	Phe	Gly	Arg
			420					425					430		
Asp	Gly	Gln	Lys	Pro	Cys	Ile	Glu	His	Gly	Gly	Ser	Trp	Phe	Phe	Cys
		435					440					445			
Phe	Cys	Leu													
		450													

(2) INFORMATIONS POUR LA SEQ ID NO: 407:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(398909..399688)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 407:

Phe	Val	Lys	Glu	Ile	Phe	Phe	Val	Lys	Thr	His	Asp	Leu	Ala	Asp	Thr
1				5					10					15	
Trp	Gln	Leu	Tyr	Trp	Ser	Thr	Lys	Glu	Ile	His	His	Arg	Asp	Val	Leu
			20					25					30		
Ile	Glu	Ser	Tyr	Leu	Pro	Leu	Val	Lys	Asn	Val	Ala	His	Arg	Leu	Ala
		35					40					45			
Ser	Gly	Met	Pro	Ser	His	Val	Lys	Met	Glu	Asp	Leu	Tyr	Ala	Leu	Gly
	50					55					60				
Val	Glu	Gly	Leu	Ile	Arg	Ala	Val	Glu	Arg	Phe	Asp	Pro	Glu	Lys	Ser
65					70					75					80
Lys	Arg	Phe	Glu	Ser	Tyr	Ala	Leu	Phe	Ile	Ile	Lys	Ala	Ala	Ile	Ile
				85					90					95	
Asp	Gly	Leu	Arg	Lys	Gln	Asp	Trp	Val	Pro	Arg	Ser	Val	Tyr	Gln	Arg
			100					105					110		
Ala	Asn	Arg	Leu	Ala	Asp	Ala	Met	Asp	Ser	Leu	Arg	Gln	Thr	Leu	Gly
		115					120					125			
Lys	Glu	Pro	Thr	Asp	Gly	Glu	Leu	Cys	Glu	Tyr	Leu	Asn	Ile	Ser	Gln
	130					135					140				
Gln	Glu	Leu	Ser	His	Trp	Phe	Ser	Ser	Ser	Arg	Pro	Ala	Leu	Val	Leu
145					150					155					160
Ser	Leu	Asn	Asp	Asp	Phe	Ser	Cys	Gln	Asp	Asp	Asp	Glu	Gly	Leu	Ala
			165						170					175	
Leu	Glu	Glu	Arg	Ile	Ala	Asp	Glu	Arg	Ala	Glu	Thr	Gly	Tyr	Asp	Val
			180					185					190		
Ile	Arg	Lys	Lys	Glu	Ala	Ile	Ser	Ile	Leu	Thr	Glu	Ala	Leu	Leu	Ala
		195					200					205			
Leu	Asp	Glu	Lys	Glu	Arg	Gln	Val	Met	Ala	Leu	Tyr	Tyr	Tyr	Asp	Asp
	210					215					220				
Leu	Val	Leu	Lys	Glu	Ile	Gly	Lys	Ile	Leu	Gly	Val	Ser	Glu	Ser	Arg
225					230					235					240
Val	Ser	Gln	Ile	His	Ser	Lys	Ala	Leu	Leu	Lys	Leu	Arg	Gly	Thr	Leu
				245					250					255	
Ser	Ser	Leu	Leu												
			260												

(2) INFORMATIONS POUR LA SEQ ID NO: 408:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui.

(viii) POSITION DANS LE GENOME: complement(399778..400167)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 408:

Met	Tyr	Met	Ala	Leu	Lys	Ser	Lys	Asn	Ser	Gln	Glu	Leu	Val	Glu	Cys
1				5					10					15	
Val	Arg	Lys	Tyr	Leu	Gly	Lys	Gln	Ile	Gly	Leu	Ser	Leu	Trp	Asn	Arg
			20					25					30		
Gln	Asp	Val	Leu	Glu	Val	Ile	Thr	Ile	Asp	Ser	Leu	Val	Glu	Gln	Phe

(2) INFORMATION POUR LA SEQ ID NO: 409:

(A) LONGUEUR: 397 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(400034..401224)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 409:

Gly 1	Ile	Ser	Phe	Pro 5	Leu	Gly	Ala	Ser	Arg 10	Leu	Ala	Leu	Thr	Val 15	Cys
Leu	Leu	Leu	Phe 20	Leu	Val	Asn	Phe	Leu 25	Val	Ile	Thr	Lys 30	Gly	Ala	Glu
Arg	Ile	Ala 35	Glu	Val	Arg	Ala 40	Arg	Phe	Ser	Leu	Glu 45	Ala	Leu	Pro	Gly
Lys	Gln 50	Met	Ser	Leu	Asp	Ala 55	Asp	Ile	Ala	Ala 60	Gly	Arg	Ile	Gly	Tyr
Ser 65	Arg	Ala	Ser	Val	Lys 70	Lys	Ser	Ser	Leu 75	Leu	Glu	Glu	Ser	Asp 80	Tyr
Phe	Ser	Ala	Met 85	Glu	Gly	Val	Phe	Arg 90	Phe	Val	Lys	Gly	Asp 95	Ala	Ile
Met	Ser	Trp 100	Val	Leu	Leu	Gly	Val 105	Asn	Ile	Leu	Ala	Ala 110	Leu	Phe	Leu
Gly	Arg	Ala 115	Thr	His	Val	Gly	Asp 120	Leu	Trp	Leu	Thr 125	Val	Leu	Gly	Asp
Ala	Leu 130	Val	Ser	Gln	Ile	Pro 135	Ala	Leu	Leu 140	Thr	Ser	Cys 145	Ala	Ala	Ala
Thr 145	Leu	Ile	Ala	Lys 150	Val	Gly	Glu	Lys	Glu 155	Ser	Leu	Ala	Gln	His	Leu 160
Leu	Asp	Tyr	Tyr 165	Glu	Gln	Ser	Arg	Gln 170	Ser	Phe	Leu	Phe 175	Ile	Ala	Leu
Ile	Leu	Cys 180	Gly	Met	Ala	Cys	Ile 185	Pro	Gly	Ala	Pro	Lys 190	Ala	Leu	Ile
Leu	Gly 195	Phe	Ser	Val	Leu	Leu 200	Phe	Leu	Gly 205	Tyr	Lys	Asn 210	Pro	Ser	Ser
Gly	Glu	Thr 210	Leu	Leu	Phe 215	Gln	Lys	Glu	Arg 220	Val	Glu	Phe 225	Val	Leu	Pro
Asp 225	Glu	Gly	Val	Gly 230	Asn	Pro	Ala	Asn	Leu 235	Tyr	Lys	Asp 240	Ala	Arg	Asn

(2) INFORMATION POUR LA SEQ ID NO: 410:

(A) LONGUEUR: 82 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 401776..402021

(xi) DESCRIPTION DE LA SEQUENCE: SEO ID NO: 410:

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 411:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: 402126..403220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 411:

Glu	Phe	Met	Phe	Thr	Ser	Leu	Ser	Ala	Ile	Gln	Asn	Ala	Ile	Arg	Pro	1	5	10	15
Ser	Cys	Gln	Leu	Pro	Val	Leu	Thr	Pro	Arg	Arg	Ala	Leu	Ile	Thr	Ser	20	25	30	
Leu	Ala	Ser	Gly	Ile	Ile	Leu	Gly	Leu	Ala	Gly	Cys	Val	Val	Gly	Val	35	40	45	
Leu	Ala	Ser	Leu	Pro	Ala	Leu	Ile	Ala	Val	Ser	Ala	Val	Ile	Leu	Gly	50	55	60	
Val	Ser	Leu	Phe	Ala	Ser	Gly	Leu	Phe	Leu	Cys	Arg	Tyr	Val	Cys	Pro	65	70	75	
Pro	Lys	Ile	Val	Ser	Arg	Arg	Pro	Ser	Thr	Glu	Leu	Pro	Ala	Glu	Pro	85	90	95	
Thr	Pro	Glu	Leu	Pro	Glu	Ile	Lys	Arg	Pro	Lys	Pro	Ile	Ala	Pro	Pro	100	105	110	
Pro	Pro	Asp	Phe	Ile	Pro	Pro	Lys	Pro	Leu	Arg	Arg	Thr	Ile	Gly	Glu	115	120	125	
Met	Leu	Phe	Gly	Trp	Asn	Cys	Ile	Glu	Ser	Ile	Arg	Gln	Met	Pro	Phe	130	135	140	
Phe	Leu	Ala	Asn	Asp	Lys	Thr	Pro	Leu	Phe	Phe	Arg	Asn	Pro	Ser	Ala	145	150	155	
Arg	Phe	Arg	Ala	Trp	Asn	Ile	Pro	Phe	Thr	His	Thr	Ile	Phe	Val	Ser	165	170	175	
Thr	Ser	Gly	Gln	Phe	Ser	Ser	Leu	Arg	Met	Gln	Ser	Asn	Leu	Pro	Ala	180	185	190	
Ala	Ile	Ala	Asn	Ala	Thr	Gln	Ser	Ala	Ala	Phe	Ala	Lys	Arg	Gly	Gln	195	200	205	
Gly	Gly	Leu	Gly	Val	Asn	Asp	Ala	Phe	Pro	Ala	Val	Leu	Thr	Asp	Lys	210	215	220	
Cys	Trp	Glu	Glu	Ser	Lys	Pro	Glu	Ser	Gly	Ile	Leu	Leu	Pro	Gly	Glu	225	230	235	
Cys	Ser	Ser	Ala	Thr	Trp	Glu	Asp	Lys	Asn	His	Leu	Val	Pro	Cys	Trp	245	250	255	
Asp	Glu	Glu	Thr	Lys	Thr	Tyr	Asn	Lys	Pro	Leu	Leu	Phe	Ile	Gln	Met	260	265	270	
Leu	Ala	Pro	Lys	Ala	Ser	Met	Ser	Lys	Ser	Cys	Tyr	Glu	Ile	Thr	Leu	275	280	285	
Arg	Ala	Tyr	Thr	Ala	Cys	Phe	Glu	Glu	Ala	Ile	Arg	Cys	Gly	Cys	Arg	290	295	300	
Met	Ile	Gln	Ile	Pro	Leu	Ile	Ala	Ser	Phe	Gly	Asp	Phe	Val	Pro	Arg	305	310	315	
Ala	Leu	Ser	Lys	Arg	Pro	Lys	Trp	Ile	Glu	Ser	Ala	Lys	Leu	Ala	Leu	325	330	335	
Leu	His	Ala	Val	Glu	Lys	Thr	Ala	Lys	Lys	His	Ala	Ser	Lys	Asp	Leu	340	345	350	
Val	Ile	Val	Leu	Thr	Asn	Ile	Pro	Gln	Pro	Val	Asn	Leu	355	360	365				

(2) INFORMATIONS POUR LA SEQ ID NO: 412:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 611 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 403348..405180

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 412:

Gln	Lys	Leu	Phe	Val	Gly	His	Leu	Val	Met	Ala	Thr	Pro	Cys	Ile	Gln
1				5					10					15	
Asn	Ala	Phe	Arg	Arg	Lys	Thr	Leu	Pro	Val	Arg	Ile	Gly	Asp	Leu	Phe
			20					25					30		
Val	Gly	Ser	Glu	His	Ser	Ile	Lys	Ile	Gln	Ser	Met	Thr	Thr	Thr	Ala
		35					40					45			
Thr	Thr	Asp	Val	Asp	Gly	Thr	Val	Arg	Gln	Ile	Cys	Ala	Leu	Gln	Glu
	50					55					60				
Leu	Gly	Cys	Asp	Ile	Val	Arg	Val	Thr	Val	Gln	Gly	Leu	Arg	Glu	Val
65					70					75					80
His	Ala	Cys	Glu	His	Ile	Lys	Asp	Arg	Leu	Ile	Gln	Gln	Asn	Ile	Ser
				85					90					95	
Ile	Pro	Leu	Val	Ala	Asp	Ile	His	Phe	Phe	Pro	Gln	Ala	Ala	Ile	His
			100					105					110		
Val	Val	Asp	Cys	Val	Asp	Lys	Val	Arg	Ile	Asn	Pro	Gly	Asn	Tyr	Val
		115					120					125			
Asp	Lys	Arg	Asn	Met	Phe	Thr	Gly	Lys	Ile	Tyr	Ser	Asp	Glu	Gln	Tyr
	130					135					140				
Ala	His	Ser	Leu	Glu	His	Leu	Met	Asn	Lys	Phe	Ser	Pro	Leu	Val	Glu
145					150					155					160
Lys	Cys	Lys	Arg	Leu	Gly	Lys	Ala	Met	Arg	Ile	Gly	Val	Asn	His	Gly
				165					170					175	
Ser	Leu	Ser	Glu	Arg	Val	Thr	Gln	Arg	Tyr	Gly	Asn	Thr	Ile	Glu	Gly
			180					185					190		
Met	Val	Tyr	Ser	Ala	Leu	Glu	Tyr	Ala	Glu	Val	Cys	Val	Ala	Met	Asp
		195					200					205			
Tyr	His	Asp	Val	Ile	Phe	Ser	Met	Lys	Ser	Ser	Asn	Pro	Lys	Val	Met
	210					215					220				
Val	Ala	Ala	Tyr	Arg	Ser	Leu	Ala	Tyr	Glu	Leu	Asp	Gln	Arg	Glu	Trp
225					230					235					240
Ser	Tyr	Pro	Leu	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Ser	Gly	Thr	Ala
				245					250					255	
Gly	Ile	Val	Lys	Ser	Ala	Val	Gly	Ile	Gly	Thr	Leu	Leu	Ser	Glu	Gly
			260					265					270		
Leu	Gly	Asp	Thr	Ile	Arg	Cys	Ser	Leu	Thr	Gly	Ser	Pro	Ile	Asn	Glu
		275					280					285			
Ile	Pro	Ile	Cys	Ile	Asp	Leu	Leu	Lys	Gln	Thr	Thr	Glu	Leu	Ser	Glu
	290					295						300			
Arg	Trp	Gly	Glu	Ala	Asp	Asn	Pro	Phe	Ala	Ile	His	Ser	Ser	Lys	Gln
305					310					315					320
Leu	Gly	Thr	Arg	Asn	Thr	Leu	Asn	Thr	Pro	Pro	Trp	Asp	Asn	Val	Tyr
				325					330					335	
Gly	Leu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Gln	Leu	Leu	Thr	Ala	Glu	Pro
			340					345					350		
Ile	Glu	Leu	Leu	Gln	Cys	Leu	Gly	Ile	Asp	Thr	Thr	Thr	Gly	Lys	Ile
		355					360					365			
Asp	Pro	Thr	Thr	Pro	Glu	Gly	Val	Val	Val	Pro	Lys	Ala	Met	Arg	Ser
	370					375					380				
Ser	Pro	Ile	Val	Ser	Glu	Ile	Glu	Lys	His	Leu	Leu	Val	Phe	Asn	Lys
385					390					395					400
Glu	Asp	Ala	Pro	Ile	Leu	Asn	Pro	Met	Asn	Glu	Glu	Glu	Trp	Leu	Ser

(2) INFORMATION POUR LA SEQ ID NO: 413:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(403276..403788)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 413:

Ala	Met	Arg	Val	Leu	Leu	Ile	Arg	Val	Asn	Phe	Pro	Ser	Lys	His	Ile
1				5					10					15	
Thr	Leu	Ile	Tyr	Ile	Val	Ser	Trp	Ile	Asp	Thr	His	Phe	Ile	Tyr	Thr
			20					25					30		
Ile	His	Asn	Met	Tyr	Gly	Cys	Leu	Arg	Lys	Glu	Met	Asp	Ile	Cys	Tyr
		35					40					45			
Lys	Arg	Asp	Gly	Asn	Val	Leu	Leu	Asn	Gln	Ala	Val	Phe	Asn	Val	Leu
	50					55					60				
Ala	Cys	Met	Asn	Leu	Ser	Gln	Thr	Leu	Tyr	Arg	Asn	Thr	Asn	Asp	Val
65					70					75					80
Ala	Thr	Gln	Leu	Leu	Gln	Ser	Thr	Asn	Leu	Ser	Asn	Arg	Ser	Ile	His
				85					90					95	
Ile	Cys	Gly	Gly	Cys	Ser	Arg	His	Arg	Leu	Asp	Phe	Asp	Gly	Val	Leu
			100					105					110		
Thr	Thr	Asn	Lys	Lys	Ile	Ser	Asp	Ser	Tyr	Trp	Glu	Gly	Phe	Ala	Ser
		115					120					125			

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Lys Arg Ile Leu Tyr Thr Gly Cys Cys His Asp Glu Val Ser Tyr Lys
  130          135          140
Gln Phe Leu Lys Leu Ala Gly Thr Val Pro Ala Glu Ser Leu Ser Pro
  145          150          155          160
Glu Gly Phe Gly Gly Leu Arg Lys Tyr Lys Leu
          165          170

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(2) INFORMATIONS POUR LA SEQ ID NO: 414:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 252 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 405165..405920

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 414:

```

Met Glu Arg Ala Arg Ile Gly Ser Leu Met Thr Leu Pro Ser Glu Ala
  1          5          10          15
Leu Arg Lys Gln Thr Phe Pro Glu Leu Glu Tyr Leu Pro Ile Arg His
          20          25          30
Gly Ile Phe Pro Lys Gln Asp Asp Lys Glu Glu Ala Ser Gln Val Ser
          35          40          45
Asp Glu Val Ile Ser Ser Ser Leu Gly Gly Asn Asp Phe Cys Asn Ala
          50          55          60
Arg Gln Val His Gly Thr Ser Val Arg Tyr Val Thr Pro Lys Thr Pro
  65          70          75          80
Lys Arg Ala Pro Ala Asp Gly Leu Phe Thr Thr Thr Pro Leu Leu Ser
          85          90          95
Leu His Ile Tyr His Ala Asp Cys Gln Ala Ala Ile Phe Tyr Asp Pro
          100          105          110
Glu Asn His Val Ile Ala Asn Val His Ala Gly Trp Arg Gly Leu Val
          115          120          125
Gly Asn Ile Tyr Ala Val Thr Val Arg Leu Leu Lys Lys Thr Phe Asn
          130          135          140
Thr Arg Pro Gln Asp Leu Ile Val Ala Ile Ser Pro Ser Leu Gly Pro
  145          150          155          160
Asp Met Ala Val Tyr Pro Asp Tyr Lys Arg Leu Phe Pro Ser Ser Phe
          165          170          175
Phe Pro Leu Met Pro Lys Glu Asn His Leu Asp Phe Arg Ala Val Ala
          180          185          190
Arg Lys Gln Leu Leu Ser Glu Gly Leu Ser Ser Asn His Ile Phe Ile
          195          200          205
Ser Glu Arg Cys Thr Cys Ser Glu Ser Asn Thr Phe Phe Ser Phe Arg
          210          215          220
Ser Trp Lys Ser Arg His Gln Gln Asp Pro Ser Ala Ile Arg Ser Arg
  225          230          235          240
Lys Asn Asn Val Thr Ala Val Leu Leu Leu Pro Arg
          245          250

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(2) INFORMATIONS POUR LA SEQ ID NO: 415:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(405955..407049)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 415:

Met	Ser	Ile	Glu	Val	Arg	Ile	Pro	Asn	Ile	Ala	Glu	Ser	Ile	Ser	Glu	1	5	10	15
Val	Thr	Ile	Ser	Ala	Leu	Leu	Ile	Pro	Ser	Gly	Asp	Leu	Val	Gln	Glu	20	25	30	
Asn	Gln	Gly	Ile	Leu	Glu	Ile	Glu	Ser	Asp	Lys	Val	Asn	Gln	Leu	Ile	35	40	45	
Tyr	Ala	Pro	Cys	Ser	Gly	Arg	Val	Glu	Trp	Ser	Val	Ser	Val	Gly	Asp	50	55	60	
Thr	Val	Ala	Val	Gly	Ser	Val	Val	Gly	Ile	Ile	Ser	Glu	Ala	Glu	Lys	65	70	75	80
Ser	Gln	Asp	Thr	Ala	Pro	Ile	His	Glu	Gln	Met	Pro	Phe	Ser	Leu	Val	85	90	95	
Glu	Gln	Glu	Ser	Asp	Ala	Gln	Ile	Ile	Ala	Phe	Pro	Ser	Ser	Val	Arg	100	105	110	
Gln	Asp	Pro	Pro	Ala	Glu	Gly	Lys	Thr	Phe	Val	Pro	Leu	Lys	Glu	Ile	115	120	125	
Gln	Pro	Ala	Ser	Ser	Asp	His	Arg	Glu	Ser	Arg	Glu	Ser	Met	Ser	Ala	130	135	140	
Ile	Arg	Lys	Thr	Ile	Ser	Arg	Arg	Leu	Val	Gln	Ser	Leu	His	Asp	Ser	145	150	155	160
Ala	Met	Leu	Thr	Thr	Phe	Asn	Glu	Ile	His	Met	Gly	Pro	Leu	Ile	Ala	165	170	175	
Leu	Arg	Lys	Glu	Arg	Gln	Glu	Asp	Phe	Val	Ala	Lys	Tyr	Gly	Val	Lys	180	185	190	
Leu	Gly	Phe	Met	Ser	Phe	Phe	Val	Arg	Ala	Val	Val	Asp	Ser	Leu	Lys	195	200	205	
Lys	Tyr	Pro	Arg	Val	Asn	Ala	Tyr	Ile	Glu	Asp	Asn	Glu	Ile	Val	Tyr	210	215	220	
Arg	His	Tyr	Tyr	Asp	Ile	Ser	Ile	Ala	Ile	Gly	Thr	Asp	Arg	Gly	Leu	225	230	235	240
Val	Val	Pro	Val	Ile	Arg	Asn	Cys	Asp	Gln	Leu	Ser	Ser	Gly	Glu	Ile	245	250	255	
Glu	Leu	Gln	Leu	Ala	Asp	Leu	Ala	Ser	Arg	Ala	Arg	Glu	Gly	Lys	Leu	260	265	270	
Ala	Ile	His	Glu	Leu	Glu	Gly	Gly	Gly	Phe	Thr	Ile	Thr	Asn	Gly	Gly	275	280	285	
Val	Tyr	Gly	Ser	Leu	Leu	Ser	Thr	Pro	Ile	Ile	Asn	Pro	Pro	Gln	Val	290	295	300	
Gly	Ile	Leu	Gly	Met	His	Lys	Ile	Glu	Lys	Arg	Pro	Val	Val	Arg	Glu	305	310	315	320
Asp	Ala	Ile	Val	Ile	Ala	Asp	Met	Met	Tyr	Val	Ala	Met	Ser	Tyr	Asp	325	330	335	
His	Arg	Ile	Ile	Asp	Gly	Lys	Glu	Ala	Val	Gly	Phe	Leu	Val	Asn	Val	340	345	350	
Lys	Glu	Gln	Leu	Glu	Gln	Pro	Glu	Leu	Leu	Leu	Lys	Met				355	360	365	

## (2) INFORMATIONS POUR LA SEQ ID NO: 416:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 906 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(407056..409773)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 416:

Ile	Arg	Leu	Met	Asp	Ser	Asp	Phe	Ala	Arg	His	Val	His	Ser	Ser	Asp
1			5					10					15		
Ile	Asp	Trp	Ile	Glu	Ser	Leu	Phe	Glu	Arg	Phe	Glu	Lys	His	Glu	Pro
		20						25				30			
Met	Asp	Ser	Ser	Trp	Lys	Tyr	Phe	Phe	Glu	Gly	Tyr	Gln	Val	Gly	Lys
		35					40					45			
Thr	Glu	Gly	Ser	Pro	Thr	Glu	Ser	Ser	His	Asp	Gln	Phe	Phe	Thr	Ser
	50					55					60				
Leu	Gln	Glu	Lys	Lys	Ala	His	Ser	Leu	Leu	Met	Ile	Tyr	Arg	Tyr	Tyr
65				70					75						80
Gly	Tyr	Leu	Gln	Gly	Gln	Val	Ser	Pro	Ile	Ser	Ser	Ser	Glu	Glu	Ser
			85					90					95		
Ser	Leu	Val	Thr	Glu	Lys	Val	Arg	Asn	Phe	Asp	Pro	Gln	Glu	Glu	Ile
			100					105				110			
Pro	Ser	Leu	Gly	Leu	Leu	Pro	Gln	Ser	Tyr	Val	Arg	Ile	Ala	Asp	Phe
		115					120					125			
Ile	Gln	Val	Leu	Lys	Glu	Lys	Tyr	Cys	Arg	Ser	Ile	Ser	Val	Glu	Thr
	130				135						140				
Leu	Asn	Cys	Ser	Pro	Glu	Ile	Gln	Glu	Tyr	Val	Trp	Lys	Leu	Met	Glu
145				150					155						160
Gly	Glu	Lys	Pro	Ser	Leu	Thr	Lys	Glu	Val	Leu	Leu	Ala	Arg	Tyr	Arg
			165					170					175		
Asp	Val	Lys	Arg	Ala	Val	Ala	Phe	Glu	Glu	Phe	Leu	Gln	Val	Lys	Phe
			180					185				190			
Thr	Gly	Lys	Lys	Arg	Phe	Ser	Leu	Glu	Gly	Gly	Glu	Ser	Leu	Val	Pro
		195					200					205			
Met	Leu	Glu	His	Leu	Ile	Ala	Cys	Gly	Val	Lys	Gln	Gly	Ile	Asn	Arg
	210				215						220				
Tyr	Val	Met	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Ala	Asn
225				230					235						240
Ile	Phe	Gly	Lys	Pro	Tyr	Arg	Gln	Ile	Phe	Met	Glu	Phe	Glu	Asp	Ala
			245						250				255		
Pro	Gln	Ile	Arg	Gly	Leu	Glu	Thr	Val	Gly	Asp	Val	Lys	Tyr	His	Lys
			260				265						270		
Gly	Tyr	Val	Ala	Asn	Arg	Pro	Glu	Gln	Asn	Val	Met	Met	Ala	Leu	Leu
		275					280					285			
Pro	Asn	Pro	Ser	His	Leu	Glu	Ser	Val	Asp	Pro	Val	Val	Glu	Gly	Ala
	290				295						300				
Val	Ala	Ala	Ile	Gln	His	Gln	Gly	Glu	Ala	Gly	Lys	Glu	Gln	Ala	Cys
305				310						315					320
Leu	Ala	Val	Leu	Met	His	Gly	Asp	Ala	Ala	Leu	Ala	Gly	Gln	Gly	Val
			325					330					335		
Val	Tyr	Glu	Thr	Phe	Gln	Leu	Ser	Gly	Ile	Pro	Gly	Tyr	Ser	Thr	Glu
			340					345				350			
Gly	Thr	Val	His	Ile	Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Ala	Gln

		355					360					365					
Pro	Arg	Glu	Ser	Arg	Ser	Thr	Pro	Tyr	Cys	Thr	Asp	Ile	Ala	Lys	Met		
	370					375					380						
Met	Gly	Ile	Pro	Val	Phe	Arg	Val	Asn	Gly	Glu	Asp	Val	Leu	Ala	Cys		
385					390					395					400		
Leu	Gln	Val	Met	Glu	Tyr	Ala	Ile	His	Ile	Arg	Glu	Arg	Phe	His	Cys		
				405					410						415		
Asp	Val	Ile	Ile	Asp	Leu	Cys	Cys	Tyr	Arg	Lys	Tyr	Gly	His	Asn	Glu		
				420				425						430			
Ser	Asp	Asp	Pro	Ser	Val	Thr	Ala	Pro	Phe	Leu	Tyr	Glu	Glu	Ile	Lys		
		435					440					445					
Lys	Lys	Lys	Gln	Gly	Ser	Glu	Leu	Phe	Lys	Glu	Ile	Leu	Leu	His	His		
	450					455					460						
Pro	Glu	Trp	Asn	Ile	Ser	Ser	Asn	Glu	Leu	Glu	Arg	Ile	Asp	Thr	Glu		
465					470					475					480		
Ile	Ala	His	Val	Leu	Asn	Gln	Glu	Tyr	Ala	Ser	Leu	Lys	Asp	Pro	Gly		
				485					490						495		
Val	Glu	Arg	Leu	Asp	Glu	Cys	Met	His	Cys	Thr	Arg	Met	Ala	Ala	Gly		
			500					505					510				
Glu	Leu	Leu	Val	Asp	Asn	Val	Asp	Thr	Ser	Leu	Asp	Lys	Glu	Ala	Leu		
		515					520					525					
Phe	Asp	Leu	Ser	Ala	Lys	Leu	Cys	Asp	Ile	Pro	Glu	His	Phe	Ser	Pro		
	530					535					540						
His	Ala	Lys	Ile	Arg	Ser	Leu	Leu	Asn	Lys	Arg	Met	Ser	Met	Ala	Asp		
545					550					555					560		
Gly	Glu	Ile	Gly	Tyr	Asp	Trp	Gly	Met	Ala	Glu	Glu	Val	Ala	Phe	Ala		
				565					570					575			
Ser	Leu	Leu	Gln	Glu	Gly	Phe	Ser	Leu	Arg	Leu	Ser	Gly	Gln	Asp	Ser		
			580					585					590				
Ile	Arg	Gly	Thr	Phe	Ser	Gln	Arg	Gln	Leu	Val	Trp	Thr	Asp	Val	Gln		
		595					600					605					
Thr	Gly	Asp	Thr	Phe	Ser	Pro	Leu	Tyr	His	Leu	Ser	Pro	Ser	Gln	Gly		
	610					615						620					
Ser	Val	Glu	Leu	Tyr	Asn	Ser	Pro	Leu	Ser	Glu	Tyr	Ala	Val	Leu	Gly		
625					630					635					640		
Phe	Glu	Tyr	Gly	Tyr	Ala	Gln	Gln	Ala	Glu	Lys	Thr	Leu	Val	Ile	Trp		
				645					650					655			
Glu	Ala	Gln	Phe	Gly	Asp	Phe	Ser	Asn	Gly	Ala	Gln	Ile	Ile	Phe	Asp		
			660					665					670				
Gln	Tyr	Ile	Ser	Ser	Gly	Ile	Gln	Lys	Trp	Asp	Leu	His	Ser	Asp	Val		
		675					680					685					

```

Ile Ser Lys Tyr Thr Glu Val His His Tyr Val Trp Leu Gln Glu Glu
      835                      840                      845
Pro Gln Asn Met Gly Ala Phe Ser Tyr Phe Ala Leu Ala Thr Asp Glu
      850                      855                      860
Ile Phe Pro Ser Lys Leu Gln Cys Val Cys Arg Pro Arg Ser Ser Ser
865                      870                      875                      880
Thr Ala Thr Gly Ser Ala Ser Leu Ser Gln Lys Glu Leu Ser Met Leu
      885                      890                      895
Met Glu Thr Leu Phe Ser Ile Gly Arg Glu
      900                      905

```

(2) INFORMATIONS POUR LA SEQ ID NO: 417:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 295 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 410532..411416

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 417:

```

Met Asn Gly Lys Thr Pro Leu Ala Leu Tyr Ile His Ile Pro Phe Cys
1      5      10      15
Ser Lys Lys Cys His Tyr Cys Ser Phe Tyr Thr Ile Pro Tyr Lys Glu
      20      25      30
Glu Leu Met Arg Ser Tyr Cys Glu Ala Val Ile Lys Glu Gly Leu Lys
      35      40      45
Lys Leu Ala Pro Leu Arg Cys Ser His Tyr Ile Asp Thr Val Phe Phe
      50      55      60
Gly Gly Gly Thr Pro Ser Leu Val Pro Pro Ala Leu Ile Gln Asp Ile
65      70      75      80
Leu Val Ala Leu Glu Ala Gln His Ala Thr Glu Ile Thr Leu Glu Ala
      85      90      95
Asn Pro Glu Asn Leu Ser Leu Glu Tyr Ile Gln Ala Leu Ala Leu Thr
      100     105     110
Ser Ile Asn Arg Ile Ser Ile Gly Val Gln Thr Phe Asn Asp Pro Leu
      115     120     125
Leu Lys Leu Leu Gly Arg Thr His Ser Ser Ser Lys Ala Ile Glu Ala
      130     135     140
Phe Met Leu Cys Ser Gln Tyr Gly Phe Ser Asn Val Ser Ala Asp Leu
145     150     155     160
Ile Tyr Gly Leu Pro Thr Gln Ser Ile Ser Asp Phe Ile Val Asp Leu
      165     170     175
Arg Gln Ala Ile Ser Leu Pro Ile Gln His Ile Ser Ile Tyr Asn Leu
      180     185     190
Thr Ile Asp Pro His Thr Ser Phe Tyr Lys His Arg Lys Arg Ile Leu
      195     200     205
Pro Ser Ile Ala Asp Asp Asp Ser Leu Ala Glu Met Ala Leu Ala Ala
      210     215     220
Glu Glu Leu Leu Glu Asn Gln Gly Phe Thr Arg Tyr Glu Leu Ala Ser
225     230     235     240
Tyr Ala Lys Asn Gln Ala Ala Ser Lys His Asn Thr Tyr Tyr Trp Thr
      245     250     255
Ala Lys Pro Phe Leu Gly Leu Gly Val Ser Ala Ser Gln Tyr Leu His

```



	260		265		270
Gly	Ile	Arg	Ser	Lys	Asn
	275		280		285
Arg	Ile	Asn	Ile	Tyr	Arg
	290		295		

(2) INFORMATIONS POUR LA SEQ ID NO: 418:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 568 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 411707..413410

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 418:

Phe	Leu	Ile	Glu	Lys	Met	Asn	Lys	Lys	Glu	Arg	Ile	Asn	Lys	Lys	Asn
1				5					10					15	
Ala	Ser	Thr	Lys	Ile	Gln	Arg	Asn	Thr	Pro	Thr	Arg	Ala	Leu	Leu	Ser
			20					25					30		
Ile	Gly	Ser	Gln	Gln	Leu	Ser	Ser	Phe	Thr	Lys	Leu	Ser	Phe	Asn	Asn
			35				40					45			
Glu	Ala	Lys	Leu	Ser	Gly	Val	Ala	Thr	Pro	Thr	Arg	Asp	Thr	Asp	Val
	50					55					60				
Val	Pro	Leu	Gln	Tyr	Leu	Gln	Ala	Arg	Tyr	Leu	Ser	Lys	Asn	Asp	Pro
65					70					75					80
Asn	Pro	Asp	Tyr	Leu	Pro	Ile	His	Gly	Gly	Ser	Met	Thr	Gly	Asn	Ile
				85					90					95	
Asn	Met	Gly	Thr	His	Ser	Val	Phe	Asn	Leu	Lys	Gln	Pro	Thr	Lys	Pro
			100					105					110		
Ser	Ala	Thr	Leu	Pro	Glu	Glu	Ser	Ser	Lys	Pro	Lys	Asp	Pro	Arg	Glu
			115					120				125			
Glu	Glu	Gly	Phe	Thr	Lys	Lys	Thr	Ala	Glu	Lys	Gln	Glu	Gln	Ala	Ile
	130					135					140				
Lys	Glu	Tyr	Asn	Thr	Lys	Leu	Ala	Glu	Tyr	Gln	Lys	Lys	Ile	Asp	Asp
145					150					155					160
Tyr	Asn	Ala	Ala	Trp	Glu	Ala	Phe	Tyr	Ser	Glu	Ala	Ala	Thr	Val	Lys
				165					170					175	
Tyr	Val	Lys	Gly	Ile	Val	Asp	Lys	Ile	Leu	Asn	Asn	Asn	Lys	Leu	Ser
			180					185					190		
Thr	Ala	Leu	Asn	Ser	Ala	Thr	Glu	Val	Glu	Lys	Lys	Ile	Ala	Leu	Ala
			195				200					205			
Gln	Lys	Ala	Leu	Gly	Ile	Glu	Ile	Thr	Ile	Asn	Pro	Asp	Ala	Asp	Thr
	210					215					220				
Asp	Pro	Val	Pro	Glu	Thr	Pro	Lys	Pro	Thr	Pro	Thr	Thr	Asp	Thr	Glu
225					230					235					240
Glu	Lys	Glu	Ser	Pro	Pro	Leu	Ser	Tyr	Asp	Asp	Leu	Pro	Ser	Val	Ile
				245					250					255	
Lys	Asn	Ala	Gln	Phe	Val	Val	Thr	Gln	Ser	Gln	Asn	Lys	Leu	Thr	Gly
			260					265					270		
Asp	Leu	Lys	Met	Thr	Asn	Ala	Gln	Ile	Ala	Asn	Ile	Lys	Thr	Pro	Asp
			275				280					285			
Thr	Gly	Asp	Ser	Asn	Tyr	Ala	Ala	Asn	Val	Thr	Tyr	Leu	Glu	Ser	Lys
	290					295					300				

Leu Lys Gln Pro Lys Arg Ala Phe Leu Ser Asn Thr Leu Pro Thr Thr  
 305 310 315 320  
 Thr Ser Ser Pro Thr Ile Ser Phe Asn Gly Tyr Ile Pro Trp Leu Ser  
 325 330 335  
 Thr Thr Asn Gly Ser Ser Ser Pro Thr Glu Pro Asp Phe Lys Ser Glu  
 340 345 350  
 Leu Ala Asp Lys Cys Phe Thr Ala Glu Gln Glu Asn Leu Lys Val Lys  
 355 360 365  
 Thr Ala Gly Leu Leu Val Leu Ser Val Arg Gly Thr Trp Ser Pro Thr  
 370 375 380  
 Thr Ala Thr Ile Ala Asp Gly Ser Thr Gln Thr Pro Lys Thr Ile Ser  
 385 390 395 400  
 Val Asn Leu Thr Val Thr Pro Asp Asn Ser Ser Gly Thr Asn Thr Pro  
 405 410 415  
 Ser Ser Gly Ser Asp Ser Ser Gly Asp Ala Ser Ala Thr Thr Leu Thr  
 420 425 430  
 Ile Pro Leu Thr Leu Tyr Ser Arg Glu Ser Val Gln Leu Gln Leu Pro  
 435 440 445  
 Ile Lys Thr Ala Ser Asp Ile Lys Met Asp Thr Ser Ser Gln Thr Ser  
 450 455 460  
 Asn Gly Gly Ser Gly Ser Val Ser Ser Ser Ala Thr Glu Thr Leu Thr  
 465 470 475 480  
 Ile Pro Leu Thr Leu Tyr Ser Gly Glu Ser Val Gln Leu Gln Leu Pro  
 485 490 495  
 Ile Thr Thr Thr Ser Ser Val Lys Met Ala Thr Thr Thr Ser Gln Thr  
 500 505 510  
 Ser Asn Gly Gly Gly Asp Thr Ser Ser Gln Ile Thr Leu Ser Ser Trp  
 515 520 525  
 Ser Trp Glu Ala Ala Leu Tyr Pro Thr Asp Val Thr Val Thr Asn Lys  
 530 535 540  
 Thr Thr Pro Pro Thr Thr Lys Thr Pro Ser Ser Pro Ser Pro Asn Ser  
 545 550 555 560  
 Lys Met Ile Lys Asn Lys Ile Val  
 565

(2) INFORMATIONS POUR LA SEQ ID NO: 419:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(412606..413433)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 419:

Ile Phe Asn Phe Val Asn Leu Tyr Thr Ile Leu Phe Leu Ile Ile Phe  
 1 5 10 15  
 Glu Leu Gly Asp Gly Asp Glu Gly Val Phe Val Val Gly Gly Val Val  
 20 25 30  
 Leu Leu Val Thr Val Thr Ser Val Gly Tyr Arg Ala Ala Ser Gln Asp  
 35 40 45  
 Gln Asp Asp Ser Val Ile Cys Asp Glu Val Ser Pro Pro Pro Leu Glu  
 50 55 60  
 Val Trp Glu Val Val Val Ala Ile Phe Thr Leu Asp Val Val Val Ile

65					70					75				80
Gly	Ser	Cys	Ser	Cys	Thr	Asp	Ser	Pro	Glu	Tyr	Ser	Val	Arg	Gly Ile
				85					90				95	
Val	Ser	Val	Ser	Val	Ala	Glu	Asp	Asp	Thr	Glu	Pro	Leu	Pro	Pro Leu
			100				105					110		
Glu	Val	Trp	Glu	Glu	Val	Ser	Ile	Phe	Met	Ser	Asp	Ala	Val	Leu Ile
		115					120				125			
Gly	Ser	Cys	Ser	Cys	Thr	Asp	Ser	Leu	Glu	Tyr	Ser	Val	Arg	Gly Ile
	130					135					140			
Val	Ser	Val	Val	Ala	Glu	Ala	Ser	Pro	Glu	Glu	Ser	Asp	Pro	Leu Leu
145					150					155				160
Gly	Val	Leu	Val	Pro	Leu	Glu	Leu	Ser	Gly	Val	Thr	Val	Arg	Phe Thr
			165						170				175	
Asp	Met	Val	Leu	Gly	Val	Cys	Val	Leu	Pro	Ser	Ala	Ile	Val	Ala Val
		180						185				190		
Val	Gly	Leu	His	Val	Pro	Leu	Thr	Asp	Lys	Thr	Ser	Arg	Pro	Ala Val
	195					200					205			
Phe	Thr	Phe	Arg	Phe	Ser	Cys	Ser	Ala	Val	Lys	His	Leu	Ser	Ala Ser
	210					215					220			
Ser	Leu	Leu	Lys	Ser	Gly	Ser	Val	Gly	Glu	Glu	Asp	Pro	Phe	Val Val
225					230					235				240
Leu	Ser	His	Gly	Met	Tyr	Pro	Leu	Asn	Glu	Ile	Val	Gly	Glu	Leu Val
			245						250				255	
Val	Val	Gly	Arg	Val	Leu	Glu	Arg	Lys	Ala	Leu	Leu	Gly	Cys	Leu Ser
		260						265				270		
Leu	Asp	Ser	Arg											
		275												

(2) INFORMATIONS POUR LA SEQ ID NO: 420:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 413404..413952

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 420:

Asp	Ser	Ile	Glu	Ile	Tyr	Glu	Val	Lys	Asp	Leu	Lys	Asn	Glu	Ile	Met
1				5					10					15	
Asn	Asp	Ile	Lys	Asn	Asn	Ile	Ser	Ser	Ser	Phe	Trp	Asn	Pro	Asn	Lys
		20					25					30			
Val	Val	Thr	Lys	Val	Leu	Leu	Lys	Val	Ser	Glu	Thr	Gly	Ile	Glu	Ser
	35						40					45			
Thr	Pro	Gly	Ile	Val	Lys	His	Asn	Gln	Pro	Ile	Thr	Gln	Ser	Glu	Asn
	50					55					60				
Pro	Lys	Asp	Pro	Thr	Asp	Ala	Val	Thr	Phe	Lys	Tyr	Leu	Lys	Glu	Asn
65				70					75					80	
Tyr	Thr	Lys	Glu	Asn	Asp	Pro	Asn	Pro	Gly	Phe	Leu	Pro	Thr	Lys	Gly
			85						90				95		
Gly	Thr	Met	Thr	Gly	Asp	Ile	Asp	Met	Gln	Gly	Asn	Asn	Val	Thr	Asp
		100						105					110		
Ile	Val	Met	Tyr	Lys	Gln	Asn	Gly	Gln	Gln	Asp	Pro	Asp	Asp	Gly	Ser
		115					120					125			

Ala Val Thr Ile Gly Tyr Leu Asn Glu Lys Ala Asp Glu Ile Lys Ser  
 130 135 140  
 Asn Asp Lys Ile Thr Arg Val Ser Gln Ala Tyr Arg Ile Leu Thr His  
 145 150 155 160  
 Lys Tyr Pro Arg Tyr Thr Asn Phe Ser Val Leu Leu Lys Ile Leu Thr  
 165 170 175  
 Leu Ser Leu Thr Gln Ile Phe  
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 421:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 424 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 413841..415112

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 421:

Gln Asn Tyr Thr Gly Val Ala Gly Leu Ser Asp Ile Asn Ser Gln Ile  
 1 5 10 15  
 Ser Thr Leu His Gln Leu Leu Gly Ile Ala Glu Asp Pro Asp Thr Val  
 20 25 30  
 Thr Asn Pro Asp Leu Leu Lys Thr Ser Gly Gly Thr Val Tyr Glu Asn  
 35 40 45  
 Ile Asp Met Asn Ser Asn Thr Val Ser Asp Leu Gly Thr Pro Thr Asn  
 50 55 60  
 Lys Asp Thr Lys Ser Ala Ile Asn Val Glu Phe Val Gln Ala Lys Ile  
 65 70 75 80  
 Thr Ser Pro Gln Met Ala Phe Leu Lys Asn Asn Asp Thr Asn Leu Ser  
 85 90 95  
 Asn Ile Thr Val Ser Glu Tyr Phe Asn Trp Leu Gln Ala Pro Thr Pro  
 100 105 110  
 Asn Pro Ala Pro Thr Thr Pro Asp Asn Ser Asn Thr Pro Asn Asn Pro  
 115 120 125  
 Pro Ser Ser Ser Asn Gly Ala Ser Ser Phe Ile Arg Glu Leu Ala Ala  
 130 135 140  
 Thr Thr Thr Gly Ser Thr Asp Thr Glu Ile Thr Pro Ala Ala Glu Gly  
 145 150 155 160  
 Thr Asp Leu Pro Asn Thr Thr Phe Ser Glu Lys Ser Pro Leu Trp Glu  
 165 170 175  
 Glu Phe Phe Ser Tyr Pro Asp Ser Ser Arg Ser Glu Met Val Ile Gln  
 180 185 190  
 Lys Thr Gly Ile Leu Thr Phe Ser Met Gln Gly Thr Trp Asn His Pro  
 195 200 205  
 Asn Asn Thr Thr Pro Thr Ser Thr Asp Pro Ile Ser Leu Glu Leu Thr  
 210 215 220  
 Val Thr Pro Pro Lys Thr Asp Thr Thr Pro Lys Ser Pro Ser Ser Ser  
 225 230 235 240  
 Pro Lys Lys Thr Thr Ser Glu Ala Thr Ser Ser Pro Ala Thr Asn Gly  
 245 250 255  
 Pro Thr Thr Ala Ser Ile Thr Lys Thr Phe Ser Arg Lys Tyr Asn Leu  
 260 265 270  
 Ser Ala Thr Pro Ser Pro Thr Pro Thr Thr Pro Thr Thr Pro Asp Pro

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      275              280              285
Ile Thr Lys Lys Phe Ser Leu Ala Ser Gly Gln Ser Cys Thr Leu Gln
  290              295              300
Ile Pro Val Gln Ala Thr Gly Ser Val Leu Lys Leu Lys Tyr Val Asn
305              310              315              320
Pro Asn Asn Asn Ser Ser Gly Gly Ser Ser Gly Ser Gly Gly Asp Ser
      325              330              335
Gln Glu Glu Asn Pro Thr Ser Ser Ser Gly Thr Asn Asn Ala Pro Ala
      340              345              350
Ser Gln Thr Ser Arg Ile Gln Ile Arg Tyr Ala Ser Thr Thr Thr Thr
      355              360              365
Asp Ser Gly Ser Thr Thr Lys Asn Pro Ile Lys Ala Gln Ala Asp Glu
      370              375              380
Ser Thr Pro Pro Glu Thr Thr Ser Thr Gly Ile Thr Leu Thr Ser Phe
385              390              395              400
Ser Trp Ser Leu Val Leu Thr Ser Gly Glu Ile Thr Lys Ala Lys Ser
      405              410              415
Thr Pro Ser Thr Pro Ser Gln Pro
      420

```

(2) INFORMATIONS POUR LA SEQ ID NO: 422:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(413978..414379)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 422:

```

Glu Lys Asn Ser Ser His Lys Gly Asp Phe Ser Glu Asn Val Val Phe
1              5              10              15
Gly Arg Ser Val Pro Ser Ala Ala Gly Val Ile Ser Val Ser Val Glu
      20              25              30
Pro Val Val Val Ala Ala Ser Ser Leu Ile Asn Glu Glu Ala Pro Phe
      35              40              45
Glu Glu Asp Gly Gly Leu Phe Gly Val Leu Leu Leu Ser Gly Val Val
      50              55              60
Gly Ala Gly Phe Gly Val Gly Ala Cys Ser Gln Leu Lys Tyr Ser Glu
      65              70              75              80
Thr Val Ile Leu Glu Arg Phe Val Ser Leu Phe Phe Arg Lys Ala Ile
      85              90              95
Cys Gly Glu Val Ile Leu Ala Cys Thr Asn Ser Thr Leu Ile Ala Leu
      100              105              110
Leu Val Ser Leu Phe Val Gly Val Pro Arg Ser Asp Thr Val Leu Leu
      115              120              125
Phe Ile Ser Ile Phe Ser
      130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 423:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 496 acides aminés

(B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(415177..416664)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 423:

Leu	Ile	Lys	Arg	Gln	Asn	Met	Asn	Lys	Lys	Ile	Ile	Lys	Glu	Arg	Val
1				5					10					15	
Ser	Ser	Ser	Val	Pro	Ser	Thr	Pro	Ser	Asp	Gln	Pro	Ala	Asp	Pro	Thr
			20					25					30		
Asn	Pro	Val	Thr	Lys	Met	Leu	Phe	Glu	Cys	Lys	Leu	Ser	Gln	Asn	Gln
		35					40					45			
Gly	Asp	Ala	Ser	Ala	Asp	Val	Asp	Ala	Met	Val	Thr	Thr	Ala	His	Val
	50					55					60				
Lys	Leu	Asp	Ala	Lys	Asn	Gln	Gln	Val	Arg	Lys	Val	Ala	Lys	Arg	Glu
65					70					75					80
Glu	Asp	Gln	Asn	Val	Ile	Val	Leu	Ser	Gln	Leu	Glu	Gly	Tyr	Leu	Gln
			85						90					95	
Lys	Gly	Ser	Arg	Ser	Ile	Ala	Gly	Leu	Phe	Leu	Pro	Thr	Ser	Gly	Gly
			100					105						110	
Ala	Met	Val	Gly	Asp	Ile	Asn	Met	Gly	Thr	Ser	Pro	Gly	Asn	Thr	Ile
		115					120					125			
Lys	Gly	Leu	Pro	Ser	Ser	Trp	Gly	Ser	Ala	Met	Phe	Leu	Gly	Asn	Glu
	130					135					140				
Tyr	Ala	Ala	Ser	Val	Gly	Ile	Val	Gln	Asp	Val	Val	Gly	Glu	Tyr	Arg
145					150					155					160
Ala	Arg	Leu	Asp	Asp	Leu	Ile	Asp	Arg	Ile	Thr	Lys	Tyr	Ala	Gly	Ser
				165					170					175	
Gly	Glu	Gly	Ser	Leu	Glu	Gln	Leu	Ile	Lys	Asp	Leu	Gly	Ser	Pro	Gln
			180					185					190		
Glu	Ser	Gln	Ala	Gly	Gln	Thr	Pro	Ser	Val	Thr	Leu	Glu	Lys	Pro	Thr
		195					200					205			
Asp	Ala	Lys	Trp	Leu	Leu	Leu	Ser	Ala	Lys	Asn	Ala	Met	Thr	Gly	Thr
	210					215					220				
Leu	Arg	Phe	Glu	Lys	Lys	Gln	Gly	Ala	Leu	Pro	Thr	Thr	Pro	Asp	Pro
225					230					235					240
Thr	Ile	Thr	Asn	Leu	Lys	Ala	Gly	Gly	Leu	Gly	Thr	Ile	Gly	Thr	Ala
				245					250					255	
Thr	Pro	Lys	Asp	Lys	Leu	Gln	Asn	Ile	Val	Ser	Val	Ala	Asp	Leu	Thr
			260					265					270		
Thr	Ile	Leu	Lys	Asp	Leu	Gln	Asn	Asn	Ala	Pro	Ser	Glu	Gly	Thr	Gly
		275					280					285			
Ser	His	Thr	Gly	Ser	Asp	Val	Gly	Ser	Arg	Ser	Gly	Ser	Gly	Thr	Asp
	290					295					300				
Ser	Val	Ser	Gly	Gly	Val	Ala	Gly	Ala	Ser	Val	Ser	Thr	Thr	Thr	Ala
305					310					315					320
Ser	Thr	Phe	Pro	Glu	Trp	Thr	Gly	Gln	Glu	Val	Pro	Tyr	Leu	Val	Glu
				325					330					335	
Gln	Ser	Pro	Asp	Ser	Gly	Ser	Gly	Ser	Leu	Ser	Val	Gln	Asn	Pro	Leu
			340					345					350		
Lys	Ser	Ser	Asn	Ala	Asp	Asn	Tyr	Ile	Lys	Lys	Asp	Asn	Gly	Thr	Tyr
		355					360					365			
Ser	Leu	Leu	Arg	Arg	Gly	Leu	Tyr	Leu	Ile	Thr	Phe	Ala	Tyr	Glu	Phe
	370					375					380				
Gly	Ser	Pro	Ile	Gln	Asn	Gly	Ala	Val	Thr	Cys	Thr	Gly	Thr	Leu	Arg

385					390					395					400
Lys	Lys	Ser	Asp	Ser	Thr	Ser	Ala	Gly	Gly	Asp	Val	Ala	Ala	Gln	Pro
				405					410					415	
Thr	Ser	Gly	Asp	Ala	Thr	Ala	Pro	Thr	Asp	Pro	Glu	Pro	Ser	Pro	Ala
			420					425					430		
Phe	Ser	Val	Val	Gly	Ser	Ser	Asp	Gly	Lys	Thr	Val	Val	Gly	Ser	Ala
		435					440					445			
Tyr	Ile	Leu	Val	Pro	Gly	Asp	Lys	Ala	Leu	Ser	Lys	His	Thr	Leu	Thr
	450					455					460				
Leu	Ala	Leu	Thr	Pro	Gly	Lys	Asn	Thr	Glu	Val	Ser	Pro	Thr	Ser	Ala
465					470					475					480
Thr	Ala	Ser	Lys	Ser	Tyr	Val	Ala	Ile	Ser	Tyr	Met	Gly	Ala	Gly	Tyr
				485					490					495	

(2) INFORMATIONS POUR LA SEQ ID NO: 424:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 237 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(416740..417450)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 424:

Met	Ala	Leu	Tyr	Leu	Leu	Pro	Asn	Thr	Leu	Gly	Ser	Lys	Arg	Ser	Glu
1				5					10					15	
Asp	Leu	Pro	Ser	Ser	Val	Gly	Glu	Ile	Val	Arg	Asn	Lys	Ile	Gln	Gly
			20					25					30		
Leu	Ile	Val	Glu	Ser	Asp	Arg	Gly	Gly	Arg	Leu	Phe	Leu	Ser	Leu	Trp
		35					40					45			
Lys	Val	Glu	Glu	Pro	His	Arg	Phe	Pro	Leu	Ala	Val	Met	Ser	Lys	Asn
	50					55					60				
Asp	Thr	Ser	Val	Lys	Ala	Cys	Asp	Phe	Tyr	Leu	Glu	Pro	Ile	Leu	Lys
65				70					75					80	
Lys	Gln	Glu	Ser	Trp	Gly	Val	Ile	Ser	Asp	Ala	Gly	Leu	Pro	Cys	Ile
			85						90				95		
Ala	Asp	Pro	Gly	Ala	Lys	Leu	Val	Arg	Arg	Ala	Arg	Thr	Leu	Gly	Ile
		100						105					110		
Pro	Val	His	Ala	Val	Ser	Gly	Pro	Cys	Ser	Ile	Thr	Gln	Ala	Leu	Met
		115					120					125			
Leu	Ser	Gly	Leu	Pro	Gly	Gln	Asn	Phe	Thr	Phe	His	Gly	Tyr	Leu	Pro
	130					135					140				
Gln	Asn	Pro	Lys	Glu	Arg	Ser	Arg	Tyr	Leu	Arg	Ser	Cys	Ser	Gly	Lys
145				150					155					160	
Ser	His	Thr	Gln	Ile	Cys	Ile	Glu	Thr	Pro	Tyr	Arg	Asn	Pro	Tyr	Thr
			165						170				175		
Phe	Asp	Ala	Leu	Leu	Asp	Gln	Leu	Pro	Asp	His	Gly	Glu	Leu	Cys	Val
		180					185					190			
Ala	Ile	Asp	Leu	Met	Gly	Asp	Gln	Glu	Tyr	Val	Ser	Thr	Arg	Ser	Ile
	195					200						205			
Ala	Val	Trp	Asn	Gln	Ser	Ser	Asp	Ile	Glu	Glu	Val	Arg	Glu	Arg	Leu
	210				215						220				
Lys	Lys	Val	Pro	Ala	Ile	Phe	Leu	Phe	Ile	Thr	Ser	Phe			
225					230				235						

(2) INFORMATIONS POUR LA SEQ ID NO: 425:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(417721..418053)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 425:

Leu	Lys	Val	Leu	Ile	Lys	Arg	Ser	Lys	Glu	Leu	Gln	Leu	Ser	Cys	Ser
1				5				10					15		
Leu	Gly	Val	Ala	Lys	Ile	Phe	Val	Ser	Lys	Phe	Pro	Gln	Thr	Gly	Leu
		20						25					30		
Phe	Glu	Ile	Leu	Ser	Glu	Phe	Gln	Lys	Leu	Ile	Cys	Gln	Met	Gly	Asp
		35					40					45			
Lys	Glu	Ser	Ile	Glu	Ala	Ser	Asp	Ile	Gln	Ser	Phe	Val	Glu	Lys	Lys
		50				55					60				
Glu	Ala	Ile	Ser	Leu	Trp	Lys	Leu	Arg	Asp	Ala	Leu	Leu	Arg	Lys	Asp
65					70					75				80	
Arg	Val	Ala	Ala	His	Ser	Leu	Met	Arg	Ser	Leu	Val	Ser	Asp	Met	Gly
				85					90					95	
Glu	Glu	Pro	Leu	Gly	Phe	Ser	Thr	Phe	Tyr	Val	Val	Ser	Thr	Ser	
			100					105					110		

(2) INFORMATIONS POUR LA SEQ ID NO: 426:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 191 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(418031..418603)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 426:

Glu	Phe	Ser	Phe	Pro	Gly	Phe	Leu	Tyr	Leu	Leu	Ala	Glu	Ser	Lys	Cys
1				5					10					15	
Leu	Lys	Lys	Ile	Lys	Ser	Gly	Asn	Lys	Lys	Asn	Asn	Pro	Arg	Ile	Ile
			20					25					30		
Gly	Phe	Trp	Arg	Trp	Ile	Met	Gly	Asn	Ser	Gln	Asn	Ser	Ile	His	Ile
		35					40					45			
Thr	Ser	Thr	Lys	Asp	Phe	Val	Gln	Tyr	Ile	Glu	Arg	Glu	Arg	Phe	Arg
		50				55					60				
Val	Ile	Val	Ile	Gly	Ser	Ser	Ser	Leu	Glu	Asp	Lys	Asp	Ile	Phe	Ser
65					70					75				80	
Glu	Leu	Tyr	Ile	Ser	Gly	Arg	Lys	Ser	Phe	Phe	Asp	Gly	Gln	Arg	Leu
				85					90					95	
Leu	Gln	Gln	Glu	Leu	Leu	Ser	Trp	Thr	Asp	His	Phe	Gly	Leu	Phe	Ala



			100						105					110			
Ser	Gln	Glu	Thr	Ile	Gly	Ile	Tyr	Gln	Ala	Glu	Lys	Met	Ser	Ser	Ser		
			115					120					125				
Leu	Gln	Glu	Phe	Ile	Ile	Asp	Tyr	Thr	Arg	His	Pro	Asn	Pro	Asn	Leu		
			130					135					140				
Thr	Leu	Phe	Leu	Phe	Thr	Asn	Lys	Ala	Glu	Leu	Phe	Ser	Ser	Leu	Ser		
145					150					155					160		
Ser	Lys	Leu	Ser	Asn	Ala	Leu	Cys	Leu	Ser	Leu	Phe	Gly	Glu	Tyr	Phe		
				165					170					175			
Ala	Glu	Arg	Asp	Ala	Arg	Ile	Ala	Gln	Gly	Phe	Asp	Lys	Thr	Phe			
			180					185					190				

(2) INFORMATIONS POUR LA SEQ ID NO: 427:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 293 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(418647..419525)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 427:

Met	Leu	Gly	Val	Gln	Lys	Lys	Arg	Ser	Thr	Arg	Lys	Thr	Ala	Ala	Arg		
1			5					10					15				
Lys	Thr	Val	Val	Arg	Lys	Pro	Ala	Ala	Lys	Lys	Thr	Ala	Ala	Lys	Lys		
			20					25					30				
Ala	Pro	Val	Arg	Lys	Val	Ala	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr		
			35				40					45					
Val	Ala	Lys	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Xaa	Ala		
50						55				60							
Thr	Ala	Arg	Lys	Ala	Pro	Val	Arg	Xaa	Ala	Val	Ala	Lys	Lys	Thr	Val		
65					70					75					80		
Ala	Arg	Lys	Thr	Val	Ala	Xaa	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val		
				85					90				95				
Ala	Lys	Lys	Ala	Ala	Lys	Lys	Ala	Pro	Val	Arg	Lys	Val	Ala	Ala			
			100					105				110					
Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	Val	Ala	Lys	Lys	Thr	Val	Ala	Ala		
			115				120					125					
Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala	Thr	Ala	Lys	Lys	Ala	Pro	Val	Arg		
130						135						140					
Lys	Ala	Val	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	Val	Ala	Lys	Lys		
145					150					155					160		
Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala	Thr	Gly	Lys	Lys		
				165					170					175			
Ala	Pro	Val	Arg	Lys	Val	Ala	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr		
			180					185				190					
Val	Ala	Lys	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala		
			195				200					205					
Thr	Ala	Lys	Lys	Ala	Pro	Val	Arg	Lys	Ala	Val	Ala	Lys	Lys	Thr	Val		
210						215						220					
Ala	Lys	Arg	Val	Ala	Ser	Thr	Lys	Lys	Ser	Ser	Val	Ala	Val	Lys	Ala		
225					230					235					240		
Gly	Val	Cys	Met	Lys	Lys	His	Lys	His	Thr	Ala	Ala	Cys	Gly	Arg	Val		
				245					250					255			

Ala Ala Ser Gly Val Lys Val Cys Ala Ser Ala Ala Lys Arg Lys Met  
                   260                  265                  270  
 Asn Pro Asn Arg Ser Arg Thr Ala His Ser Trp Arg Gln Gln Leu Met  
                   275                  280                  285  
 Lys Leu Val Ala Arg  
                   290

(2) INFORMATIONS POUR LA SEQ ID NO: 428:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(419672..420037)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 428:

Met Val Val Ser Leu Gly Glu Ser Val Ala Gly Phe Phe Ala Asn Asn  
 1                  5                  10                  15  
 Asp Val Leu Ala Arg Asp Leu Ala Glu Ala Ser Ser Glu Thr Gly Glu  
                   20                  25                  30  
 Ala Leu Trp Arg Met Pro Leu Val Glu Lys Tyr Asp Gln Ala Leu His  
                   35                  40                  45  
 Ser Asp Ile Ala Asp Met Lys Asn Ile Gly Ser Asn Arg Ala Gly Ser  
                   50                  55                  60  
 Ile Thr Ala Ala Leu Phe Leu Gln Arg Phe Leu Glu Asp Asn Pro Val  
 65                  70                  75                  80  
 Ala Trp Ala His Leu Asp Ile Ala Gly Thr Ala Tyr His Glu Lys Glu  
                   85                  90                  95  
 Glu Leu Pro Tyr Pro Lys Tyr Ala Thr Gly Phe Gly Val Arg Cys Leu  
                   100                  105                  110  
 Ile His Tyr Met Glu Lys Phe Leu Ser Lys  
                   115                  120

(2) INFORMATIONS POUR LA SEQ ID NO: 429:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(420245..421078)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 429:

Glu Ala Ala Val Val Asp Glu Asp Tyr Lys Leu Val Tyr Gln Asn Ala  
 1                  5                  10                  15  
 Leu Ser Asn Phe Ser Gly Lys Lys Gly Glu Thr Ala Phe Leu Phe Gly  
                   20                  25                  30  
 Asn Asp His Thr Lys Glu Gln Lys Ile Val Leu Leu Gly Leu Gly Lys

35				40				45							
Ser	Glu	Glu	Val	Ser	Gly	Thr	Thr	Val	Leu	Glu	Ala	Tyr	Ala	Gln	Ala
	50				55						60				
Thr	Thr	Val	Leu	Arg	Lys	Ala	Lys	Cys	Lys	Thr	Val	Asn	Ile	Leu	Phe
65				70						75					80
Pro	Thr	Ile	Ser	Gln	Leu	Arg	Phe	Ser	Val	Glu	Glu	Phe	Leu	Thr	Asn
				85				90						95	
Leu	Ala	Ala	Gly	Val	Leu	Ser	Leu	Asn	Tyr	Asn	Tyr	Pro	Thr	Tyr	His
			100					105						110	
Lys	Val	Asp	Thr	Ser	Leu	Pro	Phe	Leu	Glu	Lys	Val	Thr	Val	Met	Gly
		115					120							125	
Ile	Val	Ser	Lys	Val	Gly	Asp	Lys	Ile	Phe	Arg	Lys	Glu	Glu	Ser	Leu
	130					135					140				
Phe	Glu	Gly	Val	Tyr	Leu	Thr	Arg	Asp	Leu	Val	Asn	Thr	Asn	Ala	Asp
145				150						155					160
Glu	Val	Thr	Pro	Glu	Lys	Leu	Ala	Ala	Val	Ala	Lys	Gly	Leu	Ala	Gly
				165				170						175	
Glu	Phe	Ala	Ser	Leu	Asp	Val	Lys	Ile	Leu	Asp	Arg	Lys	Ala	Ile	Leu
			180					185						190	
Lys	Glu	Lys	Met	Gly	Leu	Leu	Ala	Ala	Val	Ala	Lys	Gly	Ala	Ala	Val
		195					200					205			
Glu	Pro	Arg	Phe	Ile	Val	Leu	Asp	Tyr	Gln	Gly	Lys	Pro	Lys	Ser	Lys
	210					215					220				
Asp	Arg	Thr	Val	Leu	Ile	Gly	Lys	Gly	Val	Thr	Phe	Asp	Ser	Gly	Gly
225				230						235					240
Leu	Asp	Leu	Lys	Pro	Gly	Lys	Ala	Met	Ile	Thr	Met	Lys	Glu	Asp	Met
				245				250						255	
Ala	Gly	Ala	Ala	Thr	Val	Leu	Gly	Ile	Phe	Ser	Ala	Phe	Ser	Phe	Pro
			260					265						270	
Trp	Ser	Phe	Arg	Ser	Met										
		275													

(2) INFORMATION POUR LA SEQ ID NO: 430:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(421518..421988)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 430:

Met 1	Leu	Phe	Gly	Tyr 5	Leu	Val	Gly	Phe	Leu 10	Ala	Ala	Asp	Pro	Glu 15	Glu
Arg	Met	Thr	Ser 20	Gly	Gly	Lys	Arg	Val 25	Val	Val	Leu	Arg	Leu 30	Gly	Val
Lys	Ser	Arg	Val 35	Gly	Ser	Lys	Asp 40	Glu	Thr	Val	Trp	Cys 45	Arg	Cys	Asn
Ile 50	Trp	Asn	Asn	Arg	Tyr	Asp 55	Lys	Met	Leu	Pro	Tyr 60	Leu	Lys	Lys	Gly
Ser 65	Ser	Val	Ile	Val 70	Ala	Gly	Glu	Leu	Ser	Leu 75	Glu	Ser	Tyr	Val 80	Gly
Arg	Asp	Gly	Ser 85	Pro	Gln	Ala	Ser	Ile 90	Ser	Val	Ser	Val	Asp	Thr 95	Leu

Lys Phe Asn Ser Gly Ser Ser Arg Pro Asp Ala Arg Gly Ser Asp Glu  
                   100                  105                  110  
 Gly Arg Gln Arg Ala Asn Asp Asn Val Ser Ile Gly Phe Asp Gly Glu  
                   115                  120                  125  
 Ser Leu Asp Thr Asp Ser Ala Leu Asp Lys Glu Val Tyr Ala Gly Phe  
                   130                  135                  140  
 Gly Glu Asp Gln Gln Tyr Ala Ser Glu Asp Val Pro Phe  
 145                  150                  155

(2) INFORMATIONS POUR LA SEQ ID NO: 431:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 186 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 422486..423043

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 431:

Lys Ile Leu Leu Lys Ser Leu Lys Leu Pro Asp Val Ala Phe Asp Gln  
 1                  5                  10                  15  
 Asn Asn Thr Cys Ile Leu Phe Val Asp Gly Glu Phe Ser Leu His Leu  
                   20                  25                  30  
 Thr Tyr Glu Glu His Ser Asp Arg Leu Tyr Val Tyr Ala Pro Leu Leu  
                   35                  40                  45  
 Asp Gly Xaa Pro Asp Asn Pro Gln Arg Lys Leu Ala Leu Tyr Glu Lys  
                   50                  55                  60  
 Leu Leu Glu Gly Ser Met Leu Gly Gly Gln Met Ala Gly Gly Gly Val  
 65                  70                  75                  80  
 Gly Val Ala Thr Lys Glu Gln Leu Ile Leu Met His Cys Val Leu Asp  
                   85                  90                  95  
 Met Lys Tyr Ala Glu Thr Asn Leu Leu Lys Ala Phe Ala Gln Leu Phe  
                   100                  105                  110  
 Ile Glu Thr Val Val Lys Trp Arg Thr Val Cys Ser Asp Ile Ser Val  
                   115                  120                  125  
 Asp Glu Asn Pro Leu Leu Ile Pro Cys His Lys Cys Leu Lys Gly Val  
                   130                  135                  140  
 Ala Glu Glu Phe Asn Leu Leu Gln Gln Glu Ser Val His Lys Ser Phe  
 145                  150                  155                  160  
 Ala Ile Ile Gln Gln Lys Glu Glu Gly Leu Leu Pro Phe Val Phe Lys  
                   165                  170                  175  
 Pro Pro Pro Ser Ser Leu His Phe Phe Gly  
                   180                  185

(2) INFORMATIONS POUR LA SEQ ID NO: 432:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 618 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 423226..425079

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 432:

Asn	Ser	Ser	Ile	Phe	Tyr	Arg	Pro	Gln	Asp	Trp	Ser	His	Leu	Ala	Tyr	1	5	10	15
Arg	Asn	Cys	Arg	His	Phe	Leu	Val	Asn	Gly	Arg	Met	Leu	Ile	Asn	Leu	20	25	30	
Arg	Gly	Thr	Asp	Leu	Ser	Ser	Gln	Lys	Phe	Ala	Thr	Asp	Ser	Tyr	Ile	35	40	45	
Ala	Asp	Pro	Tyr	Ser	Lys	Asn	Ile	Tyr	Ser	Pro	Gln	Leu	Phe	Gly	Ser	50	55	60	
Pro	Lys	Gln	Glu	Lys	Asp	Tyr	Ala	Phe	Ser	Tyr	Leu	Lys	Tyr	Glu	Asp	65	70	75	80
Phe	Asp	Trp	Glu	Gly	Asp	Thr	Pro	Leu	His	Leu	Pro	Lys	Glu	Asn	Tyr	85	90	95	
Phe	Ile	Tyr	Glu	Met	His	Val	Arg	Ser	Phe	Thr	Arg	Asp	Pro	Ser	Ser	100	105	110	
Gln	Val	Ser	His	Pro	Gly	Thr	Phe	Leu	Gly	Ile	Ile	Glu	Lys	Ile	Asp	115	120	125	
His	Leu	Lys	Gln	Leu	Gly	Val	His	Ala	Val	Glu	Leu	Leu	Pro	Ile	Phe	130	135	140	
Glu	Phe	Asp	Glu	Thr	Val	His	Pro	Phe	Lys	Asn	Gln	Asp	Phe	Pro	His	145	150	155	160
Leu	Cys	Asn	Tyr	Trp	Gly	Tyr	Ser	Ser	Val	Asn	Phe	Phe	Cys	Pro	Ser	165	170	175	
Arg	Arg	Tyr	Thr	Tyr	Gly	Ala	Asp	Pro	Cys	Ala	Pro	Ala	Arg	Glu	Phe	180	185	190	
Lys	Thr	Leu	Val	Lys	Ala	Leu	His	Arg	Ala	Gly	Ile	Glu	Val	Ile	Leu	195	200	205	
Asp	Val	Val	Phe	Asn	His	Thr	Gly	Phe	Glu	Gly	Thr	Ser	Cys	Pro	Leu	210	215	220	
Pro	Trp	Ile	Asp	Leu	Lys	Ser	Tyr	Tyr	Met	Val	Asn	Asp	His	Gly	Asp	225	230	235	240
Leu	Met	Asn	Phe	Ser	Gly	Cys	Gly	Asn	Thr	Val	Asn	Thr	Asn	Thr	Pro	245	250	255	
Thr	Thr	Leu	Lys	Trp	Ile	Leu	Asp	Ala	Leu	Arg	Tyr	Trp	Val	Gln	Glu	260	265	270	
Met	His	Val	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Ala	Ser	Val	Phe	Ser	Arg	275	280	285	
Asp	Pro	Gln	Gly	Val	Pro	Leu	Pro	Leu	Thr	Pro	Ile	Leu	Gln	Ala	Ile	290	295	300	
Ser	Ser	Asp	Ser	Ile	Leu	Ser	Glu	Thr	Lys	Leu	Ile	Ala	Glu	Pro	Trp	305	310	315	320
Asp	Ala	Gly	Gly	Leu	Tyr	Gln	Leu	Gly	His	Phe	Pro	Ser	Ile	Ser	Thr	325	330	335	
Arg	Trp	Ser	Glu	Trp	Asn	Gly	Cys	Tyr	Arg	Asp	His	Val	Lys	Ala	Phe	340	345	350	
Leu	Asn	Gly	Asp	Ala	His	Gln	Val	Ser	Ser	Phe	Ala	Ser	Arg	Ile	Ser	355	360	365	
Gly	Ser	His	Asp	Ile	Tyr	Pro	Asn	Gly	Lys	Pro	Thr	Asn	Ser	Ile	Asn	370	375	380	
Tyr	Ile	Cys	Ser	His	Asp	Gly	Phe	Thr	Leu	Tyr	Asp	Thr	Val	Ala	Tyr	385	390	395	400
Asn	Asp	Lys	His	Asn	Glu	Glu	Asn	Gly	Glu	Tyr	Asn	Arg	Asp	Gly	Thr	405	410	415	
Ser	Ala	Asn	Tyr	Ser	Tyr	Asn	Phe	Gly	Cys	Glu	Gly	Glu	Thr	Thr	Asp	420	425	430	

```

Pro Thr Ile Cys Ala Leu Arg Glu Arg Gln Met Lys Asn Phe Phe Leu
      435      440      445
Ala Leu Phe Leu Ser Gln Gly Ile Pro Met Ile Gln Ser Gly Asp Glu
      450      455      460
Tyr Gly His Thr Ala Tyr Gly Asn Asn Asn His Trp Cys Leu Asp Thr
465      470      475      480
Lys Ile Asn Tyr Phe Leu Trp Asp Arg Leu Ala Glu Arg Lys Glu Leu
      485      490      495
Phe Ser Phe Leu Cys Gln Val Ile Ala Leu Arg Lys Ala Tyr Thr Glu
      500      505      510
Leu Phe Asn Thr Ser Phe Leu Ser Glu Asp Thr Ile Thr Trp Leu Asn
      515      520      525
Thr Lys Gly Ser Pro Arg Glu Trp Gly Ala Asp His Tyr Leu Ala Phe
      530      535      540
Xaa Leu Lys His Leu Asn Tyr Ser Leu Phe Val Xaa Phe Tyr Ser Gly
545      550      555      560
Asn Glu Arg Ile Glu Ile Ser Leu Pro Lys Pro Arg Lys Glu His Leu
      565      570      575
Ala Tyr Glu Lys Ile Val Asp Ser Thr Thr Gly Phe Phe Ser Gln Ile
      580      585      590
Leu Ser Pro Lys Leu Ser Leu Glu Pro Tyr Ser Ser Leu Val Ala Ile
      595      600      605
Ser Arg Arg Lys Thr Ser Leu Glu Ser Arg
      610      615

```

(2) INFORMATIONS POUR LA SEQ ID NO: 433:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 303 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(425146..426054)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 433:

```

Arg Val Trp Phe Ser Glu Pro Gln Glu Asp Gly Leu Gln Pro Leu Trp
1      5      10      15
His Met Asn Ile Leu Thr Gly Thr Leu Arg Thr Gly Gly Glu Lys Asn
      20      25      30
Lys Val Lys Lys Leu Asn Leu Leu Val Leu Leu Gly Val Phe Cys Gly
      35      40      45
Val Ser Gly Val Gly Asp Ala Asp Val Lys Val Ser Asp Ala Leu Ser
      50      55      60
Gln Ser Ile Leu Val Glu Pro Lys Ile Arg Val Leu Leu Leu Ser Glu
65      70      75      80
Ser Thr Thr Ala Leu Ile Glu Ala Lys Gly Ala Phe Ser Val Phe Gly
      85      90      95
Asp Gly Glu Leu Leu Arg Val Ser Ser Gln Gly Gln Arg Cys Ala Ala
      100      105      110
His Ala Leu Tyr Gly Gly Ile Arg Trp Gly Glu Asn Tyr Pro Asn Val
      115      120      125
Glu Cys Leu Lys Ile Glu Pro Leu Asp Gly Ala Ala Ser Leu Phe Val
      130      135      140
Asn Gly Ile Gln Tyr Lys Gly Ala Ile Tyr Ile His Arg Thr Asp Arg

```

145					150					155				160	
Ser	Cys	Leu	Phe	Ile	Val	Asn	Glu	Leu	Ala	Leu	Glu	Asp	Tyr	Leu	Lys
				165					170					175	
Ser	Thr	Leu	Ser	Val	Lys	Tyr	Leu	Lys	Glu	Leu	Asp	Lys	Glu	Ala	Leu
			180					185					190		
Ser	Ala	Cys	Val	Ile	Leu	Glu	Arg	Thr	Ala	Leu	Tyr	Glu	Arg	Leu	Leu
		195					200					205			
Ala	Gly	Asn	Ser	His	Ser	Phe	Trp	His	Val	Asn	Ala	Gln	Glu	Asp	Arg
	210					215					220				
Tyr	Gly	Gly	Phe	Gly	Val	Thr	Ser	Gln	Phe	Tyr	Gly	Val	Glu	Glu	Ala
225					230					235					240
Val	Asp	Trp	Thr	Ser	Arg	Leu	Val	Leu	Asp	Asn	Pro	Glu	Gly	Leu	Val
				245					250					255	
Phe	Asn	Ala	Asp	Tyr	Leu	Leu	Arg	Ala	Asn	Val	Asp	His	Leu	Ala	Ile
			260					265					270		
Glu	Gly	Tyr	Asn	Ala	Arg	Gln	Ile	Leu	Glu	Lys	Phe	Tyr	Lys	Asp	Ala
		275				280						285			
Asp	Leu	Val	Val	Ile	Glu	Ser	Trp	Glu	Asp	Asp	Cys	Lys	Gly	Ala	
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 434:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 247 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(426245..426985)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 434:

Thr	Ile	Ala	Asn	Thr	Tyr	Met	Thr	His	Lys	Ile	Ser	Val	Leu	His	Gln
1				5					10					15	
Asp	Lys	Lys	Phe	Asp	Phe	Ser	Leu	Arg	Pro	Lys	Lys	Leu	Thr	Glu	Phe
			20					25					30		
Cys	Gly	Gln	Lys	Gln	Leu	Lys	Glu	Arg	Leu	Asp	Leu	Phe	Leu	Arg	Ala
		35					40					45			
Ala	Val	Gln	Arg	Asn	Glu	Val	Pro	Gly	His	Cys	Leu	Phe	Tyr	Gly	Pro
	50					55				60					
Pro	Gly	Leu	Gly	Lys	Thr	Ser	Leu	Ala	His	Ile	Met	Ala	Asn	Thr	Ile
65				70						75				80	
Gly	Lys	Gly	Leu	Val	Ile	Ala	Ser	Gly	Pro	Gln	Leu	Leu	Lys	Pro	Ser
				85					90					95	
Asp	Leu	Ile	Gly	Leu	Leu	Thr	Gly	Leu	Gln	Glu	Gly	Asp	Ile	Phe	Phe
			100				105						110		
Ile	Asp	Glu	Ile	His	Arg	Met	Gly	Lys	Ala	Ala	Glu	Glu	Tyr	Leu	Tyr
	115						120					125			
Pro	Ala	Met	Glu	Asp	Phe	Lys	Val	Asp	Ile	Thr	Leu	Asp	Ser	Gly	Pro
	130					135					140				
Gly	Ala	Arg	Ser	Val	Arg	Leu	Asp	Leu	Ala	Pro	Phe	Thr	Leu	Val	Gly
145					150				155					160	
Ala	Thr	Thr	Arg	Ala	Gly	Met	Leu	Ser	Glu	Pro	Leu	Arg	Thr	Arg	Phe
				165					170					175	
Ala	Phe	Thr	Gly	Arg	Val	Asp	Tyr	Tyr	Thr	Asp	Glu	Asp	Leu	Val	Ser
			180					185					190		

```

Ile Leu Ser Arg Ser Ser Gln Leu Leu Ala Ile Glu Ala Asn Gln Glu
    195                200                205
Thr Leu Leu Glu Ile Ala Arg Arg Ala Arg Gly Thr Pro Arg Leu Ala
    210                215                220
Asn Asn Leu Leu Arg Trp Val Arg Asp Phe Ala Gln Met Arg Glu Gly
225                230                235                240
Asn Cys Ile Asn Ser Arg Pro
                245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 435:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 427248..427817

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 435:

```

Met Gly Ile Lys Glu Asp Asn Trp Ile Arg Lys Met Ala Ile Glu Glu
1          5          10          15
Gly Met Ile Glu Pro Phe Ala Asp Ser Gln Val Lys Leu His Pro Glu
    20          25          30
Thr Gly Glu Lys Leu Ile Ser Tyr Gly Leu Ser Ser Tyr Gly Tyr Asp
    35          40          45
Leu Arg Ile Ser Arg Glu Phe Lys Val Phe Thr Asn Val Tyr Asn Ser
    50          55          60
Leu Val Asp Pro Lys Cys Phe Thr Glu Asp Ala Leu Ile Ser Ile Val
65          70          75          80
Asp Asp Val Cys Ile Ile Pro Pro Asn Ser Phe Ala Leu Ala Arg Ser
    85          90          95
Val Glu Tyr Phe Arg Ile Pro Arg Asn Val Leu Thr Val Cys Ile Gly
    100          105          110
Lys Ser Thr Tyr Ala Arg Cys Gly Leu Ile Val Asn Val Thr Pro Phe
    115          120          125
Glu Pro Glu Trp Glu Gly Tyr Val Thr Ile Glu Ile Ser Asn Thr Thr
    130          135          140
Pro Leu Pro Ala Lys Val Tyr Ala Asn Glu Gly Ile Ala Gln Val Leu
145          150          155          160
Phe Phe Glu Gly Asp Ala Ala Cys Asp Val Ser Tyr Ala Glu Arg Gln
    165          170          175
Gly Lys Tyr Gln Lys Gln Gln Gly Ile Thr Ile Pro Phe Val
    180          185          190

```

(2) INFORMATIONS POUR LA SEQ ID NO: 436:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 436:

(2) INFORMATION POUR LA SEQ ID NO: 437:

(A) LONGUEUR: 168 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(429857..430360)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 437:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 438:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(430323..430637)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 438:

Gly	Lys	Glu	Met	Lys	Arg	Ile	Leu	Val	Tyr	Ser	Asp	Lys	Gly	Val	Ser
1				5					10					15	
Pro	Tyr	Tyr	Leu	Arg	His	Thr	Val	Arg	Trp	Leu	Lys	Gln	Val	Ala	Ala
			20					25					30		
Pro	Phe	Gln	Met	Glu	Val	Cys	Arg	Val	Asn	Gly	Arg	Phe	Leu	Ile	His
			35				40					45			
Glu	Pro	Leu	Trp	Glu	Asp	Thr	Thr	Gln	Leu	Leu	Val	Ile	Pro	Gly	Gly
	50					55					60				
Ala	Asp	Val	Pro	Tyr	His	Asn	Val	Leu	His	Gly	Leu	Gly	Thr	Ala	Arg
65					70					75					80
Ile	Asp	Asn	Tyr	Val	Arg	Glu	Gly	Gly	Cys	Tyr	Leu	Gly	Ile	Leu	Arg
				85					90					95	
Arg	Ser	Leu	Phe	Trp	Leu	Arg	Ala	Val							
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 439:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 285 acides aminés.

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire.

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 430933..431787

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 439:

Ser	Ala	Val	Phe	Lys	Leu	Glu	Ser	Leu	Leu	Ser	Met	Met	Ser	Ser	Pro
1				5					10					15	
His	Pro	Met	Ser	Ser	Ser	Arg	Asn	Thr	Pro	Leu	Gly	Val	Phe	Tyr	Ser
			20					25					30		
Leu	Leu	Ala	Cys	Phe	Tyr	Trp	Gly	Met	Val	Phe	Val	Ile	Pro	Ser	Met
			35				40					45			
Leu	Gly	Asn	Phe	Ala	Asp	Leu	Asp	Ile	Val	Leu	Thr	Arg	Tyr	Ser	Val
	50					55					60				
Phe	Gly	Ile	Cys	Ser	Leu	Ile	Thr	Ile	Leu	Tyr	Lys	Arg	Ser	Asn	Ile
65					70					75					80
Phe	Lys	Thr	Val	Pro	Phe	Phe	Leu	Trp	Lys	Lys	Gly	Ile	Leu	Trp	Ala
				85					90					95	
Phe	Leu	Ile	Asn	Ile	Ala	Tyr	Tyr	Phe	Gly	Ile	Ala	Gln	Ala	Val	Arg
			100					105					110		
Tyr	Ser	Gly	Ser	Ala	Val	Thr	Val	Ile	Ile	Ala	Gly	Leu	Ala	Pro	Ile

(2) INFORMATION POUR LA SEQ ID NO: 440:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 431658..431987

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 440:

(2) INFORMATION POUR LA SEQ ID NO: 441:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 748 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 432232..434475

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 441:

Lys	Asp	Met	Gly	Cys	Glu	Glu	Lys	Leu	Ser	Gly	Ile	Leu	Glu	Leu	Ile
1				5					10					15	
Leu	Pro	Glu	Asp	Pro	Leu	Ser	Asp	Gln	Thr	Gly	Tyr	Ala	Phe	Leu	Arg
			20					25					30		
Val	Pro	Tyr	Lys	Asn	Ser	Leu	Val	Thr	Val	Cys	Gly	His	Leu	Pro	Leu
		35					40					45			
Ser	Leu	Phe	Lys	Ile	Gly	Ser	Ser	Val	Asp	Leu	Thr	Gly	His	Trp	Ser
	50					55					60				
Val	Asp	Ala	Ser	Gly	Ala	Leu	Val	Phe	Arg	Phe	Thr	Ser	Ala	Ala	Thr
65					70				75						80
Tyr	Ser	Pro	Asp	Ser	Gly	Ile	Ile	Ala	Tyr	Leu	Asn	Ala	Gln	Ile	Lys
				85					90					95	
Gly	Val	Gly	Pro	Lys	Leu	Ala	Gln	Lys	Ile	Val	Ser	Thr	Phe	Gly	Glu
			100					105					110		
Asp	Thr	Leu	Thr	Val	Leu	Asp	Ser	Cys	Pro	Ser	Lys	Leu	Val	Glu	Val
		115					120					125			
Asp	Gly	Ile	Ser	Pro	Ala	Arg	Cys	Glu	Asp	Phe	Ser	Lys	Gln	Leu	Gln
	130					135					140				
Glu	Gln	Arg	Asp	Leu	Arg	His	Ala	Leu	Leu	Phe	Leu	Gln	Arg	His	Gly
145					150					155					160
Ile	Ala	Ile	His	Tyr	Gly	Leu	Arg	Leu	Tyr	Lys	Lys	Tyr	Gln	Asn	Gln
			165						170					175	
Thr	Ile	Glu	Lys	Val	Cys	Gln	Asp	Pro	Phe	Leu	Leu	Ala	Lys	Glu	Met
			180					185					190		
Tyr	Gly	Ile	Gly	Phe	Lys	Thr	Ala	Asp	Leu	Ile	Ala	Thr	Cys	Leu	Gly
		195					200					205			
Val	Pro	Leu	Asn	Ser	Pro	Asn	Arg	Ile	Val	Ala	Gly	Ile	Gln	Tyr	Ser
	210					215					220				
Leu	Asp	Glu	Leu	Gln	Glu	Glu	Gly	His	Thr	Cys	Tyr	Pro	Leu	Asn	Asp
225				230						235					240
Phe	Ile	Val	Leu	Val	Glu	Lys	Leu	Leu	Asn	Glu	Glu	Ala	Pro	Glu	Glu
			245						250					255	
Ile	Ile	Arg	Lys	Glu	Glu	Ile	Arg	Thr	Gln	Ile	His	Phe	Leu	Ser	Arg
		260						265					270		
Gln	Lys	Thr	Val	Tyr	Val	Lys	Glu	Leu	Glu	Gln	Asp	Thr	Tyr	Ile	Trp
		275					280					285			
Ser	Arg	Gln	Leu	Phe	Leu	Ala	Glu	Gln	Gln	Ile	Ala	Ile	Asp	Ile	Arg
	290					295					300				
Arg	Leu	Leu	Phe	Ser	Ser	Lys	Arg	Ile	Arg	Ser	Ile	Asn	Thr	Gln	Glu
305				310						315					320
Ala	Ile	Leu	Glu	Val	Glu	Asn	Leu	Leu	Asp	Leu	Lys	Leu	Glu	Glu	Lys
			325						330					335	
Gln	Lys	Glu	Ala	Leu	His	Ala	Ser	Ser	Ser	Gln	Lys	Ile	His	Ile	Ile
			340					345					350		
Ser	Gly	Gly	Pro	Gly	Thr	Gly	Lys	Ser	Thr	Ile	Thr	Arg	Ala	Ile	Leu
		355					360					365			
Ser	Ile	Phe	Glu	Lys	Ile	Ser	Ser	Pro	Lys	Lys	Ile	Ile	Leu	Ala	Ala
	370					375					380				
Pro	Thr	Gly	Lys	Ala	Ala	Lys	Arg	Met	Thr	Glu	Ile	Thr	Gly	Lys	Arg
385				390						395					400
Thr	Gln	Thr	Ile	His	Ser	Leu	Leu	Gln	Tyr	Asp	Phe	Lys	Thr	Leu	Ser

(2) INFORMATION POUR LA SEQ ID NO: 442:

(A) LONGUEUR: 563 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(434620..436308)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 442:

Lys	Arg	Ser	Phe	Ser	Val	Gln	Leu	Glu	Arg	Arg	Glu	Ile	Val	Glu	Ser
1				5					10					15	
Ser	Arg	Ile	Leu	Ile	Thr	Ser	Ala	Leu	Pro	Tyr	Ala	Asn	Gly	Pro	Leu
			20					25					30		
His	Phe	Gly	His	Ile	Thr	Gly	Ala	Tyr	Leu	Pro	Ala	Asp	Val	Tyr	Ala
		35					40					45			
Arg	Phe	Gln	Arg	Leu	Gln	Gly	Lys	Glu	Val	Leu	Tyr	Ile	Cys	Gly	Ser
	50					55					60				
Asp	Glu	Tyr	Gly	Ile	Ala	Ile	Thr	Leu	Asn	Ala	Glu	Leu	Ala	Gly	Met
65					70					75					80
Gly	Tyr	Gln	Glu	Tyr	Val	Asp	Met	Tyr	His	Lys	Leu	His	Lys	Asp	Thr
				85					90					95	
Phe	Lys	Lys	Leu	Gly	Ile	Ser	Val	Asp	Phe	Phe	Ser	Arg	Thr	Thr	Asn
			100					105						110	
Ala	Tyr	His	Pro	Ala	Ile	Val	Gln	Asp	Phe	Tyr	Arg	Asn	Leu	Gln	Glu
		115					120						125		
Arg	Gly	Leu	Val	Glu	Asn	Gln	Val	Thr	Glu	Gln	Leu	Tyr	Ser	Glu	Glu
	130					135						140			
Glu	Gly	Lys	Phe	Leu	Ala	Asp	Arg	Tyr	Val	Val	Gly	Thr	Cys	Pro	Lys
145					150					155					160
Cys	Gly	Phe	Asp	Arg	Ala	Arg	Gly	Asp	Glu	Cys	Gln	Gln	Cys	Gly	Ala
				165					170					175	
Asp	Tyr	Glu	Ala	Arg	Asp	Leu	Lys	Glu	Pro	Arg	Ser	Lys	Leu	Thr	Gly
			180					185						190	
Ala	Ala	Leu	Ser	Leu	Arg	Asp	Thr	Glu	His	Ala	Tyr	Leu	His	Leu	Glu
		195					200						205		
Arg	Met	Lys	Glu	Asp	Leu	Leu	Ala	Phe	Val	Gln	Gly	Ile	Tyr	Leu	Arg
	210					215					220				
Pro	His	Met	Arg	Asn	Phe	Val	Thr	Asp	Tyr	Ile	Glu	His	Leu	Arg	Pro
225				230						235					240
Arg	Ala	Val	Thr	Arg	Asp	Leu	Ser	Trp	Gly	Ile	Pro	Val	Pro	Asp	Leu
				245					250					255	
Glu	Asn	Lys	Val	Phe	Tyr	Val	Trp	Phe	Asp	Ala	Pro	Ile	Gly	Tyr	Ile
			260					265						270	
Ser	Gly	Thr	Met	Asp	Trp	Ala	Ala	Ser	Ile	Gly	Asp	Pro	Glu	Ala	Trp
		275					280						285		
Lys	Lys	Phe	Trp	Leu	Asp	Asp	Thr	Val	Thr	Tyr	Ala	Gln	Phe	Ile	Gly
	290					295					300				
Lys	Asp	Asn	Thr	Ser	Phe	His	Ala	Val	Ile	Phe	Pro	Ala	Met	Glu	Ile
305					310					315					320
Gly	Gln	Ser	Leu	Pro	Tyr	Lys	Lys	Val	Asp	Ala	Leu	Val	Thr	Ser	Glu
				325					330					335	
Phe	Leu	Leu	Leu	Glu	Gly	Phe	Gln	Phe	Ser	Lys	Ser	Asp	Gly	Asn	Phe
			340					345					350		
Ile	Asp	Met	Asp	Ala	Phe	Leu	Glu	Thr	Tyr	Ser	Leu	Asp	Lys	Leu	Arg
		355					360						365		
Tyr	Val	Leu	Ala	Ala	Ile	Ala	Pro	Glu	Thr	Ser	Asp	Ser	Glu	Phe	Ser
	370					375					380				
Phe	Gln	Glu	Phe	Lys	Thr	Arg	Cys	Asn	Ser	Glu	Leu	Val	Gly	Lys	Tyr
385					390					395					400
Gly	Asn	Phe	Val	Asn	Arg	Val	Leu	Ala	Phe	Ala	Val	Lys	Asn	Gly	Cys
				405					410					415	
Thr	Glu	Leu	Ser	Pro	Gln	Leu	Glu	Gln	Lys	Asp	Leu	Asp	Phe	Ile	
			420				425						430		
Ser	Lys	Ser	Gln	Lys	Leu	Ala	Lys	Asp	Ala	Ala	Glu	His	Tyr	Ala	Gln
		435					440						445		
Tyr	Ser	Leu	Arg	Lys	Ala	Cys	Ser	Thr	Ile	Met	Glu	Leu	Ala	Ala	Leu
	450					455					460				
Gly	Asn	Gly	Tyr	Phe	Asn	Asp	Glu	Ala	Pro	Trp	Lys	Leu	Ala	Lys	Glu

465		470		475		480									
Gly	Asn	Trp	Asn	Arg	Val	Arg	Ala	Ile	Leu	Phe	Cys	Ala	Cys	Tyr	Cys
			485						490					495	
Gln	Lys	Leu	Leu	Ala	Leu	Ile	Ser	Tyr	Pro	Ile	Met	Pro	Glu	Thr	Ala
		500						505					510		
Leu	Lys	Ile	Leu	Glu	Met	Ile	Ala	Pro	Tyr	Ser	Leu	Asp	Leu	Gly	Ser
		515					520					525			
Gln	Asp	Pro	Asp	Arg	Leu	His	Ser	Leu	Trp	Thr	Asp	Ser	Phe	Phe	Asp
	530					535					540				
Tyr	Ser	Glu	Glu	Lys	Phe	Ser	Leu	Lys	Glu	Pro	Glu	Leu	Leu	Phe	Thr
545					550					555					560
Met	Val	Glu													

(2) INFORMATIONS POUR LA SEQ ID NO: 443:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(436272..436574)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 443:

Val	Met	Ala	Arg	Lys	Asp	Arg	Leu	Thr	Asn	Glu	Arg	Leu	Asn	Lys	Leu
1				5					10					15	
Phe	Asp	Ser	Pro	Phe	Ser	Leu	Val	Asn	Tyr	Val	Ile	Lys	Gln	Ala	Lys
			20					25					30		
Asn	Lys	Ile	Ala	Arg	Gly	Asp	Val	Arg	Ser	Ser	Asn	Val	Ala	Ile	Glu
		35					40					45			
Ala	Leu	Asn	Phe	Leu	Asp	Leu	Tyr	Gly	Ile	Gln	Ser	Glu	Tyr	Ala	Glu
	50					55					60				
Arg	Asp	Asp	Arg	Glu	Arg	His	Leu	Ser	Ala	Thr	Gly	Glu	Arg	Arg	Arg
65					70					75					80
Glu	Gln	Gly	Phe	Gly	Thr	Ser	Arg	Arg	Lys	Asp	Pro	Ser	Leu	Tyr	Asn
				85					90					95	
Trp	Ser	Asp	Val	Lys											
				100											

(2) INFORMATIONS POUR LA SEQ ID NO: 444:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 373 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(436567..437685)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 444:

Ala	Cys	Ile	Leu	Pro	Arg	Gly	Lys	Val	Phe	Leu	Gly	Ile	Asp	Asp	Ser
1				5					10					15	
Lys	Lys	Leu	Thr	Pro	Lys	Gln	Arg	Arg	Tyr	Leu	Tyr	Glu	Leu	Leu	
			20					25					30		
Glu	Asp	Pro	Glu	Val	Asp	Cys	Gly	Val	Gly	Val	Ile	Ser	Val	Glu	Arg
		35					40					45			
Ile	Asp	Glu	Ile	Asn	Ile	Leu	Glu	Ala	Thr	Lys	Glu	Ala	Met	Val	Gln
	50					55					60				
Ala	Ile	Ala	Ser	Leu	Arg	Ser	Thr	Pro	Asp	Phe	Leu	Leu	Val	Asp	Gly
65					70					75					80
Leu	Phe	Leu	Pro	His	Lys	Ile	Pro	Ser	Leu	Lys	Ile	Ile	Lys	Gly	Asp
			85						90					95	
Ala	Arg	Ser	Val	Ser	Ile	Ala	Ala	Ala	Ser	Ile	Ile	Ala	Lys	Glu	Tyr
			100					105						110	
Arg	Asp	Glu	Leu	Met	Arg	Lys	Leu	His	Val	Glu	Tyr	Pro	Glu	Tyr	Gly
		115					120					125			
Phe	Asp	Lys	His	Lys	Gly	Tyr	Gly	Thr	Ala	Ala	His	Leu	Gln	Ala	Leu
	130					135					140				
Lys	His	Phe	Gly	Pro	Cys	Val	Tyr	His	Arg	Lys	Ser	Phe	Ser	Pro	Val
145					150					155					160
Lys	Glu	Ser	Ile	Xaa	Arg	Gly	Ser	Met	Ser	Val	Lys	Val	Ile	Ser	Pro
			165						170					175	
Phe	Ser	Gln	Asp	Gly	Val	Gln	Phe	Phe	Pro	Lys	Leu	Phe	Ile	Ile	Ser
			180					185					190		
Ala	Pro	Ala	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Thr	His	Met	Leu	Gln	Arg
		195					200					205			
Glu	Phe	Pro	Asp	Ala	Phe	Glu	Lys	Thr	Val	Ser	Ser	Thr	Thr	Arg	Ser
	210					215					220				
Ala	Arg	Pro	Gly	Glu	Val	His	Gly	Val	Asp	Tyr	Leu	Phe	Val	Ser	Glu
225					230					235					240
Asp	Asp	Phe	Lys	Gln	Ser	Leu	Asp	Arg	Glu	Asp	Phe	Leu	Glu	Trp	Val
			245						250					255	
Phe	Leu	Phe	Gly	Thr	Tyr	Tyr	Gly	Thr	Ser	Lys	Ala	Glu	Ile	Ser	Arg
			260					265					270		
Val	Leu	Gln	Lys	Gly	Lys	His	Cys	Ile	Ala	Val	Ile	Asp	Val	Gln	Gly
		275					280					285			
Ala	Leu	Ala	Leu	Lys	Lys	Gln	Met	Pro	Ala	Val	Thr	Ile	Phe	Ile	Gln
	290					295					300				
Ala	Pro	Ser	Gln	Glu	Glu	Leu	Glu	Arg	Arg	Leu	Asn	Ala	Arg	Asp	Ser
305					310					315					320
Glu	Lys	Asp	Phe	Gln	Lys	Lys	Glu	Arg	Leu	Glu	His	Ser	Ala	Val	Glu
			325						330					335	
Ile	Ala	Ala	Ala	Ser	Glu	Phe	Asp	Tyr	Val	Val	Val	Asn	Asp	Asp	Leu
			340					345					350		
Ile	Thr	Ala	Tyr	Gln	Val	Leu	Arg	Ser	Ile	Phe	Ile	Ala	Glu	Glu	His
		355					360						365		
Arg	Met	Ser	His	Gly											
															370

(2) INFORMATIONS POUR LA SEQ ID NO: 445:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: complement(437894..438262)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 445:

Asn	Thr	Met	Gly	Asn	Leu	Ile	Lys	Glu	Leu	Gln	Asp	Glu	Gln	Cys	Arg
1				5				10						15	
Thr	Asp	Leu	Ala	Asp	Phe	Cys	Val	Gly	Asp	Thr	Ile	Arg	Val	Ala	Thr
		20						25					30		
Asn	Ile	Ser	Glu	Gly	Gly	Lys	Glu	Arg	Val	Gln	Val	Phe	Gln	Gly	Thr
		35				40						45			
Val	Met	Ala	Arg	Lys	Gly	Gly	Ala	Gly	Glu	Thr	Val	Ser	Leu	His	
	50				55				60						
Arg	Val	Ala	Tyr	Gly	Glu	Gly	Met	Glu	Lys	Ser	Phe	Leu	Leu	Asn	Ser
65				70					75					80	
Pro	Lys	Ile	Val	Ser	Ile	Glu	Val	Val	Lys	Arg	Gly	Lys	Val	Ser	Arg
			85						90					95	
Ala	Arg	Leu	Phe	Tyr	Leu	Arg	Gly	Lys	Thr	Gly	Lys	Ala	Ala	Lys	Val
		100					105						110		
Lys	Glu	Leu	Ile	Gly	Ser	Arg	Ala	Ala	Lys	Lys					
		115					120								

(2) INFORMATIONS POUR LA SEQ ID NO: 446:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 281 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(438285..439127)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 446:

Lys	His	Lys	Lys	Lys	Glu	Val	Gln	Gly	His	Ile	Leu	Ile	Ser	Ala	Gly
1				5				10						15	
Gln	Leu	Leu	Ser	Ala	Lys	Lys	Ser	Arg	Glu	Leu	Ala	Ser	Cys	Ser	His
		20						25					30		
Leu	Val	Leu	Leu	Cys	Gly	His	Tyr	Glu	Gly	Ile	Asp	Glu	Arg	Ala	Leu
		35				40					45				
Thr	Ala	Glu	Val	Asp	Glu	Glu	Ile	Ser	Ile	Gly	Asp	Tyr	Val	Leu	Thr
	50					55				60					
Asn	Gly	Cys	Ala	Ala	Ala	Leu	Val	Leu	Val	Asp	Ala	Leu	Ala	Arg	Phe
65				70					75					80	
Ile	Pro	Gly	Ile	Leu	Gly	Asn	Gln	Glu	Ser	Ala	Glu	Tyr	Asp	Ser	Leu
			85					90					95		
Glu	Asn	Gly	Leu	Leu	Glu	Gly	Pro	Gln	Tyr	Thr	Arg	Pro	Arg	Val	Phe
		100					105						110		
Glu	Gly	Glu	Ser	Val	Pro	Glu	Val	Leu	Leu	Cys	Gly	Asp	His	Gln	Lys
		115				120					125				
Ile	Ala	Asp	Trp	Arg	Lys	Gln	Val	Ser	Leu	Glu	Arg	Thr	Arg	Glu	Arg
	130					135					140				
Arg	Pro	Asp	Leu	Tyr	Leu	Gln	Tyr	Phe	Tyr	Gly	Asn	Ser	Ala	Cys	Leu
145				150					155					160	
Ser	Thr	Gln	Glu	Asp	Leu	Pro	Arg	Ile	Glu	Val	Val	Ser	Pro	Lys	Thr
			165						170					175	

Phe	Ser	Val	Val	Leu	Glu	Val	Gln	Asp	Leu	Arg	Lys	Ala	Lys	Lys	Phe
			180					185					190		
Tyr	Ser	Arg	Met	Phe	Gly	Lys	Glu	Cys	Trp	Asp	Gly	Asp	Lys	Leu	Phe
		195					200					205			
Leu	Leu	Gly	Lys	Thr	Ser	Leu	Tyr	Leu	Gln	Gln	Thr	Lys	Glu	Thr	Arg
	210					215					220				
Gly	Pro	Thr	Thr	Val	Phe	Ile	Glu	Leu	Glu	Thr	Asp	His	Asp	Phe	Val
225					230					235					240
Arg	Phe	Leu	Lys	Arg	Trp	Glu	Met	Leu	Gly	Gly	Glu	Leu	Gly	Glu	Gln
				245					250					255	
Gly	Thr	Gly	Gly	Phe	Pro	Leu	Arg	Gln	Val	Phe	Asp	Leu	Asp	Gly	His
			260					265					270		
Ile	Trp	Val	Val	Ser	Cys	Val	Gln	Lys							
		275					280								

(2) INFORMATIONS POUR LA SEQ ID NO: 447:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(438986..439339)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 447:

Met	Glu	Ile	Asp	Ile	Leu	Ser	Leu	Phe	Pro	Asp	Tyr	Phe	Ala	Ser	Pro
1			5					10						15	
Leu	Gln	Ala	Thr	Ile	Leu	Gly	Arg	Ala	Ile	Lys	Gln	Gly	Ala	Leu	Ser
		20					25						30		
Val	Arg	Ser	Arg	Asp	Ile	Arg	Glu	Phe	Gly	Leu	Gly	Lys	Trp	Lys	Gln
		35				40					45				
Val	Asp	Asp	Ser	Pro	Tyr	Asn	Gly	Glu	Gly	Met	Leu	Leu	Met	Ala	Glu
	50					55				60					
Pro	Val	Val	Gln	Ala	Ile	Arg	Ser	Ile	Arg	Arg	Lys	Lys	Ser	Lys	Val
65				70					75						80
Ile	Tyr	Leu	Ser	Pro	Gln	Asp	Asn	Phe	Phe	Pro	Gln	Arg	Lys	Val	Val
			85					90						95	
Asn	Trp	Arg	Arg	Val	Arg	Ile	Trp	Tyr	Cys	Tyr	Val	Asp	Thr	Met	Arg
		100					105						110		
Glu	Leu	Met	Lys	Gly	Arg										
		115													

(2) INFORMATIONS POUR LA SEQ ID NO: 448:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 115 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(439358..439702)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 448:

```

Ala Leu Lys Ile Arg Leu Arg Gln Gln Gly Arg Lys Asn His Val Val
1           5           10           15
Tyr Arg Leu Val Leu Ala Asp Val Glu Ser Pro Arg Asp Gly Lys Tyr
          20           25           30
Ile Glu Leu Leu Gly Trp Tyr Asp Pro His Ser Glu Gln Asn Tyr Gln
          35           40           45
Leu Lys Ser Glu Arg Ile Phe Tyr Trp Leu Asn Gln Gly Ala Glu Leu
          50           55           60
Thr Glu Lys Ala Gly Ala Leu Val Lys Gln Gly Ala Pro Gly Val Tyr
65           70           75           80
Ala Glu Leu Met Ala Lys Lys Val Ala Arg Arg Ala Val Val Arg Gln
          85           90           95
Lys Arg Arg Ala Tyr Arg Gln Arg Leu Ala Ala Arg Lys Ala Glu Ala
          100          105          110
Ala Ala Lys
          115

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 449:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 448 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(439699..441042)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 449:

```

Met Ile Ser Ser Leu Ser Gln Lys Leu Ser Asn Ile Phe Ser Ser Leu
1           5           10           15
Phe Thr Ala Lys Arg Val Thr Glu Glu Gly Ile Ser Asp Ser Ile Arg
          20           25           30
Glu Val Arg Leu Ala Leu Leu Asp Ala Asp Val Asn Tyr Gln Ala Val
          35           40           45
Lys Asp Phe Ile Ala Lys Val Lys Gln Lys Val Val Gly Glu Glu Val
          50           55           60
Trp Lys His Val Ser Pro Gly Gln Gln Phe Ile Lys Cys Leu His Glu
65           70           75           80
Glu Leu Ser Ser Ser Leu Ala Ser Glu Gln Thr Ala Val Ser Leu Arg
          85           90           95
Gly Cys Pro Ala Val Ile Leu Leu Cys Gly Leu Gln Gly Ala Gly Lys
          100          105          110
Thr Thr Thr Cys Ala Lys Leu Ala Asp Tyr Phe Leu Arg Glu Lys Lys
          115          120          125
Ala Lys Lys Val Leu Val Ala Ser Cys Asp Leu Lys Arg Phe Ser Ala
          130          135          140
Val Glu Gln Leu Glu Gly Leu Val Lys Gln Thr Gly Ala Asp Phe Phe
145          150          155          160
Arg Arg Glu Gly Asn Asp Pro Val Asp Met Ala Ala Glu Ala Val Gln
          165          170          175
His Ala Lys Ser Gln Gly Tyr Asp Leu Val Leu Val Asp Thr Ala Gly
          180          185          190

```

Arg	Leu	His	Val	Asp	Asp	Ala	Leu	Met	Asp	Glu	Leu	Val	Ala	Ile	Ala		
		195					200					205					
Arg	Val	Thr	Ser	Pro	Cys	Glu	Thr	Leu	Phe	Val	Met	Asn	Leu	Ala	Met		
	210					215					220						
Gly	Gln	Asp	Ala	Val	Val	Val	Thr	Ala	Lys	Ala	Phe	Asp	Glu	Arg	Leu	Gly	
225					230						235					240	
Leu	Thr	Gly	Val	Val	Val	Ser	Met	Ala	Asp	Gly	Asp	Ala	Arg	Ala	Gly		
			245						250						255		
Ala	Val	Leu	Ser	Val	Lys	Ser	Leu	Leu	Asn	Lys	Pro	Ile	Lys	Phe	Glu		
		260					265						270				
Gly	Cys	Gly	Glu	Lys	Ile	Lys	Asp	Leu	Arg	Pro	Phe	Asn	Ala	Gln	Ser		
	275						280					285					
Met	Ala	Glu	Arg	Ile	Leu	Gly	Met	Gly	Asp	Thr	Ile	Ser	Leu	Val	Asp		
	290					295					300						
Lys	Met	Arg	Glu	Cys	Ile	Ser	Glu	Glu	Glu	Asn	Lys	Glu	Leu	Glu	Glu		
305				310						315					320		
Lys	Leu	Thr	Lys	Ala	Thr	Phe	Thr	Tyr	Glu	Asp	Phe	His	Lys	Gln	Ile		
			325						330					335			
Leu	Ala	Phe	Arg	Arg	Leu	Gly	Pro	Leu	Arg	Lys	Ile	Met	Asn	Met	Met		
			340					345					350				
Pro	Ser	Phe	Gly	Gly	Ala	Lys	Pro	Ser	Asp	Lys	Asp	Leu	Glu	Glu	Ser		
	355						360					365					
Glu	Lys	Gln	Met	Lys	Arg	Asn	Glu	Ala	Ile	Ile	Leu	Ser	Met	Thr	Pro		
	370					375					380						
Glu	Glu	Arg	Lys	Glu	Leu	Val	Glu	Leu	Ser	Met	Ser	Arg	Met	Lys	Arg		
385				390					395						400		
Ile	Ala	Ala	Gly	Cys	Gly	Leu	Thr	Leu	Gly	Asp	Val	Asn	Gln	Phe	Arg		
			405						410					415			
Lys	Gln	Met	Met	Gln	Ser	Lys	Lys	Phe	Phe	Lys	Gly	Met	Thr	Arg	Glu		
		420						425				430					
Lys	Met	Glu	Gln	Met	Gly	Lys	Lys	Met	Ser	Gly	Gly	Asn	Leu	Trp	Arg		
	435						440					445					

(2) INFORMATIONS POUR LA SEQ ID NO: 450:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 290 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(441042..441911)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 450:

Met	Lys	Lys	Leu	Leu	Arg	Glu	Ala	Ser	Glu	Tyr	Leu	Leu	Ser	Arg	Gly		
1			5						10					15			
Ile	Arg	Phe	Pro	Gln	Arg	Glu	Ala	Glu	Asp	Ile	Leu	Met	Asp	Leu	Leu		
		20						25					30				
Glu	Ile	Ser	Ser	Arg	Ser	Ala	Leu	His	Gln	Ala	Lys	Leu	Ser	Ser	Glu		
		35					40					45					
Glu	Gln	Ser	Leu	Tyr	Trp	Lys	Arg	Leu	Arg	Lys	Arg	Gly	Asp	Arg	Cys		
	50					55				60							
Pro	Thr	Ala	Tyr	Ile	His	Gly	Lys	Val	His	Phe	Leu	Gly	Val	Glu	Leu		
65				70						75				80			
Gln	Val	Thr	Pro	Gln	Val	Leu	Ile	Pro	Arg	Gln	Glu	Thr	Glu	Ile	Phe		

				85					90					95					
Val	Glu	Gln	Ile	Ile	Gly	Tyr	Leu	Gln	Met	His	Lys	Glu	Lys	Thr	Thr				
			100					105					110						
Phe	Tyr	Asp	Val	Cys	Cys	Gly	Ser	Gly	Cys	Ile	Gly	Leu	Ala	Val	Arg				
		115					120					125							
Lys	His	Cys	Pro	His	Val	Arg	Val	Thr	Leu	Ser	Asp	Ile	Ser	Pro	Glu				
		130				135					140								
Ala	Leu	Ala	Ile	Ala	Glu	Ser	Asn	Ala	Arg	Ser	Asn	Ala	Leu	Ala	Val				
145					150				155						160				
Asp	Phe	Leu	Leu	Gly	Asp	Leu	Phe	Asp	Pro	Phe	Ser	Phe	Pro	Ala	Asp				
			165					170						175					
Val	Leu	Val	Cys	Asn	Pro	Pro	Tyr	Leu	Ser	Tyr	Lys	Glu	Phe	Phe	Glu				
		180						185				190							
Ser	Asp	Pro	Glu	Val	Arg	Cys	His	Glu	Pro	Trp	Lys	Ala	Leu	Val	Gly				
		195				200					205								
Gly	Val	Ser	Gly	Leu	Glu	Phe	Tyr	His	Arg	Ile	Ala	Thr	His	Ile	His				
210					215				220										
Lys	Ile	Leu	Val	Ser	Gly	Gly	Val	Gly	Trp	Leu	Glu	Ile	Gly	Ser	Thr				
225				230					235					240					
Gln	Gly	Glu	Asp	Val	Lys	Gln	Ile	Phe	His	Ala	Lys	Gly	Ile	Arg	Gly				
			245					250						255					
Arg	Val	Leu	Lys	Asp	Tyr	Ala	Gln	Leu	Asp	Arg	Phe	Phe	Phe	Leu	Xaa				
		260						265					270						
Asn	Gln	Ala	Asn	Asp	Ala	Val	Ser	Ser	Gly	Glu	Val	Ser	Gly	Phe	Ser				
		275					280					285							
Glu	Arg																		
290																			

(2) INFORMATIONS POUR LA SEQ ID NO: 451:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 232 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(441898..442593)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 451:

Gly	Xaa	Cys	Val	Arg	Met	Tyr	His	Leu	Tyr	Ala	Ala	Ser	Lys	Gly	Trp				
1				5				10					15						
Gln	Cys	Glu	Val	Leu	Ser	Ala	Ser	Glu	Ser	Asp	Leu	Gly	Gly	Tyr	Lys				
		20					25					30							
Glu	Tyr	Val	Met	Gly	Ile	Ser	Gly	Ala	Ser	Val	Lys	Arg	Phe	Leu	Gln				
		35				40					45								
Tyr	Glu	Ala	Gly	Thr	His	Arg	Val	Gln	Arg	Val	Pro	Glu	Thr	Glu	Thr				
	50				55					60									
Gln	Gly	Arg	Val	His	Thr	Ser	Ala	Val	Thr	Val	Ala	Val	Leu	Pro	Glu				
65				70				75					80						
Pro	Ala	Glu	Asp	Asp	Glu	Glu	Val	Phe	Ile	Asp	Glu	Lys	Asp	Leu	Arg				
			85				90					95							
Ile	Asp	Thr	Phe	Arg	Ser	Ser	Gly	Ala	Gly	Gly	Gln	His	Val	Asn	Val				
		100					105					110							
Thr	Asp	Ser	Ala	Val	Arg	Ile	Thr	His	Ile	Pro	Ser	Gly	Val	Val	Val				
		115					120					125							

```

Thr Cys Gln Asp Glu Arg Ser Gln His Lys Asn Lys Ala Lys Ala Met
 130      135      140
Arg Val Leu Lys Ala Arg Ile Arg Asp Ala Glu Val Gln Lys Arg Ala
 145      150      155      160
Gln Glu Ala Ser Ala Met Arg Ser Ala Gln Val Gly Ser Gly Asp Arg
      165      170      175
Ser Glu Arg Ile Arg Thr Tyr Asn Phe Pro Gln Asn Arg Val Thr Asp
      180      185      190
His Arg Ile Gly Leu Thr Leu Tyr Asn Leu Asp Arg Val Met Glu Gly
      195      200      205
Glu Leu Asp Met Ile Thr Thr Ala Leu Val Thr His Val His Arg Gln
 210      215      220
Leu Phe Gly His Glu Glu Thr Ala
 225      230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 452:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 567 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 444688..446388

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 452:

```

Leu Phe Ala Lys Gln Ala Gln Ala Ile Gln Lys Arg Phe Pro Lys Ser
 1      5      10      15
Lys Leu Arg Ala Thr Phe Asp Leu Ile Tyr Ala Leu Thr Phe Ala Ala
      20      25      30
Ile Leu Ala Phe Leu Ile Arg Gln Phe Trp Phe Glu Leu Tyr Glu Val
      35      40      45
Pro Thr Gly Ser Met Arg Pro Thr Ile Leu Glu Gln Asp Arg Ile Leu
 50      55      60
Val Ser Lys Thr Thr Phe Gly Leu Arg Leu Pro Phe Ser Asn Arg Ser
 65      70      75      80
Ile Gly Tyr Thr Pro Glu Ala Ile Thr Arg Gly Glu Leu Val Val Phe
      85      90      95
Thr Val Gly Asp Leu Pro Ile Pro Asn Ala Asp Thr Lys Tyr Phe Gly
      100      105      110
Ile Ile Pro Gly Lys Lys Arg Tyr Ile Lys Arg Cys Met Gly Lys Pro
      115      120      125
Gly Asp Thr Val Tyr Phe Tyr Gly Gly Lys Ile Tyr Gly Ile Asp Cys
      130      135      140
Asp Gly Glu Pro Ile Phe Pro Gln Asn Thr Glu Asn Xaa Tyr His Val
 145      150      155      160
Pro Tyr Ile Ser Phe Asp Gly Thr Pro Glu Ile Leu Thr His Ser Glu
      165      170      175
Glu Gln Thr Asp Val Ile Phe Asn Gln Phe His Thr Pro Cys Gly Lys
      180      185      190
Ile Ser Leu Pro Gln Gln Ala Ser Tyr Gly Gln Phe Phe Tyr Lys Asn
      195      200      205
Ala Trp His Asn Asp Thr Pro Tyr Ala Leu Lys Asp Pro His Asn Glu
 210      215      220
Pro Val Ser Tyr Ala Asp Leu Phe Gly Ile Lys Asn Phe Ala Met Val

```

225					230					235				240
Arg	Ile	Leu	Thr	Lys	Lys	Gln	Ala	Ala	Leu	Thr	His	Val	Leu	Pro Ser
				245					250				255	
Pro	Leu	Ser	Asp	Thr	Tyr	Leu	Glu	Ile	Ala	His	Thr	Pro	Asn	Val Ser
			260					265					270	
Tyr	Xaa	His	Pro	His	Leu	Arg	Pro	Phe	Glu	Thr	Gln	Arg	Ile	Pro Thr
		275					280					285		
Ile	Glu	Pro	Met	Lys	Thr	Leu	Leu	Pro	Leu	Arg	Lys	Glu	His	Ile His
	290					295					300			
Leu	Ile	Arg	Asn	Asn	Leu	Thr	Thr	Ser	Arg	Phe	Thr	Val	Val	Asp Gly
305					310					315				320
Tyr	Ala	Tyr	Lys	Tyr	Gln	Pro	Ala	Pro	Met	Asn	Thr	Ser	Gly	Met Val
				325					330					335
Arg	Met	Phe	Ala	Leu	Pro	Met	Pro	Asn	Ile	Pro	Asp	Gly	Cys	Tyr Glu
			340					345					350	
Phe	Ser	Lys	Gly	Asp	Val	Phe	Lys	Ile	Asn	Met	Gly	Gly	Phe	Arg Thr
		355				360						365		
Lys	Leu	Lys	Gln	Pro	His	Pro	Leu	Thr	Gln	Leu	Ser	Asn	Ser	Gln Val
	370					375					380			
Ile	Asp	Leu	Phe	Asn	Cys	Gly	Ile	Ser	Phe	His	Thr	Ile	Tyr	Ile Pro
385					390					395				400
Lys	Asn	Pro	Gln	Tyr	Ala	Pro	Phe	Pro	Asn	Arg	Tyr	Ala	Phe	Phe Asn
				405					410					415
Gln	Gly	Asn	Leu	Phe	Val	Met	Asp	Ser	Pro	Val	Phe	Ile	Asp	Ser Asp
			420					425					430	
Pro	Ala	Leu	Gln	Lys	Phe	Ile	Val	Ser	Glu	Glu	Glu	Lys	Glu	Leu Gln
		435					440					445		
Ser	Ser	Glu	Asp	Lys	Pro	Tyr	Ile	Ala	Phe	Ile	Asp	Arg	Gly	Pro Pro
	450				455						460			
Pro	Glu	Ser	Thr	Glu	Glu	Phe	Val	Ser	Phe	Ile	Thr	Asn	Phe	Gly Leu
465					470					475				480
Lys	Ile	Pro	Glu	Gly	His	Val	Leu	Val	Leu	Gly	Asp	Asn	Cys	Pro Met
				485					490					495
Ser	Ala	Asp	Ser	Arg	Asp	Phe	Gly	Phe	Val	Pro	Val	Glu	Asn	Leu Leu
			500				505						510	
Gly	Ser	Pro	Val	Gly	Ile	Phe	Trp	Pro	Ile	Asn	Arg	Leu	Gly	Leu Leu
		515					520					525		
Ser	Ser	Asn	Ile	Thr	Pro	Leu	Ser	Leu	Pro	Gly	Tyr	Leu	Val	Asn Gly
	530				535						540			
Leu	Ala	Leu	Gly	Ala	Phe	Leu	Tyr	Cys	Ile	Gly	Leu	Trp	Tyr	Tyr Arg
545					550					555				560
Lys	Asn	His	Arg	Leu	Phe	Pro								
				565										

(2) INFORMATIONS POUR LA SEQ ID NO: 453:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 539 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(446452..448068)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 453:

Lys	Leu	Thr	Arg	Thr	Gly	Asn	Leu	Ser	Glu	Glu	Ser	Leu	Met	Phe	Ser
1				5					10					15	
Ile	Val	Gly	Leu	Ile	Leu	Glu	Leu	Cys	His	Met	Leu	Arg	Ile	Ile	Thr
			20					25					30		
Leu	Leu	Lys	Glu	Gln	Lys	Lys	Arg	Arg	Leu	Cys	Phe	Pro	Ala	Asp	Phe
		35					40					45			
Ile	Ala	Glu	Gly	Leu	Asp	Gln	Thr	Arg	Gly	Trp	Phe	Tyr	Thr	Leu	Thr
	50					55					60				
Val	Ile	Ala	Ala	Ala	Leu	Phe	Asp	Gln	Pro	Ala	Phe	Lys	Asn	Val	Ile
65					70					75					80
Val	Asn	Gly	Ile	Ile	Leu	Ala	Glu	Asp	Gly	Asn	Lys	Met	Ser	Lys	Arg
				85					90					95	
Leu	Asn	Asn	Tyr	Pro	Ser	Pro	Lys	Met	Ile	Met	Asp	Ala	Tyr	Gly	Ala
			100					105					110		
Asp	Ala	Leu	Arg	Leu	Tyr	Leu	Leu	Asn	Ser	Val	Val	Val	Lys	Ala	Glu
		115					120					125			
Asp	Leu	Arg	Phe	Ser	Asp	Lys	Gly	Val	Glu	Ser	Val	Leu	Lys	Gln	Val
		130				135					140				
Leu	Leu	Pro	Leu	Ser	Asn	Ala	Leu	Ala	Phe	Tyr	Asn	Thr	Tyr	Ala	Glu
145					150					155					160
Leu	Tyr	Gly	Phe	Asp	Pro	Lys	Glu	Thr	Asp	Asn	Ile	Glu	Leu	Ala	Glu
				165					170					175	
Ile	Asp	Arg	Trp	Ile	Leu	Ser	Ser	Leu	Tyr	Ser	Leu	Leu	Gly	Lys	Thr
			180					185					190		
Arg	Glu	Ser	Met	Ser	Gln	Tyr	Asp	Leu	His	Ala	Ala	Val	Asn	Pro	Phe
		195					200					205			
Val	Asp	Phe	Ile	Glu	Asp	Leu	Thr	Asn	Trp	Tyr	Ile	Arg	Arg	Ser	Arg
	210					215					220				
Arg	Arg	Phe	Trp	Asp	Ala	Glu	Asp	Ser	Thr	Asp	Arg	Arg	Ala	Ala	Phe
225					230					235					240
Ser	Thr	Leu	Tyr	Glu	Val	Leu	Val	Val	Phe	Ser	Lys	Val	Ile	Ala	Pro
				245					250					255	
Phe	Ile	Pro	Phe	Ile	Ser	Glu	Asp	Met	Tyr	Gln	Gln	Leu	Arg	Gly	Glu
			260					265					270		
Thr	Asp	Pro	Glu	Ser	Val	His	Leu	Cys	Asp	Phe	Pro	His	Val	Val	Leu
		275					280					285			
Glu	Lys	Ile	Leu	Pro	Asn	Leu	Glu	Arg	Lys	Met	Gln	Asp	Ile	Arg	Glu
	290					295					300				
Ile	Val	Ala	Leu	Gly	His	Ser	Leu	Arg	Lys	Glu	His	Lys	Leu	Lys	Val
305					310					315					320
Arg	Gln	Pro	Leu	Gln	Asn	Val	Tyr	Ile	Val	Gly	Ser	Gln	Glu	Arg	Met
				325					330					335	
Glu	Ala	Leu	Ser	Gln	Val	Gly	Ser	Leu	Ile	Gly	Glu	Glu	Leu	Asn	Val
			340					345					350		
Lys	Asp	Val	His	Phe	Cys	Ser	Glu	Thr	Pro	Glu	Tyr	Val	Thr	Thr	Leu
		355					360					365			
Ile	Lys	Pro	Asn	Phe	Arg	Thr	Leu	Gly	Lys	Lys	Val	Gly	Asn	Arg	Leu
	370					375					380				
Pro	Glu	Ile	Gln	Arg	Ala	Leu	Ala	Gly	Leu	Pro	Gln	Glu	Gln	Ile	Gln
385					390					395					400
Ala	Phe	Met	His	Lys	Gly	Gln	Met	Val	Val	Ser	Leu	Gly	Glu	Glu	Thr
				405					410					415	
Ile	Ser	Leu	Asp	Lys	Glu	Asp	Ile	Thr	Val	Ser	Trp	Ala	Ser	Ala	Glu
			420					425					430		
Gly	Phe	Val	Ala	Arg	Ser	Ser	Ala	Ser	Phe	Val	Ala	Val	Leu	Asp	Cys
		435					440					445			
Gln	Leu	Thr	Glu	Pro	Leu	Ile	Met	Glu	Gly	Ile	Ala	Arg	Glu	Leu	Val
	450					455					460				
Asn	Lys	Ile	Asn	Thr	Met	Arg	Arg	Asn	Gly	Lys	Leu	His	Val	Ser	Asp



```

465          470          475          480
Arg Ile Ala Ile Arg Leu His Ala Pro Val Ile Val Gln Glu Ala Phe
          485          490          495
Ala Leu His Lys Glu Tyr Ile Cys Glu Glu Thr Leu Thr Thr Ser Val
          500          505          510
Ser Val Ile Asp Tyr Lys Glu Gly Glu Glu Trp Asp Ile Asn Gly His
          515          520          525
Ala Val Ser Phe Val Leu Glu Arg Val Glu Arg
          530          535

```

(2) INFORMATIONS POUR LA SEQ ID NO: 454:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 543 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(447932..449560)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 454:

```

Met Asp Asn Glu Asp Lys Ile Ser Ile Ser Ala Lys Glu Glu Lys Ile
1          5          10          15
Leu Ser Phe Trp Lys Glu Gln Asp Ile Phe Gln Lys Thr Leu Asp Asn
          20          25          30
Arg Glu Gly Cys Pro Thr Phe Ser Phe Tyr Asp Gly Pro Pro Phe Ala
          35          40          45
Thr Gly Leu Pro His Tyr Gly His Leu Leu Ala Gly Thr Ile Lys Asp
          50          55          60
Val Val Cys Arg Tyr Ala Ser Met Asp Gly His Tyr Val Pro Arg Arg
65          70          75          80
Phe Gly Trp Asp Cys His Gly Val Pro Val Glu Tyr Glu Val Glu Lys
          85          90          95
Ser Leu Gly Leu Thr Glu Pro Gly Ala Ile Glu Arg Phe Gly Val Ala
          100          105          110
Asn Phe Asn Glu Glu Cys Arg Lys Ile Val Phe Arg Tyr Ala Asp Glu
          115          120          125
Trp Lys Tyr Phe Val Asp Arg Ile Gly Arg Trp Val Asp Phe Ser Ala
          130          135          140
Thr Trp Arg Thr Met Asp Leu Ser Phe Met Glu Ser Val Trp Trp Val
145          150          155          160
Phe Arg Ser Leu Tyr Asp Gln Gly Leu Val Tyr Glu Gly Thr Lys Val
          165          170          175
Val Pro Phe Ser Thr Lys Leu Gly Thr Pro Leu Ser Asn Phe Glu Ala
          180          185          190
Gly Gln Asn Tyr Lys Glu Val Asp Asp Pro Ser Val Val Val Lys Phe
          195          200          205
Ala Leu Gln Asp Asn Gln Gly Phe Leu Leu Ala Trp Thr Thr Thr Pro
210          215          220
Trp Thr Leu Val Ser Asn Met Ala Leu Ala Val His Pro Glu Leu Thr
225          230          235          240
Tyr Val Arg Ile Lys Asp Lys Glu Ser Gly Asp Glu Tyr Ile Leu Gly
          245          250          255
Gln Glu Ser Leu Pro Arg Trp Phe Pro Asp Arg Glu Ser Tyr Glu Trp
          260          265          270

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Ile Gly Gln Leu Ser Gly Lys Ser Leu Val Gly Gln Ser Tyr Glu Pro
    275          280          285
Leu Phe Pro Tyr Phe Gln Asp Lys Lys Glu Leu Gly Ala Phe Arg Ile
    290          295          300
Leu Pro Ala Asp Phe Ile Glu Glu Ser Glu Gly Thr Gly Ile Val His
    305          310          315          320
Met Ala Pro Ala Phe Gly Glu Ala Asp Phe Phe Ala Cys Gln Glu His
          325          330          335
Asn Val Pro Leu Val Cys Pro Val Asp Asn Gln Gly Cys Tyr Thr Ala
          340          345          350
Glu Val Lys Asp Phe Val Gly Glu Tyr Ile Lys Ser Ala Asp Lys Gly
    355          360          365
Ile Ala Arg Arg Leu Lys Asn Glu Asn Lys Leu Phe Tyr Gln Gly Thr
    370          375          380
Val Arg His Arg Tyr Pro Phe Cys Trp Arg Thr Asp Ser Pro Leu Ile
    385          390          395          400
Tyr Lys Ala Val Asn Ser Trp Phe Val Ala Val Glu Lys Val Lys Ser
          405          410          415
Lys Met Leu Lys Ala Asn Glu Ser Ile His Trp Thr Pro Gly His Ile
          420          425          430
Lys Gln Gly Arg Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp Trp Ala
    435          440          445
Ile Ser Arg Asn Arg Tyr Trp Gly Thr Pro Ile Pro Ile Trp Arg Ser
    450          455          460
Asp Asp Gly Glu Leu Leu Val Ile Gly Ser Ile Gln Glu Leu Glu Ala
    465          470          475          480
Leu Ser Gly Gln Lys Ile Val Asp Leu His Arg His Phe Ile Asp Glu
          485          490          495
Ile Glu Ile Asn Gln Asn Gly Lys Ser Phe Arg Arg Ile Pro Tyr Val
    500          505          510
Phe Asp Cys Trp Phe Asp Ser Gly Ala Met Pro Tyr Ala Gln Asn His
    515          520          525
Tyr Pro Phe Glu Arg Ala Glu Glu Thr Glu Ala Leu Leu Pro Ser
    530          535          540

```

(2) INFORMATIONS POUR LA SEQ ID NO: 455:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui \_

(viii) POSITION DANS LE GENOME: 450546..451076

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 455:

```

Lys Leu Tyr Leu Phe Lys Gly Val Phe Phe Val Tyr Val Phe Ser Asn
1          5          10          15
Thr Phe Phe Phe Met Gln His Ala His Asn Ala Asp Ser Phe Pro Ala
    20          25          30
Trp Asp Cys Leu Gln His Asn Tyr Leu Arg Arg Asn Ala Leu Thr Ser
    35          40          45
Phe Cys Ser Tyr Val Pro Ile Leu Ser Thr Val Val Gly Ile Arg Thr
    50          55          60
Leu Tyr Asn Met Arg Lys Leu His Gln Ala Phe Val Arg Arg Thr Gly

```

65					70					75					80
Gly	Phe	Leu	Cys	Gln	Asn	Asp	Pro	Asn	Ile	Pro	Cys	Asn	Lys	Phe	Pro
				85					90					95	
Cys	Ser	Ile	Ile	Arg	Lys	Glu	Trp	Pro	Gln	Val	His	Thr	Lys	Ala	Met
			100					105					110		
Gln	Glu	Val	Phe	Gly	Ile	Lys	Ala	Leu	Val	Cys	Leu	Gly	Ser	Leu	Ile
		115					120					125			
Leu	Lys	Ile	Phe	Arg	Ala	Val	Lys	Ala	Phe	Phe	His	Arg	Thr	Phe	Ser
	130						135				140				
Pro	Ser	Leu	Leu	Pro	Glu	Gln	Asp	Ala	Ser	Ile	Gln	Leu	Pro	Asp	Ser
145					150					155				160	
Pro	Gln	Ser	Gly	Ile	Pro	Glu	Glu	Thr	Leu	Ser	Glu	Thr	Pro	Arg	Ser
				165					170					175	
Ser															

## (2) INFORMATIONS POUR LA SEQ ID NO: 456:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(451144..451623)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 456:

Lys	Asn	Lys	Arg	Leu	Gln	Arg	Phe	Leu	Phe	Leu	Leu	Pro	Ala	Val	Val
1				5				10					15		
Thr	Glu	Leu	Ala	Gln	Asp	Leu	Ser	Ser	Val	Lys	Gly	Ser	Leu	Leu	Ser
			20				25					30			
His	Tyr	Ile	Arg	Lys	Lys	Gly	Phe	Val	Lys	Ala	Ser	Pro	Val	Ile	Glu
	35					40					45				
Gly	Arg	Glu	Ser	Phe	Glu	Arg	Ser	Leu	Phe	Ala	Val	Trp	Val	Ser	Leu
50					55					60					
Gln	Pro	Glu	Glu	Ile	Arg	His	Gln	Leu	Thr	Met	Glu	Ser	Phe	Tyr	Arg
65				70				75					80		
Asp	Glu	Gln	Lys	Lys	Lys	Arg	Val	Leu	Thr	Gly	Glu	Leu	Glu	Val	Tyr
			85					90					95		
Pro	His	Ile	Val	Lys	Asn	Asn	Pro	Gly	Asp	Tyr	Leu	Leu	Lys	Asn	Gly
			100				105						110		
Glu	Asp	Val	Val	Ala	Phe	Val	Tyr	Ala	Thr	Ser	Ile	Asp	Leu	Ser	Lys
	115						120					125			
Trp	Leu	Gly	Lys	Pro	Val	Val	Leu	Glu	Cys	Val	Ser	Arg	Pro	Asn	Asn
	130					135					140				
His	Phe	Ala	Phe	Pro	Ala	Tyr	Ile	Val	Leu	Ser	Val	Lys	Glu	Gly	Ala
145				150					155					160	

## (2) INFORMATIONS POUR LA SEQ ID NO: 457:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 359 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(451517..452593)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 457:

```

Lys Ile Glu Gln Ser Arg Leu Thr Phe Ser Phe Lys Ser Ile Ile Ile
1      5      10      15
Pro Ser Leu Glu Asp Glu Ser Ser Arg Ala Val Asn Ala Ser Leu Glu
20      25      30
Ala Gln Ile Leu Ala Asn Cys Arg Ser Phe Cys Val Arg Thr Leu Ser
35      40      45
Ile Ser Met Leu Ile Phe Ala Leu Ser Cys Gly Ala Asp Ala Cys Leu
50      55      60
Cys Ala Ala Asp Leu Ser Lys Ala Lys Val Glu Ala Ser Val Gly Asp
65      70      75      80
Arg Ala Ala Phe Ser Pro Phe Thr Gly Glu Ile Lys Gly Asn Arg Val
85      90      95
Arg Leu Arg Leu Ala Pro His Thr Asp Ser Phe Ile Ile Lys Glu Leu
100     105     110
Ser Lys Gly Asp Cys Leu Ala Val Leu Gly Glu Ser Lys Asp Tyr Tyr
115     120     125
Val Val Ala Ala Pro Glu Gly Val Arg Gly Tyr Val Phe Arg Thr Phe
130     135     140
Val Leu Asp Asn Val Ile Glu Gly Glu Lys Val Asn Val Arg Leu Glu
145     150     155     160
Pro Ser Thr Ser Ala Pro Ile Leu Ala Arg Leu Ser Lys Gly Thr Val
165     170     175
Val Lys Thr Leu Gly Ala Ala Gln Gly Lys Trp Ile Glu Ile Ala Leu
180     185     190
Pro Lys Gln Cys Val Phe Tyr Val Ala Lys Asn Phe Val Lys Asn Val
195     200     205
Gly Ala Leu Asp Leu Tyr Asn Gln Lys Glu Gly Gln Lys Lys Leu Ala
210     215     220
Leu Asp Leu Leu Ser Ser Ala Met Asp Phe Ala Asp Ala Glu Leu Gln
225     230     235     240
Lys Lys Ile Glu Asp Ile Asp Leu Asp Ala Ile Tyr Lys Lys Met Asn
245     250     255
Leu Ala Gln Ser Glu Glu Phe Lys Asp Val Pro Gly Leu Gln Ser Leu
260     265     270
Val Gln Lys Ala Leu Glu Arg Phe Gln Glu Ala Phe Leu Ala Lys Ser
275     280     285
Leu Glu Lys Ser Ala Val Lys Val Pro Gly Ile Gln His Lys Val Leu
290     295     300
Glu Xaa Ile Ala Val Val Ser Pro Ala Val Glu Glu Thr Pro Val Val
305     310     315     320
Thr Lys Ile Glu Glu Gln Lys Val Thr Thr Val Pro Val Pro Ala Pro
325     330     335
Ser Cys Cys Tyr Arg Ala Gly Ser Arg Phe Lys Leu Cys Gln Arg Phe
340     345     350
Phe Ile Ile Ala Leu Tyr Pro
355

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(2) INFORMATIONS POUR LA SEQ ID NO: 458:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 458:

(2) INFORMATION POUR LA SEQ ID NO: 459:

(A) LONGUEUR: 434 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 453567..454868

Met	Lys	Lys	Thr	Ser	Val	Ile	Asp	Thr	Ser	Val	Leu	Ile	Tyr	Asp	Pro
1				5					10					15	
Lys	Ala	Leu	Ser	Ser	Phe	Ser	Asn	Thr	Arg	Ile	Ile	Ile	Pro	Phe	Thr
			20					25					30		
Val	Ile	Glu	Glu	Leu	Glu	Ser	Cys	Ala	Lys	Phe	Arg	Asp	Glu	Ser	Gly
		35					40					45			
Lys	Asn	Ala	Ser	Arg	Ala	Leu	Ser	Asn	Ile	Arg	Leu	Leu	Leu	Glu	Gln
	50					55					60				

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Ser Glu Arg Pro Ser Ser Gly Gln Ile Leu Leu Lys Asn Gly Ser Glu
65      70      75      80
Leu Cys Ile Glu Val Ser Pro Leu Val Asn Leu Ser Asn His Glu Lys
      85      90      95
Gln Lys Lys His Leu Thr Leu Glu Leu Leu Gln Ile Ile Ser Gln Arg
      100      105      110
Glu Pro Val Val Phe Val Thr Lys Ser Leu Gly Arg Arg Val His Ala
      115      120      125
Glu Ala Leu Gly Ile Glu Ala Lys Asp Tyr Glu Asn Lys Cys Val Ser
      130      135      140
Phe Arg Ser Leu Tyr Arg Gly His Arg Lys Leu Lys Val Ala Asn Ser
145      150      155      160
Thr Ile Glu Tyr Phe Tyr Lys Asp Gly Ser Ile Ala Phe Pro Ser Asp
      165      170      175
Leu Ser Pro Leu Pro Ser Pro Asn Glu Tyr Phe Phe Leu Ser Gly Asp
      180      185      190
Ser Asp Asn Tyr Ser Ala Val Gly Arg Tyr Ser Ser Lys Asp Asn Lys
      195      200      205
Ile Leu Ser Leu Lys Pro Ala Pro Glu Lys Ile Trp Gly Val Lys Pro
      210      215      220
Leu Asn Ile Glu Gln Arg Cys Ala Leu Asp Leu Leu Leu Arg Asp Asp
225      230      235      240
Ile Lys Leu Val Thr Leu Met Gly Gln Ala Gly Ser Gly Lys Thr Ile
      245      250      255
Leu Ala Leu Ala Ala Ala Met Tyr Gln Val Phe Glu Lys Pro Lys Tyr
      260      265      270
Asn Lys Leu Leu Val Ser Arg Pro Ile Ile Pro Met Gly Lys Asp Ile
      275      280      285
Gly Phe Leu Pro Gly Ile Lys Glu Ala Lys Leu Met His Trp Met Gln
      290      295      300
Pro Ile Tyr Asp Asn Met Glu Phe Leu Phe Asp Val Asn Asn Met Gly
305      310      315      320
Asp Phe Ser Glu Thr Leu His Ser Leu Met Glu Thr Lys Lys Leu Glu
      325      330      335
Met Glu Ala Leu Thr Tyr Ile Arg Gly Arg Ser Leu Pro Lys Val Phe
      340      345      350
Met Ile Ile Asp Glu Ala Gln Asn Leu Thr Pro His Glu Ile Lys Thr
      355      360      365
Ile Ile Ser Arg Ala Gly Lys Gly Thr Lys Ile Val Leu Thr Gly Asp
      370      375      380
Pro Thr Gln Ile Asp Ser Leu Tyr Phe Asp Glu Asn Ser Asn Gly Leu
385      390      395      400
Thr Tyr Leu Val Gly Lys Phe His His Leu Pro Leu Tyr Gly His Met
      405      410      415
Phe Met Thr Arg Thr Glu Arg Ser Glu Leu Ala Ala Ala Ala Ala Thr
      420      425      430
Ile Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 460:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 153 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(454972..455430)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 460:

Ile	Phe	Leu	Tyr	Val	Leu	Ser	Ser	Tyr	Leu	Val	Leu	Tyr	Leu	Ser	Leu
1				5					10					15	
Leu	Ile	Ala	Thr	Ile	Leu	Gly	Met	Pro	Gln	Thr	Leu	Gly	Val	Cys	Cys
			20					25					30		
Arg	Ile	Glu	Gly	Ala	Pro	Gly	Met	Pro	Ala	Tyr	Pro	Leu	Ile	Ile	Leu
		35					40					45			
Leu	Ser	Val	Val	Thr	Leu	Ser	Cys	Cys	Tyr	Ala	Glu	Lys	Arg	Ala	Val
	50					55					60				
Ser	Ile	Gly	Lys	Tyr	Gly	Lys	Ala	Phe	Val	Leu	Ser	Cys	Ile	Asn	Leu
65					70					75				80	
Leu	Ser	Pro	Ile	Leu	Ala	Tyr	Asn	Ile	Leu	Leu	Phe	Pro	Asn	Leu	Leu
				85					90					95	
Val	Ser	Thr	Val	Asp	Asn	Arg	Tyr	Thr	Met	Thr	Val	Phe	Asn	Ala	Ala
			100					105					110		
Ala	Glu	Thr	Arg	Thr	Leu	Gln	His	Leu	Val	Thr	Ile	Val	Leu	Ile	Gly
		115					120					125			
Leu	Pro	Phe	Val	Val	Ala	Tyr	Ala	Ile	Tyr	Ile	Tyr	Arg	Val	Phe	Arg
	130					135					140				
Gly	Lys	Thr	Asp	Phe	Pro	Ser	Ile	Tyr							
145						150									

(2) INFORMATIONS POUR LA SEQ ID NO: 461:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(455367..456032)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 461:

Met	Glu	Phe	Ser	Leu	Ala	Thr	Ile	Leu	Pro	Val	Val	Trp	Tyr	Val	Ile
1				5					10					15	
Leu	Cys	Ile	Ala	Val	Phe	Ala	Tyr	Ser	Leu	Gly	Asp	Gly	Phe	Asp	Leu
			20					25					30		
Gly	Leu	Ser	Thr	Ile	Tyr	Phe	Leu	Ser	Lys	Asp	Glu	Lys	Glu	Arg	Arg
		35					40					45			
Leu	Leu	Leu	Asn	Ser	Ile	Gly	Pro	Val	Trp	Asp	Gly	Asn	Glu	Val	Trp
	50					55					60				
Phe	Val	Ile	Met	Phe	Ala	Gly	Leu	Phe	Ala	Gly	Phe	Pro	Thr	Ala	Tyr
65					70					75				80	
Gly	Thr	Leu	Leu	Ser	Ile	Phe	Tyr	Met	Pro	Ile	Trp	Xaa	Met	Val	Met
				85				90					95		
Leu	Tyr	Ile	Phe	Arg	Gly	Cys	Ser	Leu	Glu	Phe	Arg	Ser	Lys	Ala	Glu
			100					105					110		
Ser	Asn	Arg	Trp	Lys	Leu	Phe	Trp	Asp	Val	Leu	Phe	Ser	Ile	Ser	Gly
		115					120					125			
Met	Ser	Ile	Ser	Phe	Phe	Leu	Gly	Thr	Leu	Ala	Gly	Asn	Leu	Leu	Val
	130					135					140				

Gly	Phe	Pro	Ile	Ala	Pro	Asp	Thr	Ser	Tyr	Ser	Ser	Leu	Ser	Trp	Lys
145					150					155					160
Leu	Phe	Phe	Arg	Pro	Tyr	Gln	Val	Leu	Cys	Gly	Leu	Phe	Val	Val	Ala
				165					170						175
Ala	Phe	Ala	Leu	His	Gly	Ile	Ser	Phe	Ala	Leu	Met	Lys	Thr	Thr	Glu
			180					185					190		
Gly	Leu	His	Glu	Arg	Leu	Lys	Asn	Lys	Phe	Ser	Phe	Met	Phe	Cys	Leu
		195				200						205			
Val	Thr	Trp	Phe	Cys	Ile	Phe	Pro	Cys	Ser	Leu	Arg	Leu	Phe		
	210					215					220				

## (2) INFORMATIONS POUR LA SEQ ID NO: 462:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 446 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(456047..457384)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 462:

Met	Ser	Ala	Glu	Ile	Leu	Ala	Arg	Val	Gln	Phe	Ala	Leu	Phe	Ile	Gly
1				5					10					15	
Phe	His	Tyr	Leu	Phe	Val	Pro	Ile	Ser	Leu	Gly	Leu	Ser	Ile	Met	Ile
			20					25					30		
Val	Leu	Met	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Lys	Lys	Ser	Ile	Tyr	Lys
		35					40					45			
Gln	Leu	Thr	Trp	Phe	Trp	Ile	Lys	Ile	Phe	Thr	Leu	Thr	Phe	Val	Val
	50					55					60				
Gly	Val	Val	Thr	Gly	Leu	Met	Gln	Ile	Phe	Ser	Phe	Gly	Ala	Asn	Trp
65					70					75					80
Ser	Arg	Phe	Ala	Glu	Tyr	Thr	Gly	Asn	Val	Phe	Gly	Met	Phe	Leu	Gly
				85				90					95		
Ser	Glu	Gly	Met	Phe	Ala	Phe	Phe	Leu	Glu	Ser	Gly	Phe	Leu	Gly	Val
			100					105					110		
Leu	Leu	Phe	Gly	Arg	Tyr	Lys	Val	Ser	Lys	Lys	Met	His	Phe	Phe	Ser
		115					120					125			
Ala	Cys	Met	Val	Ala	Leu	Gly	Ala	His	Met	Ser	Ala	Phe	Trp	Ile	Val
	130					135					140				
Cys	Ala	Asn	Ser	Trp	Met	Gln	Thr	Pro	Ser	Gly	Tyr	Glu	Met	Val	Met
145					150					155					160
Arg	Asn	Gly	Met	Leu	Val	Pro	Gln	Met	Thr	Ser	Phe	Trp	Ala	Ala	Val
			165						170					175	
Leu	Ser	Pro	Ser	Ala	Leu	Gln	Arg	Phe	Thr	His	Val	Val	Leu	Gly	Ala
			180					185					190		
Trp	Leu	Ser	Gly	Ile	Phe	Leu	Val	Leu	Ser	Val	Ser	Ala	His	Tyr	Leu
		195					200					205			
Arg	Lys	Glu	Arg	His	Lys	Asp	Phe	Ala	Asn	Gln	Gly	Leu	Lys	Ile	Ser
	210					215					220				
Met	Phe	Cys	Ala	Phe	Leu	Val	Leu	Ala	Leu	Gln	Leu	Trp	Ser	Ala	Asp
225					230					235					240
Val	Thr	Ala	Arg	Gly	Val	Ala	Lys	His	Gln	Pro	Ala	Lys	Leu	Ala	Ala
				245					250					255	
Phe	Glu	Gly	Val	Phe	Lys	Thr	Gln	Glu	His	Thr	Pro	Ile	Tyr	Leu	Leu



				260						265					270				
Gly	Ile	Val	Asp	Met	Lys	Lys	Glu	Arg	Val	Ile	Gly	Ile	Pro	Ile	Pro				
		275						280					285						
Ser	Gly	Leu	Ser	Leu	Leu	Val	His	Arg	Asn	Ala	Lys	Thr	Pro	Val	Thr				
	290						295					300							
Gly	Leu	Asp	Gln	Phe	Pro	Lys	Asp	Glu	Trp	Pro	Asn	Val	Ala	Phe	Val				
305					310					315					320				
Phe	Gln	Thr	Tyr	His	Leu	Met	Val	Met	Leu	Trp	Gly	Val	Met	Val	Leu				
				325					330					335					
Leu	Ala	Leu	Ile	Ala	Phe	Ala	Val	Tyr	Lys	Lys	Lys	Ser	Trp	Ser	Cys				
		340						345					350						
Lys	Lys	Gly	Ile	Leu	Trp	Ile	Leu	Ser	Leu	Ser	Val	Leu	Phe	Pro	Glu				
	355						360					365							
Leu	Cys	Asn	Glu	Ile	Gly	Trp	Ile	Ser	Thr	Glu	Val	Gly	Arg	Gln	Pro				
	370					375					380								
Trp	Val	Val	Tyr	Gly	Leu	Leu	Lys	Thr	Lys	Asp	Ala	Thr	Ser	Pro	Ile				
385					390					395				400					
Val	Asn	Ala	Gly	Gln	Ile	Trp	Gln	Ser	Leu	Ile	Leu	Phe	Ser	Ile	Ile				
				405					410					415					
Phe	Ile	Cys	Leu	Leu	Ser	Val	Phe	Val	Ser	Leu	Leu	Leu	Lys	Lys	Ile				
		420						425					430						
Gly	Glu	Gly	Pro	Asp	Glu	Gln	Asp	Leu	Ile	Glu	Val	Asp	Leu						
	435						440					445							

(2) INFORMATIONS POUR LA SEQ ID NO: 463:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 457659..458450

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 463:

Met	Phe	Val	Gly	Ile	Thr	Tyr	Tyr	Thr	Thr	Pro	Leu	Leu	Glu	Ile	Ala				
1				5					10					15					
Leu	Ile	Trp	Val	Val	Leu	Asn	Tyr	Leu	Leu	Lys	Phe	Phe	Trp	Gly	Thr				
		20						25					30						
Gly	Ala	Met	Asp	Leu	Val	Phe	Gly	Leu	Leu	Ser	Phe	Leu	Cys	Leu	Phe				
	35						40					45							
Val	Leu	Ala	Glu	Lys	Leu	His	Leu	Pro	Val	Ile	Arg	Asn	Leu	Met	Leu				
	50					55					60								
His	Val	Val	Asn	Ile	Ala	Ala	Ile	Val	Val	Phe	Ile	Ile	Phe	Gln	Pro				
65				70						75				80					
Glu	Ile	Arg	Leu	Ala	Leu	Ser	Arg	Ile	Arg	Leu	Arg	Arg	Gly	Lys	Phe				
		85						90					95						
Val	Ile	Asn	Met	Gln	Asp	Glu	Phe	Ile	Asp	His	Leu	Thr	Ala	Cys	Ile				
		100						105					110						
Tyr	Arg	Met	Ala	Glu	Arg	Gln	Ile	Gly	Ala	Leu	Ile	Val	Leu	Glu	Asn				
	115					120						125							
Glu	Arg	Leu	Leu	Asn	Asp	Leu	Leu	Asn	Leu	Ser	Ala	Val	Lys	Ile	Asn				
	130					135					140								
Ala	Asp	Phe	Ser	Glu	Glu	Leu	Leu	Glu	Ala	Ile	Phe	Glu	Pro	Ser	Ser				
145					150					155					160				

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His Leu His Asp Gly Ala Val Leu Met Arg Gly Glu Thr Ile Ser Tyr
      165      170      175
Ala Arg Val Ile Leu Pro Leu Ala His Asp Thr Thr Gln Leu Ser Arg
      180      185      190
Ser Met Gly Thr Arg His Arg Ala Ala Leu Gly Ala Ser Gln Arg Thr
      195      200      205
Asp Ala Leu Val Ile Val Val Ser Glu Glu Thr Gly Ala Val Ser Leu
      210      215      220
Ala Arg Asp Gly Ile Leu Thr Arg Gly Val Lys Met Asp Arg Phe Lys
      225      230      235      240
Ala Ile Leu Arg Ser Ile Leu Thr Arg Asn Glu Arg Lys Thr Asn Pro
      245      250      255
Ile Ile Ser Trp Met Arg Lys Lys
      260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 464:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 375 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 458508..459632

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 464:

```

Val Leu Pro Leu Leu Ser Gly Arg Leu Gln Ile Lys Ser Ile Thr Ile
1      5      10      15
Thr Arg Thr Phe His Asn Ile Pro Val Arg Val Ile Asp Leu Ala Pro
      20      25      30
Glu Gln Thr Val Ile Gly Leu Gln Ala Asn Gly Leu Leu Lys Lys Lys
      35      40      45
Val Ala Met Met Ile Thr Gly Asn Lys Ser Val Val Glu Lys Leu Arg
      50      55      60
Pro Ser Asn Leu Glu Ile Val Ile Ser Ala Lys Gly Arg Thr Glu Ser
      65      70      75      80
Trp Ile Glu Thr Ile Asp Pro Tyr Asn Leu Val Cys Leu Asp Thr Asp
      85      90      95
Ile His Leu Arg Lys Asn Ile Lys Ser Val Thr Ser Glu Asp Ile Phe
      100      105      110
Ile Arg Leu Thr Gln Phe Val Thr Glu Asp Val Ser Val Thr Ile Thr
      115      120      125
Lys Pro Ile Gly Arg Ala Pro Lys Gly Tyr Glu Tyr Leu Asp Thr Trp
      130      135      140
Pro Lys Tyr Leu Val Gln Lys Val Ser Gly Pro Lys Glu Tyr Val Ser
      145      150      155      160
Ser Leu Lys Asp His Gly Leu Glu Leu Thr Phe Asn Leu Asn Lys Val
      165      170      175
Ser Phe Glu Glu Leu Asp Arg Asn Arg Leu Ala Gln Gly Asn Leu Asp
      180      185      190
Glu Val Val Tyr Leu Val Pro Glu Asp Trp Lys Lys Val Tyr Ile Pro
      195      200      205
Phe Asp Asn Ser Tyr Met Glu Leu Asn Asp Pro Gln Ala Asp Phe Leu
      210      215      220
Arg Leu Leu Phe Leu Lys Gln Glu Phe Ile Pro Leu Asn Ile Asn Leu

```

225					230					235				240
Pro	Val	Leu	Leu	Phe	Pro	Val	Glu	Asn	Ser	Gln	Leu	Val	Asn	Pro
				245				250					255	
Gln	Asn	Tyr	Tyr	Leu	Glu	Glu	Asn	Ala	Pro	Leu	Val	Leu	Asn	His
			260					265					270	Gly
Ile	Tyr	Gln	Met	Asp	Leu	Pro	Leu	Tyr	Val	Lys	Asp	Val	Ser	His
		275					280					285		Leu
Phe	Leu	Asp	Val	Val	Lys	Asn	Asn	Ile	Ala	Leu	Thr	Ile	Ile	Met
	290					295					300			Glu
Pro	Pro	Val	Lys	Ser	Gln	Arg	Glu	His	Phe	Ile	His	Trp	Ala	Val
305					310					315				Glu
Phe	Leu	Asp	Glu	Lys	Thr	Leu	Glu	Asn	Thr	Phe	Val	Gln	Ala	Val
				325				330						Met
Ala	Gln	Glu	Gln	Lys	Thr	Asn	Lys	His	Met	Ile	Leu	Asp	Glu	Ala
			340					345					350	Gly
Ile	Arg	His	Arg	Phe	Arg	Glu	Tyr	Leu	Arg	Lys	Leu	Thr	Leu	Phe
		355				360						365		Asp
Gln	Asn	Gly	Glu	Pro	Leu	Pro								
	370					375								

(2) INFORMATIONS POUR LA SEQ ID NO: 465:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 455 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 459839..461203

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 465:

Met	Leu	Phe	Lys	Arg	Leu	Arg	Thr	Gly	Gly	Lys	Ile	Leu	Val	Asp	His
1				5					10					15	
Leu	Val	Tyr	Gly	Leu	Gly	Leu	Gly	Val	Leu	Thr	Ile	Leu	Arg	Leu	Leu
			20					25					30		
Pro	Arg	Ser	Ser	Leu	Arg	Leu	Phe	Ser	Lys	Gly	Leu	Gly	Thr	Ala	Leu
		35					40					45			
Phe	Tyr	Phe	Ile	Ser	Asp	Phe	Arg	Lys	Thr	Ala	Leu	Thr	Asn	Leu	Ala
	50					55					60				
Leu	Ala	Phe	Pro	Glu	Lys	Ser	Phe	Ala	Glu	Arg	Tyr	Gln	Ile	Ala	Arg
65				70					75					80	
Gln	Ser	Val	Gln	Gln	Met	Ile	Ile	Thr	Phe	Val	Glu	Leu	Ala	Thr	Val
				85					90					95	
Asp	Lys	Phe	Ala	Lys	His	Ile	Asp	Glu	Met	Ile	Ala	Ile	Ala	Thr	Ser
		100						105					110		
Glu	Asp	Ala	Pro	Glu	Gly	Phe	Phe	Pro	Glu	Glu	Val	Ser	Ser	Gln	Gln
		115					120					125			
Glu	Leu	Asp	His	Phe	Phe	Ser	Arg	Leu	Asp	Arg	Gln	Glu	Gly	Ala	Ile
	130					135					140				
Leu	Phe	Cys	Gly	His	Gln	Ala	Asn	Trp	Glu	Leu	Pro	Phe	Leu	Tyr	Ile
145				150					155					160	
Thr	Lys	Arg	Tyr	Pro	Gly	Leu	Ala	Phe	Ala	Lys	Pro	Val	Lys	Asn	Arg
			165					170						175	
Arg	Leu	Asn	Gln	Lys	Ile	Ile	Ser	Leu	Arg	Glu	Ser	Phe	Gln	Gly	Lys
			180					185					190		

```

Ile Val Pro Pro Gln Asn Ala Ile Asn Gln Ala Leu Arg Ala Leu His
      195      200      205
Arg Gly Glu Val Val Gly Ile Val Gly Asp Gln Val Leu Leu Ser Ser
      210      215      220
Glu Tyr Ser Tyr Pro Leu Phe Gly Ser Gln Ala Phe Thr Thr Thr Ser
225      230      235      240
Pro Ala Leu Leu Ala Tyr Lys Thr Lys Lys Thr Val Ile Ala Val Ala
      245      250      255
Ile Tyr Arg Lys Pro Asn Gly Asn Tyr Leu Val Val Pro Ser Lys Ala
      260      265      270
Phe His Ala Asn Thr Glu Leu Ser Ile Arg Glu Ser Thr Glu Gln Leu
      275      280      285
Met Asp Arg Leu Met Arg Phe Leu Glu Lys Gly Ile Thr Cys Lys Pro
      290      295      300
Glu Gln Trp Leu Trp Leu His Lys Arg Trp Lys Arg Lys Leu Arg His
305      310      315      320
Lys Phe Lys Arg Arg Tyr Ala Phe Ser His Ile Leu Ile Ile Val Lys
      325      330      335
Gly Thr Ser Leu Gln Ala Leu Gln Arg Phe Leu Ile Glu Phe Gly Glu
      340      345      350
Phe Tyr Ala Asp Ala Ser Leu Ser Leu Ala Ile Ile Gly Ala Thr Asp
      355      360      365
Thr Val Leu Ala Asn Ser Phe Ala Pro Tyr Ser Leu Gln Phe Phe Ser
      370      375      380
Ser Glu Glu Glu Leu Leu Ala Ala Pro Asn Phe Phe Pro Ala Ile Val
385      390      395      400
Asp Leu Phe Gly Leu Ser Arg Lys Thr Arg Leu His Tyr Lys Arg Thr
      405      410      415
Gly Ser Arg Lys Ile Phe Thr Arg Asn Glu Leu Lys Asp Ser Leu Leu
      420      425      430
Gln Lys Gln Ser Leu Ile Gln Ser Phe His Lys Leu Leu Arg Arg Val
      435      440      445
Asp Thr Arg Ser Arg Lys Gly
450      455

```

(2) INFORMATIONS POUR LA SEQ ID NO: 466:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 143 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(461196..461624)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 466:

```

Met Ser Glu His Val His Lys Glu Leu Leu His Leu Gly Glu Val Phe
1      5      10      15
Arg Ser Gln Arg Glu Glu Arg Ala Leu Ser Leu Lys Asp Val Glu Ala
      20      25      30
Ala Thr Ser Ile Arg Leu Ser Ala Leu Glu Ala Ile Glu Ala Gly His
      35      40      45
Leu Gly Lys Leu Ile Ser Pro Val Tyr Ala Gln Gly Phe Met Lys Lys
      50      55      60
Tyr Ala Ala Phe Leu Asp Met Asp Gly Asp Arg Leu Leu Lys Glu His

```

(2) INFORMATION POUR LA SEQ ID NO: 467:

(A) LONGUEUR: 245 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 461887..462621

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 467:

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(462895..463758)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 468:

Trp 1	Ser	Gly	Met	Leu 5	Lys	Val	Leu	Phe	His 10	Thr	Met	Thr	Leu	Phe 15	Gly
His	Leu	Leu	Ser 20	Thr	Pro	Ile	Tyr	Ile	Val	Gly	Asp	Ala	Cys 30	Gly	Lys
Asp	Arg	Asp 35	Glu	Tyr	Lys	Asn	Pro 40	Pro	Leu	Arg	Ala	Phe 45	Ser	Phe	Glu
Ser	Gln	Phe 50	Leu	Gln	Ile	Glu	Asn 55	Ala	Lys	Phe	Lys 60	Thr	Leu	Pro	Asp
Gln 65	Ser	Leu	Gly	Tyr 70	Arg	Gln	Ala	Asp	Thr	Ser 75	Leu	Phe	Ala	Thr 80	Ile
Pro	Val	Thr	Glu	Met 85	Ser	Gly	Phe	Leu	Leu 90	Ser	Ser	Arg	Tyr 95	Leu	Gly
Ala	Glu	Val 100	Ser	Trp	Lys	Ser	Ser 105	Lys	Glu	Leu	Gln	Asp	Thr 110	Asp	Pro
Gln	Ala	Val 115	Gly	Tyr	Phe	Ala	Phe 120	Gln	Asp	Lys	Ser	Phe 125	Tyr	Gln	Tyr
Ile	Thr 130	Leu	Ser	Val	Gly	Ala	Tyr 135	Thr	Leu	Ala	Leu 140	Thr	Asn	Trp	Gln
Trp 145	Ser	Val	Leu	Phe	Ser 150	Gly	Met	Val	Asp	Pro 155	Glu	Asn	Ile	Glu 160	Ile
Gly	Ser	Gly	Leu	Tyr 165	Gln	Val	Val	Leu	Ser 170	Ser	Lys	Tyr	His 175	Ala	Ser
Lys	Ser	Leu 180	Ser	Val	Ile	Met	Gly 185	Val	Ile	Asn	Glu	Val 190	Gly	Leu	His
Asp	Lys 195	Gln	Ala	Trp	Pro	Leu	Leu 200	Gly	Phe	Ser	Tyr	Lys 205	Pro	Glu	Asp
Arg	Leu 210	Thr	Leu	Asn	Cys	Ile 215	Tyr	Pro	Val	Asn	Phe 220	Ser	Ala	Glu	Tyr
Gln 225	Cys	Thr	Pro	Val	Cys 230	Asp	Leu	Gly	Val	Ala 235	Tyr	Arg	Leu	Thr 240	Arg
Leu	Arg	Lys	Lys	Phe 245	Pro	Lys	Asn	Ser	Leu 250	Ala	Thr	Ser	Glu	Gly 255	Ile
Phe	Glu	Tyr 260	Ser	Gly	Arg	Glu	Ile	Glu 265	Gly	Asn	Ile	Lys 270	Leu	Ile	Phe
Trp	Pro	Gly 275	Gln	Asn	Leu	Lys	Met 280	Phe	Gly	Gly	Tyr	Phe 285	Arg	Arg	Glu

(2) INFORMATION POUR LA SEQ ID NO: 469:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 464048..464629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 469:

His	Leu	Val	Gly	Lys	Met	Pro	Ser	Thr	Val	Ala	Pro	Ile	Lys	Gly	Gln	1	5	10	15
Asp	His	Phe	Leu	Asn	Leu	Val	Phe	Pro	Glu	Arg	Val	Ala	Ala	Ala	Tyr	20	25	30	
Met	Ser	Pro	Leu	Ala	Gln	Lys	Tyr	Pro	Lys	Ala	Ala	Leu	Ser	Ile	Ala	35	40	45	
Ser	Leu	Ala	Gly	Phe	Leu	Leu	Gly	Ile	Leu	Lys	Leu	Ile	Thr	Phe	Pro	50	55	60	
Val	Leu	Cys	Ala	Ala	Gly	Leu	Phe	Val	Phe	Pro	Ile	Arg	Gly	Leu	Ile	65	70	75	
Ser	Cys	Leu	Phe	His	Lys	Ser	Phe	Gln	Gly	Cys	Ser	Gly	Tyr	Val	Leu	85	90	95	
Ala	Thr	Phe	Leu	Ser	Leu	Phe	Ser	Leu	Ala	Leu	Thr	Ile	Val	Gly	Ile	100	105	110	
Val	Ser	Cys	Ile	Thr	Trp	Ala	Pro	Gly	Phe	Ile	Phe	Pro	Met	Ile	Ser	115	120	125	
Val	Ser	Ile	Ala	Phe	Ala	Thr	Val	Glu	Thr	Cys	Phe	Gln	Ile	Tyr	Thr	130	135	140	
His	Leu	Phe	Pro	Ala	Leu	Glu	His	Lys	Pro	Ser	Ser	Ser	Leu	Lys	Ile	145	150	155	
Glu	Ile	Ala	Ala	Ala	Lys	Leu	Pro	Arg	Ser	Ser	Ser	Ala	Pro	Asp	Leu	165	170	175	
Asn	Cys	Pro	Ser	Leu	Pro	Thr	Gln	Ser	Ala	Ser	Pro	Ser	Gln	Arg	Phe	180	185	190	
Ser	Ala																		

(2) INFORMATIONS POUR LA SEQ ID NO: 470:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 376 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 464721..465848

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 470:

Ile	Leu	Val	Leu	Ser	Val	Phe	Cys	Phe	Trp	Asp	Asn	Phe	Met	Thr	Pro	1	5	10	15
Val	Thr	Pro	Val	Pro	Pro	Gln	Ser	Pro	Gln	Gln	Val	Lys	Gly	Leu	Leu	20	25	30	
Ser	Arg	Phe	Leu	Thr	Ala	Pro	Asp	Arg	His	Pro	Lys	Leu	Arg	Tyr	Val	35	40	45	
Tyr	Asp	Ile	Ala	Leu	Ile	Ala	Ile	Ser	Ile	Leu	Cys	Ile	Val	Ser	Ile	50	55	60	
Ile	Leu	Trp	Thr	Gln	Gly	Ser	Gly	Leu	Ala	Leu	Phe	Ala	Ile	Ala	Pro	65	70	75	80

```

Ala Leu Ala Ile Gly Ala Leu Gly Val Thr Leu Leu Val Ser Asp Leu
      85                      90                      95
Ala Glu Ser Gln Lys Ser Lys Glu Ile Ala Asp Thr Val Ala Ala Val
      100                    105                    110
Ser Leu Pro Phe Ile Leu Thr Gly Thr Ala Ala Gly Leu Met Phe Ser
      115                    120                    125
Ala Ile Ala Val Gly Lys Gly Ala Val Ile Leu Ala Asn Pro Leu Phe
      130                    135                    140
Leu Met Gly Ser Met Thr Leu Gly Phe Ala Leu Met Ser Leu His Arg
      145                    150                    155
Val Thr Tyr Gln Tyr Leu Ser Asn Arg Glu Gln Trp Lys Gln Gln Lys
      165                    170                    175
Lys Leu Glu Gln Val Glu Leu Ala Ala Trp Glu Ser His Leu Pro Lys
      180                    185                    190
Glu Ser Lys Ser Ser Ala Leu Glu Glu Val Arg Tyr Ser Pro Arg Leu
      195                    200                    205
Met Lys Arg Gly Lys Thr Trp Arg Lys Arg Ala Ile Arg Arg Lys Asn
      210                    215                    220
Tyr Ile Pro Ile Pro Leu Val Asp Lys Thr Leu Gln Thr Met Gln Pro
      225                    230                    235
Asp Ala Leu Phe Ser Ser Thr Thr Thr His Ser Thr Asp Ser Glu Gln
      245                    250                    255
Ile Leu Thr Ser Val Ser Pro Gln Ser Ser Asp Thr Glu Ser Ser Ser
      260                    265                    270
Ser Ser Ser Phe His Thr Pro Pro Asn Ser Asp Lys Glu Leu Ser Asp
      275                    280                    285
Ser Asn Ser Ser Asp Ser Ser Ser Ser Ser Glu Tyr Met Asp Ala Leu
      290                    295                    300
Glu Thr Val Ala Ala Gly Asp Val Ser Gly Ile Thr Pro Pro Ser Lys
      305                    310                    315
Pro Ser Ser Ser Pro Lys Thr Thr Arg Arg Val Val Lys Leu Ser Arg
      325                    330                    335
Ser Glu Arg Asn Ala Gln His His Arg Asn Lys Asp Gln Glu Gln Arg
      340                    345                    350
Gln Asp Ser Ser Glu Ser Ser Asp Glu Glu Ser Ser Ser Asp Ser Ser
      355                    360                    365
Gln Lys Lys Lys Pro Ser Arg Lys
      370                      375

```

(2) INFORMATIONS POUR LA SEQ ID NO: 471:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 436 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(466113..467420)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 471:

```

Asn Asn Met Gly Ile Ala His Thr Glu Trp Glu Ser Val Ile Gly Leu
1      5      10      15
Glu Val His Val Glu Leu Asn Thr Glu Ser Lys Leu Phe Ser Pro Ala
      20      25      30
Arg Asn His Phe Gly Asp Glu Pro Asn Thr Asn Ile Ser Pro Val Cys

```



(2) INFORMATION POUR LA SEQ ID NO: 472:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 491 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(467419..468891)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 472:

Met	Tyr	Arg	Lys	Ser	Ala	Leu	Glu	Leu	Arg	Asp	Ala	Val	Val	Asn	Arg
1				5					10					15	
Glu	Leu	Ser	Val	Thr	Ala	Ile	Thr	Glu	Tyr	Phe	Tyr	His	Arg	Ile	Glu
			20					25					30		
Ser	His	Asp	Glu	Gln	Ile	Gly	Ala	Phe	Leu	Ser	Leu	Cys	Lys	Glu	Arg
		35					40					45			
Ala	Leu	Leu	Arg	Ala	Ser	Arg	Ile	Asp	Asp	Lys	Leu	Ala	Lys	Gly	Asp
	50					55					60				
Pro	Ile	Gly	Leu	Leu	Ala	Gly	Ile	Pro	Ile	Gly	Val	Lys	Asp	Asn	Ile
65					70					75				80	
His	Ile	Thr	Gly	Val	Lys	Thr	Thr	Cys	Ala	Ser	Lys	Met	Leu	Glu	Asn
			85						90					95	
Phe	Val	Ala	Pro	Phe	Asp	Ser	Thr	Val	Val	Arg	Arg	Ile	Glu	Met	Glu
			100					105					110		
Asp	Gly	Ile	Leu	Leu	Gly	Lys	Leu	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly
		115					120					125			
Ser	Thr	Thr	Arg	Tyr	Ser	Ala	Phe	His	Pro	Thr	Asn	Asn	Pro	Trp	Asp
	130					135					140				
Leu	Glu	Arg	Val	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	Ala	Ala	Val
145					150					155					160
Ser	Ala	Arg	Phe	Cys	Pro	Ile	Ala	Leu	Gly	Ser	Asp	Thr	Gly	Gly	Ser
			165						170					175	
Ile	Arg	Gln	Pro	Ala	Ala	Phe	Cys	Gly	Val	Val	Gly	Phe	Lys	Pro	Ser
			180					185					190		
Tyr	Gly	Ala	Val	Ser	Arg	Tyr	Gly	Leu	Val	Ala	Phe	Gly	Ser	Ser	Leu
		195					200					205			
Asp	Gln	Ile	Gly	Pro	Leu	Thr	Thr	Val	Val	Glu	Asp	Val	Ala	Leu	Ala
	210					215					220				
Met	Asp	Ala	Phe	Ala	Gly	Arg	Asp	Pro	Lys	Asp	Ser	Thr	Thr	Arg	Asp
225					230					235					240
Phe	Phe	Lys	Gly	Thr	Phe	Ser	Gln	Ala	Leu	Ser	Leu	Glu	Val	Pro	Lys
			245						250					255	
Leu	Ile	Gly	Val	Pro	Arg	Gly	Phe	Leu	Asp	Gly	Leu	Gln	Glu	Asp	Cys
		260						265					270		
Lys	Glu	Asn	Phe	Phe	Glu	Ala	Leu	Ala	Val	Met	Glu	Arg	Glu	Gly	Ser
		275					280					285			
Arg	Ile	Ile	Asp	Val	Asp	Leu	Ser	Val	Leu	Lys	His	Ala	Val	Pro	Val
	290					295					300				
Tyr	Tyr	Ile	Val	Ala	Ser	Ala	Glu	Ala	Ala	Thr	Asn	Leu	Ala	Arg	Phe
305					310					315					320
Asp	Gly	Val	Arg	Tyr	Gly	His	Arg	Cys	Ala	Gln	Ala	Asp	Asn	Met	His
			325						330					335	
Glu	Met	Tyr	Ala	Arg	Ser	Arg	Lys	Glu	Gly	Phe	Gly	Lys	Glu	Val	Thr
			340					345					350		
Arg	Arg	Ile	Leu	Leu	Gly	Asn	Tyr	Val	Leu	Ser	Ala	Glu	Arg	Gln	Asn
		355					360					365			
Ile	Phe	Tyr	Lys	Lys	Gly	Met	Ala	Val	Arg	Ala	Arg	Leu	Ile	Asp	Ala
	370					375					380				
Phe	Gln	Ala	Ala	Phe	Glu	Arg	Cys	Asp	Val	Ile	Ala	Met	Pro	Val	Cys
385					390					395					400
Ala	Thr	Pro	Ala	Ile	Arg	Asp	Gln	Asp	Val	Leu	Asp	Pro	Val	Ser	Leu

				405					410					415			
Tyr	Leu	Gln	Asp	Ile	Tyr	Thr	Val	Ala	Val	Asn	Leu	Ala	Tyr	Leu	Pro		
			420					425						430			
Ala	Ile	Ser	Val	Pro	Ser	Gly	Leu	Ser	Lys	Glu	Gly	Leu	Pro	Leu	Gly		
		435					440					445					
Val	Gln	Phe	Ile	Gly	Glu	Arg	Gly	Ser	Asp	Gln	Gln	Ile	Cys	Gln	Val		
	450					455				460							
Gly	Tyr	Ser	Phe	Gln	Glu	His	Ser	Gln	Ile	Lys	Gln	Leu	Tyr	Pro	Lys		
465					470					475					480		
Ala	Val	Asn	Gly	Leu	Phe	Asp	Gly	Gly	Ile	Glu							
				485					490								

(2) INFORMATIONS POUR LA SEQ ID NO: 473:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(468906..469280)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 473:

Gly	Phe	Phe	Cys	Phe	Lys	Lys	Phe	Gly	Gly	Phe	Phe	Phe	Phe	Leu	Gly		
1			5					10						15			
Ser	Cys	Leu	Pro	Phe	Phe	Gly	Leu	Glu	Val	Ala	Gly	Phe	Phe	Phe	Asn		
		20					25					30					
Gln	Gly	Gly	Ile	Leu	Phe	Phe	Ala	Lys	Asn	Ala	Ala	Leu	Glu	Leu	Glu		
	35					40						45					
Asp	Ala	His	Val	Glu	Glu	Phe	Val	Thr	Ser	Met	Asn	Asp	Val	Ile	Ala		
	50				55				60								
Leu	Met	Gln	Glu	Val	Ile	Ala	Ile	Asp	Ile	Ser	Asp	Ile	Ile	Leu	Glu		
65				70				75						80			
Ala	Thr	Val	His	His	Phe	Val	Gly	Pro	Glu	Asp	Leu	Arg	Glu	Asp	Met		
		85				90						95					
Val	Thr	Ser	Asp	Phe	Thr	Gln	Glu	Glu	Phe	Leu	Ser	Asn	Val	Pro	Val		
		100				105						110					
Ser	Leu	Gly	Gly	Leu	Val	Lys	Val	Pro	Thr	Val	Ile	Lys					
		115				120						125					

(2) INFORMATIONS POUR LA SEQ ID NO: 474:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 469349..469675

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 474:

```

Ile Val Lys Lys Ile Thr Lys Ser Glu Leu Ser Ile His Leu Arg Trp
1          5          10          15
Arg Asp Val Met Leu Cys Lys Val Cys Arg Gly Leu Ser Ser Leu Ile
          20          25          30
Val Val Leu Gly Ala Ile Asn Thr Gly Ile Leu Gly Val Thr Gly Tyr
          35          40          45
Lys Val Asn Leu Leu Thr His Leu Leu Gly Glu Gly Thr Met Trp Thr
          50          55          60
Gln Ala Ala Tyr Val Val Thr Gly Ile Ala Gly Val Met Val Cys Leu
65          70          75          80
Asn Phe Leu Lys Cys Cys Phe Lys Lys Arg His Glu Asp Cys Cys Ser
          85          90          95
Ser Lys Gly Gly Cys His His His His Met Asp Arg Glu
          100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 475:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 467 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(469826..471226)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 475:

```

Ser Tyr Cys Ser Trp Cys Lys Phe Trp Glu Glu Tyr Ser Pro Ser Ala
1          5          10          15
Ala Arg Gly Leu Arg Leu Met Phe Thr Asp Phe Trp Arg Thr Arg Val
          20          25          30
Leu Arg Gln Thr Ser Pro Met Asp Val Val Phe Gly Asn Leu Asp Val
          35          40          45
Asn Glu Ala Arg Leu Met Ala Ala Tyr Thr Ser Glu Cys Ala Asp Tyr
          50          55          60
Leu Glu Ala His Asp Leu Ala Gly Pro Asp Gly Val Ala Ala Ala Arg
65          70          75          80
Glu Ile Ala Gln Arg Trp Asp Lys Arg Val Arg Asp Leu Gln Asp Lys
          85          90          95
Gly Ala Ala Gln Lys Leu Leu Asn Asp Pro Leu Gly Arg Arg Thr Pro
          100          105          110
Asn Tyr Gln Ser Lys Asn Pro Gly Glu Tyr Thr Val Gly Asn Ser Met
          115          120          125
Phe Tyr Asp Gly Pro Gln Val Ala Asn Leu Gln Asn Val Asp Thr Gly
          130          135          140
Phe Trp Leu Asp Met Ser Asn Phe Ser Asp Val Val Leu Ser Arg Glu
145          150          155          160
Ile Gln Thr Gly Leu Arg Ala Arg Ala Thr Leu Glu Glu Ser Met Pro
          165          170          175
Met Leu Glu Asn Leu Glu Glu Arg Phe Arg Arg Leu Gln Glu Thr Cys
          180          185          190
Asp Ala Ala Arg Thr Glu Ile Glu Glu Ser Gly Trp Thr Arg Glu Ser
          195          200          205
Ala Ser Arg Met Gly Gly Asp Glu Thr Gln Gly Pro Ser Arg Ala Gln
210          215          220
Gln Ala Phe Gln Ser Phe Val Asn Glu Cys Asn Ser Ile Glu Phe Ser

```

```

225          230          235          240
Phe Gly Ser Phe Gly Glu His Val Arg Val Leu Cys Ala Arg Val Ser
          245          250          255
Arg Gly Leu Val Ala Ala Gly Glu Ala Ile Arg Arg Cys Phe Ser Cys
          260          265          270
Cys Lys Gly Ser Thr His Arg Tyr Ala Pro Arg Asp Asp Leu Ser Pro
          275          280          285
Glu Gly Ala Ser Leu Ala Glu Thr Leu Ala Arg Phe Ala Asp Asp Met
          290          295          300
Gly Ile Glu Gln Gly Ala Asp Gly Thr Tyr Asp Ile Pro Trp Val Asp
305          310          315          320
Asp Trp Arg Arg Gly Val Pro Ser Ile Glu Gly Glu Gly Ser Ala Ser
          325          330          335
Ile Tyr Glu Ile Met Met Pro Ile Tyr Glu Val Met Asn Met Asp Leu
          340          345          350
Glu Thr Arg Arg Ser Phe Ala Val Gln Gln Gly His Tyr Gln Asp Pro
          355          360          365
Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ala Ser Asp Tyr Asp Leu Pro
          370          375          380
Arg Ser Pro Tyr Pro Thr Pro Pro Leu Pro Ser Arg Tyr Gln Leu Gln
385          390          395          400
Asn Met Asp Val Glu Ala Gly Phe Arg Glu Ala Val Tyr Ala Ser Phe
          405          410          415
Val Ala Gly Met Tyr Asn Tyr Val Val Thr Gln Pro Gln Glu Arg Ile
          420          425          430
Pro Asn Ser Gln Gln Val Glu Gly Ile Leu Arg Asp Met Leu Thr Asn
          435          440          445
Gly Ser Gln Thr Phe Ser Asn Leu Met Gln Arg Trp Asp Arg Glu Val
          450          455          460
Asp Arg Glu
465

```

(2) INFORMATIONS POUR LA SEQ ID NO: 476:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 173 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(471106..471624)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 476:

```

Val Phe Ile Leu Val Leu Gly Trp Phe Val Met Ser Ile Gly Gly Val
1          5          10          15
Gly Gly Asn Gly Asn Ser Arg Ile Pro Ser His Asn Gly Asp Gly Ser
          20          25          30
Asn Arg Arg Ser Gln Asn Thr Lys Gly Asn Asn Lys Val Glu Asp Arg
          35          40          45
Val His Ser Leu Tyr Ser Ser Leu Ser Asn Glu Asn Arg Glu Ser Pro
          50          55          60
Tyr Pro Val Val Asp Val Ser Ser Met Ile Glu Ser Thr Pro Thr Ser
65          70          75          80
Gly Glu Thr Pro Arg Ala Ser Arg Gly Val Phe Ser Arg Phe Gln Arg
          85          90          95

```

Gly	Leu	Gly	Arg	Val	Ala	Asp	Lys	Val	Arg	Arg	Ala	Val	Gln	Cys	Ala
			100					105					110		
Trp	Gly	Ser	Val	Ser	Thr	Arg	Arg	Ser	Ser	Ala	Thr	Arg	Ala	Val	Glu
		115					120					125			
Ser	Gly	Ser	Ser	Ser	Arg	Thr	Ala	Arg	Gly	Ala	Ser	Ser	Gly	Arg	Ser
		130				135					140				
Ile	Leu	Leu	Gln	Gln	Leu	Glu	Gly	Cys	Val	Leu	Cys	Ser	Gln	Ile	Ser
145					150					155					160
Gly	Glu	Leu	Gly	Phe	Tyr	Ala	Arg	Pro	Leu	Leu	Trp	Met			
				165					170						

(2) INFORMATIONS POUR LA SEQ ID NO: 477:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 471954..473267

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 477:

Val	Lys	Pro	Pro	Ser	Ser	Leu	Lys	Ile	Leu	Ile	Met	Ser	Ser	Val	His
1				5					10					15	
Phe	Leu	Arg	Thr	Val	Pro	Trp	Arg	Ala	Ser	Phe	Leu	Leu	Phe	Val	Leu
			20					25					30		
Met	His	His	Lys	Thr	Ile	Pro	Leu	Tyr	Val	Leu	Gly	Asn	Ser	Tyr	Cys
		35					40					45			
Trp	Phe	Val	Ser	Lys	Leu	His	Ile	Thr	Asp	Pro	Lys	Glu	Ala	Leu	Phe
	50				55						60				
Lys	Glu	Lys	Gly	Asp	Leu	Ser	Ile	Gln	Asn	Phe	Arg	Phe	Leu	Ser	Phe
65					70					75					80
Thr	Asp	Cys	Ser	Ser	Lys	Glu	Ser	Ser	Pro	Ser	Ile	Ile	His	Gln	Lys
				85					90					95	
Asn	Gly	Gln	Leu	Ser	Leu	Arg	Asn	Asn	Gly	Ser	Met	Ser	Phe	Cys	Arg
			100					105					110		
Asn	His	Ala	Glu	Gly	Ser	Gly	Gly	Ala	Ile	Ser	Ala	Asp	Ala	Phe	Ser
		115				120						125			
Leu	Gln	His	Asn	Tyr	Leu	Phe	Thr	Ala	Phe	Glu	Glu	Asn	Ser	Ser	Lys
	130					135					140				
Gly	Asn	Gly	Gly	Ala	Ile	Gln	Ala	Gln	Thr	Phe	Ser	Leu	Ser	Arg	Asn
145					150					155					160
Val	Ser	Pro	Ile	Ser	Phe	Ala	Arg	Asn	Arg	Ala	Asp	Leu	Asn	Gly	Gly
				165					170					175	
Ala	Ile	Cys	Cys	Ser	Asn	Leu	Ile	Cys	Ser	Gly	Asn	Val	Asn	Pro	Leu
			180					185					190		
Phe	Phe	Thr	Gly	Asn	Ser	Ala	Thr	Asn	Gly	Gly	Ala	Ile	Cys	Cys	Ile
		195					200					205			
Ser	Asp	Leu	Asn	Thr	Ser	Glu	Lys	Gly	Ser	Leu	Ser	Leu	Ala	Cys	Asn
	210					215					220				
Gln	Glu	Thr	Leu	Phe	Ala	Ser	Asn	Ser	Ala	Lys	Glu	Lys	Gly	Gly	Ala
225					230					235					240
Ile	Tyr	Ala	Lys	His	Met	Val	Leu	Arg	Tyr	Asn	Gly	Pro	Val	Ser	Phe
				245					250					255	
Ile	Asn	Asn	Ser	Ala	Lys	Ile	Gly	Gly	Ala	Ile	Ala	Ile	Gln	Ser	Gly

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 479:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 182 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 473982..474527

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 479:

Lys	Gln	Asn	Ile	Gly	Ser	Phe	Ser	Lys	Glu	Gly	Phe	Gly	Ser	Trp	His
1				5					10					15	
Ser	Val	Ala	Val	Ser	Gly	Glu	Val	Cys	Ala	Ser	Ile	Pro	Ile	Val	Ser
			20					25					30		
Asn	Gly	Ser	Gly	Leu	Phe	Ser	Ser	Phe	Ser	Ile	Phe	Ser	Lys	Leu	Gln
		35				40					45				
Gly	Phe	Ser	Gly	Thr	Gln	Asp	Gly	Phe	Glu	Glu	Ser	Ser	Gly	Glu	Ile
	50				55					60					
Arg	Ser	Phe	Ser	Ala	Ser	Ser	Phe	Arg	Asn	Ile	Ser	Leu	Pro	Ile	Gly
65				70					75					80	
Ile	Thr	Phe	Glu	Lys	Lys	Ser	Gln	Lys	Thr	Arg	Thr	Tyr	Tyr	Tyr	Phe
			85					90				95			
Leu	Gly	Ala	Tyr	Ile	Gln	Asp	Leu	Lys	Arg	Asp	Val	Glu	Ser	Gly	Pro
		100					105					110			
Val	Val	Leu	Leu	Lys	Asn	Ala	Val	Ser	Trp	Asp	Ala	Pro	Met	Ala	Asn
		115				120					125				
Leu	Asp	Ser	Arg	Ala	Tyr	Met	Phe	Arg	Leu	Thr	Asn	Gln	Arg	Ala	Leu
	130			135						140					
His	Arg	Leu	Gln	Thr	Leu	Leu	Asn	Val	Ser	Cys	Val	Leu	Arg	Gly	Gln
145			150						155				160		
Ser	Ile	Val	Thr	Pro	Trp	Ile	Trp	Gly	His	Leu	Gln	Val	Leu	Val	Pro
			165					170					175		
Leu	Pro	Ser	Ile	Ala	Phe										
			180												

(2) INFORMATIONS POUR LA SEQ ID NO: 480:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 199 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(474602..475198)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 480:

Ile	Met	Val	Cys	Pro	Leu	Arg	Asn	Cys	Cys	Thr	Ser	His	Thr	Ser	Thr
1			5					10					15		
Glu	Asn	Leu	Pro	Met	Glu	Glu	Thr	Ser	Pro	Leu	Val	Glu	Ala	Ile	Val



			20					25					30				
Gln	Ala	Val	Gln	Thr	Cys	Leu	Thr	Val	Ala	Lys	His	Thr	Glu	Asn	Ala		
		35						40				45					
Lys	Val	Tyr	Asn	Gln	Lys	Arg	Lys	Arg	Tyr	His	Gln	Thr	Gly	Cys	Trp		
	50					55					60						
Arg	Gln	Leu	Lys	Lys	Leu	Leu	Cys	Cys	Cys	Cys	Pro	Lys	Glu	Lys	Pro		
65					70				75						80		
Val	Ser	Gly	Ser	Ile	Thr	Ala	Leu	Ser	Leu	Trp	Met	Gln	Ser	His	Ile		
			85					90						95			
Pro	Thr	Arg	Gly	Leu	Leu	Val	Val	Gly	Tyr	Ala	Val	Tyr	Ser	Ser	Gly		
			100					105						110			
Val	Arg	Trp	Glu	Ala	Ile	Leu	Glu	Gly	Glu	Thr	Leu	Ser	Pro	Gly	Asp		
		115					120						125				
Arg	Ala	Gln	Leu	Asp	Ala	Cys	Leu	Glu	Ser	Ala	Gln	Val	Arg	Leu	Ala		
	130					135					140						
Gly	Leu	Met	Leu	Asn	Tyr	Trp	Asp	Gly	Asp	Phe	Pro	Gly	Tyr	Gly	Thr		
145					150					155					160		
Ser	Gly	Gly	Arg	Phe	Ser	Pro	Arg	Met	Gln	Glu	Asp	Ile	Ile	Ala	Arg		
			165					170						175			
Phe	Arg	Asp	Lys	Val	Gly	Ile	Cys	Glu	Leu	Thr	Asp	Ala	Val	Ala	Leu		
			180					185					190				
Lys	His	Phe	Cys	Arg	Arg	Thr											
			195														

(2) INFORMATIONS POUR LA SEQ ID NO: 481:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 305 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(475613..476527)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 481:

Glu	Thr	Phe	Thr	Asn	Gly	Leu	Lys	Glu	His	Tyr	Val	Ser	Arg	Asp	Val		
1				5				10						15			
Gly	Phe	Val	Ala	Ser	Leu	His	Ala	Leu	Gly	Asp	Tyr	Ile	Leu	Asn	Tyr		
		20					25						30				
Thr	Gln	Asp	Asp	Arg	Asp	Gly	Phe	Leu	Ala	Arg	Tyr	Gly	Gly	Phe	Gln		
		35				40					45						
Ala	Thr	Ala	Ala	Cys	His	Tyr	Glu	Asn	Gly	Ser	Ile	Phe	Gly	Val	Ala		
	50				55					60							
Phe	Gly	Gln	Leu	Tyr	Gly	Gln	Thr	Lys	Ser	Arg	Met	Tyr	Tyr	Ser	Lys		
65				70					75						80		
Asp	Ala	Gly	Asn	Met	Thr	Met	Leu	Ser	Cys	Phe	Gly	Arg	Ser	Tyr	Val		
			85					90						95			
Asp	Ile	Lys	Gly	Thr	Glu	Thr	Val	Val	Tyr	Trp	Glu	Thr	Ala	Tyr	Gly		
		100					105						110				
Tyr	Ser	Val	His	Arg	Met	His	Thr	Gln	Tyr	Phe	Asn	Asp	Lys	Thr	Gln		
		115					120					125					
Lys	Phe	Asp	His	Ser	Lys	Cys	His	Trp	His	Asn	Asn	Asn	Tyr	Tyr	Ala		
	130					135					140						
Phe	Val	Gly	Ala	Glu	His	Asn	Phe	Leu	Glu	Tyr	Cys	Ile	Pro	Thr	Arg		
145					150					155					160		

Gln Phe Ala Arg Asp Tyr Glu Leu Ala Gly Phe Met Arg Phe Glu Met  
 165 170 175  
 Ala Gly Gly Trp Ser Ser Ala Thr Gln Glu Thr Gly Ser Leu Thr Arg  
 180 185 190  
 Tyr Phe Ala Arg Gly Ala Gly His Asn Met Ser Leu Pro Ile Gly Ile  
 195 200 205  
 Val Val His Ala Val Ser His Val Arg Arg Ser Pro Leu Ser Lys Leu  
 210 215 220  
 Thr Leu Asn Met Gly Tyr Xaa Pro Asp Ile Trp Arg Val Thr Pro His  
 225 230 235 240  
 Cys Asn Met Glu Ile Ala Asn Gly Val Lys Thr Pro Ile Gln Gly  
 245 250 255  
 Ser Pro Leu Ala Arg His Ala Phe Phe Leu Glu Val His Asp Thr Leu  
 260 265 270  
 Tyr Ile His His Phe Gly Arg Ala Tyr Met Asn Tyr Ser Leu Asp Ala  
 275 280 285  
 Arg Arg Arg Gln Thr Ala His Phe Val Ser Met Gly Leu Asn Arg Ile  
 290 295 300  
 Phe  
 305

(2) INFORMATIONS POUR LA SEQ ID NO: 482:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 708 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(476517..478640)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 482:

Val Leu Ala Met Pro Phe Ser Leu Arg Ser Thr Ser Phe Cys Phe Leu  
 1 5 10 15  
 Ala Cys Leu Cys Ser Tyr Ser Tyr Gly Phe Ala Ser Ser Pro Gln Val  
 20 25 30  
 Leu Thr Pro Asn Val Thr Thr Pro Phe Lys Gly Asp Asp Val Tyr Leu  
 35 40 45  
 Asn Gly Asp Cys Ala Phe Val Asn Val Tyr Ala Gly Ala Glu Glu Gly  
 50 55 60  
 Ser Ile Ile Ser Ala Asn Gly Asp Asn Leu Thr Ile Thr Gly Gln Asn  
 65 70 75 80  
 His Thr Leu Ser Phe Thr Asp Ser Gln Gly Pro Val Leu Gln Asn Tyr  
 85 90 95  
 Ala Phe Ile Ser Ala Gly Glu Thr Leu Thr Leu Arg Asp Phe Ser Ser  
 100 105 110  
 Leu Met Phe Ser Lys Asn Val Ser Cys Gly Glu Lys Gly Met Ile Ser  
 115 120 125  
 Gly Lys Thr Val Ser Ile Ser Gly Ala Gly Glu Val Ile Phe Trp Asp  
 130 135 140  
 Asn Ser Val Gly Tyr Ser Pro Leu Ser Thr Val Pro Thr Ser Ser Ser  
 145 150 155 160  
 Thr Pro Pro Ala Pro Thr Val Ser Asp Ala Arg Lys Gly Ser Ile Phe  
 165 170 175  
 Ser Val Glu Thr Ser Leu Glu Ile Ser Gly Val Lys Lys Gly Val Met

180							185					190				
Phe	Asp	Asn	Asn	Ala	Gly	Asn	Phe	Gly	Thr	Val	Phe	Arg	Gly	Lys	Asn	
		195					200					205				
Asn	Asn	Asn	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Ala	Thr	Pro	Ser	Ser	
		210				215					220					
Thr	Thr	Phe	Thr	Val	Lys	Asn	Cys	Lys	Gly	Lys	Val	Ser	Phe	Thr	Asp	
225					230					235					240	
Asn	Val	Ala	Ser	Cys	Gly	Gly	Gly	Val	Val	Tyr	Lys	Gly	Ile	Val	Leu	
				245					250					255		
Phe	Lys	Asp	Asn	Glu	Gly	Gly	Ile	Phe	Phe	Arg	Gly	Asn	Thr	Ala	Tyr	
			260					265					270			
Asp	Asp	Leu	Arg	Ile	Leu	Ala	Ala	Thr	Asn	Gln	Asp	Gln	Asn	Thr	Glu	
		275					280				285					
Thr	Gly	Gly	Gly	Gly	Gly	Val	Ile	Cys	Ser	Pro	Asp	Asp	Ser	Val	Lys	
		290				295					300					
Phe	Glu	Gly	Asn	Lys	Gly	Ser	Ile	Val	Phe	Asp	Tyr	Asn	Phe	Ala	Lys	
305					310					315					320	
Gly	Arg	Gly	Gly	Ser	Ile	Leu	Thr	Lys	Glu	Phe	Ser	Leu	Val	Ala	Asp	
				325					330					335		
Asp	Ser	Val	Val	Phe	Ser	Asn	Asn	Thr	Ala	Glu	Lys	Gly	Gly	Gly	Ala	
			340					345					350			
Ile	Tyr	Ala	Pro	Thr	Ile	Asn	Met	Ser	Thr	Asn	Gly	Gly	Ser	Ile	Leu	
		355					360				365					
Phe	Glu	Arg	Asn	Arg	Ala	Ala	Glu	Gly	Gly	Ala	Ile	Cys	Val	Ser	Ala	
		370				375					380					
Ala	Ser	Ser	Gly	Ser	Thr	Gly	Lys	Leu	Thr	Leu	Ser	Ala	Ser	Asp	Gly	
385					390					395					400	
Asp	Ile	Val	Phe	Ser	Gly	Asn	Met	Thr	Ser	Asp	Arg	Pro	Gly	Glu	Arg	
				405					410					415		
Ser	Ala	Val	Arg	Ile	Leu	Ser	Ser	Gly	Thr	Thr	Val	Ala	Leu	Asn	Ala	
			420					425					430			
Ser	Gly	Leu	Ser	Lys	Leu	Ile	Phe	His	Asp	Pro	Val	Val	Gln	Ile	Asn	
		435					440					445				
Ser	Ala	Ala	Ala	Ala	Ser	Thr	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Thr	Pro	
		450				455					460					
Ala	Ala	Val	Thr	Ile	Asn	Gln	Ser	Gly	Asn	Gly	Ser	Val	Ile	Phe	Thr	
465					470					475					480	
Ala	Glu	Ser	Leu	Thr	Pro	Ser	Glu	Lys	Leu	Gln	Val	Leu	Asn	Ser	Thr	
				485					490					495		
Ser	Asn	Phe	Pro	Gly	Thr	Leu	Thr	Val	Ser	Gly	Gly	Glu	Leu	Val	Val	
			500					505					510			
Thr	Glu	Gly	Ala	Thr	Leu	Thr	Thr	Gly	Thr	Ile	Thr	Ala	Thr	Ser	Gly	
		515					520					525				
Arg	Val	Ser	Leu	Gly	Ser	Gly	Ala	Ser	Leu	Ser	Ala	Val	Ala	Gly	Ala	
		530				535					540					

Ala Lys Gly Met Val Pro Pro Asn Thr Ser Asn Thr Leu Tyr Leu Thr  
                   660                  665                  670  
 Trp Arg Pro Ala Ser Asn Tyr Gly Glu Tyr Arg Leu Asp Pro Gln Arg  
                   675                  680                  685  
 Lys Gly Glu Leu Val Pro Asn Ser Leu Trp Val Ala Gly Ser Ala Leu  
                   690                  695                  700  
 Arg Asn Leu Tyr  
 705

(2) INFORMATIONS POUR LA SEQ ID NO: 483:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(478665..479084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 483:

Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr  
 1                  5                  10                  15  
 Ala Asp His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe  
                   20                  25                  30  
 Lys Ser Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe  
                   35                  40                  45  
 Asp Arg Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala  
                   50                  55                  60  
 Tyr Ile Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu  
                   65                  70                  75                  80  
 Leu Ser His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg  
                   85                  90                  95  
 His Gly Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn  
                   100                  105                  110  
 Ile Glu Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg  
                   115                  120                  125  
 Gly Tyr Gly Leu Ser Ala Gly Ser Arg Val Arg Phe  
                   130                  135                  140

(2) INFORMATIONS POUR LA SEQ ID NO: 484:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 212 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479088..479723)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 484:

Gly Met Arg Cys Leu Ser Met Ala Ile Lys Glu Ala Gly Ser Leu Arg

```

1           5           10           15
Gly Ile Leu Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr
20           25           30
Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu
35           40           45
Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His
50           55           60
Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu
65           70           75           80
Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu
85           90           95
Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn
100          105          110
Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe
115          120          125
Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys
130          135          140
Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr
145          150          155          160
Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln
165          170          175
His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp
180          185          190
Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val
195          200          205
Ile Thr Pro Ser
210

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 485:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 115 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479668..480012)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 485:

```

Ser Val Asp His Ala Phe Gln Ser Ala Phe Val Ser Phe Phe Phe Val
1           5           10           15
Ser Lys Gln Cys Ser Tyr Glu Ser Ser Tyr Gln Ser Ser Ser Ala Arg
20           25           30
Phe Ser Ile Leu Gln Ser Leu Val Ala Gln Leu Leu Val Leu Leu Gln
35           40           45
Leu Val Gly Leu Ser Phe Leu Arg Ile Trp Met Ile Gln Leu Asn Asp
50           55           60
Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu
65           70           75           80
Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu
85           90           95
Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala
100          105          110
Trp Asp Ser
115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 486:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 524 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479895..481466)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 486:

Val	Val	Phe	Gly	Asn	Leu	Leu	Gly	Ser	Phe	Thr	Val	Leu	Gly	Arg	Gly
1				5				10						15	
His	Ser	Leu	Thr	Phe	Glu	Asn	Ile	Arg	Thr	Ser	Thr	Asn	Gly	Ala	Ala
		20						25					30		
Leu	Ser	Asn	Ser	Ala	Ala	Asp	Gly	Leu	Phe	Thr	Ile	Glu	Gly	Phe	Lys
		35					40					45			
Glu	Leu	Ser	Phe	Ser	Asn	Cys	Asn	Ser	Leu	Leu	Ala	Val	Leu	Pro	Ala
	50					55					60				
Ala	Thr	Thr	Asn	Lys	Gly	Ser	Gln	Thr	Pro	Thr	Thr	Thr	Ser	Thr	Pro
65				70					75						80
Ser	Asn	Gly	Thr	Ile	Tyr	Ser	Lys	Thr	Asp	Leu	Leu	Leu	Leu	Asn	Asn
				85				90						95	
Glu	Lys	Phe	Ser	Phe	Tyr	Ser	Asn	Leu	Val	Ser	Gly	Asp	Gly	Gly	Ala
		100						105					110		
Ile	Asp	Ala	Lys	Ser	Leu	Thr	Val	Gln	Gly	Ile	Ser	Lys	Leu	Cys	Val
	115						120					125			
Phe	Gln	Glu	Asn	Thr	Ala	Gln	Ala	Asp	Gly	Gly	Ala	Cys	Gln	Val	Val
	130					135					140				
Thr	Ser	Phe	Ser	Ala	Met	Ala	Asn	Glu	Ala	Pro	Ile	Ala	Phe	Val	Ala
145				150					155						160
Asn	Val	Ala	Gly	Val	Arg	Gly	Gly	Gly	Ile	Ala	Ala	Val	Gln	Asp	Gly
				165					170					175	
Gln	Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser
		180						185					190		
Phe	Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val
		195					200					205			
Gly	Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly
	210					215					220				
Lys	Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Phe	Pro	Val	Tyr	Ile	Ala	Ala
225				230						235					240
Lys	Gln	Pro	Thr	Ser	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asn	Asn	Tyr	Gly
				245					250					255	
Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Val	Gly	Ser	Asn
		260						265					270		
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		275					280					285			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
	290					295					300				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn	Ile	Ala	Asn
305				310						315					320
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
				325				330						335	
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala

(2) INFORMATION POUR LA SEQ ID NO: 487:

(A) LONGUEUR: 79 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(481496..481732)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 487:

(2) INFORMATION POUR LA SEQ ID NO: 488:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 522 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 481864..483429

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 488:

Pro	Ala	Met	Ile	Lys	Arg	Thr	Ser	Leu	Ser	Phe	Ala	Cys	Leu	Ser	Phe	1	5	10	15
Phe	Tyr	Leu	Ser	Thr	Ile	Ser	Ile	Leu	Gln	Ala	Asn	Glu	Thr	Asp	Thr	20	25	30	
Leu	Gln	Phe	Arg	Arg	Phe	Thr	Phe	Ser	Asp	Arg	Glu	Ile	Gln	Phe	Val	35	40	45	
Leu	Asp	Pro	Val	Ser	Leu	Ile	Thr	Ala	Gln	Asn	Val	Thr	Phe	Ser	Asn	50	55	60	
Ile	Asn	Ser	Trp	Gly	Arg	Gly	Val	Cys	Thr	Ile	Ala	Asp	Asn	Thr	Gln	65	70	75	80
Thr	Gln	Ile	Phe	Ser	Asn	Ser	Ile	Asn	Thr	Thr	Ser	Ala	Ala	Gly	Gly	85	90	95	
Val	Phe	Asp	Met	Val	Thr	Ile	Ser	Phe	Thr	Ala	Ser	Asn	Asn	Ala	Asn	100	105	110	
Leu	Leu	Phe	Cys	Asn	Asn	Tyr	Cys	Thr	His	Asn	Lys	Gly	Gly	Gly	Ala	115	120	125	
Ile	Arg	Ser	Lys	Gly	Pro	Ile	Arg	Phe	Ser	Asn	Asn	Gln	Asp	Val	Leu	130	135	140	
Phe	Tyr	Asn	Asn	Thr	Thr	Ala	Gly	Ala	Gln	Tyr	Thr	Gly	Thr	Gly	Asn	145	150	155	160
Lys	Ser	Glu	Lys	Asn	Arg	Gly	Gly	Ala	Leu	Tyr	Ala	Lys	Asn	Ile	Thr	165	170	175	
Leu	Thr	Gly	Asn	Arg	Thr	Leu	Ala	Phe	Ile	Asn	Asn	Met	Ser	Gly	Asp	180	185	190	
Cys	Gly	Gly	Ala	Ile	Ala	Ala	Asn	Thr	Gln	Ile	Ser	Ile	Thr	Asp	Thr	195	200	205	
Ala	Lys	Gly	Val	Leu	Phe	Glu	Asn	Asn	His	Thr	Leu	Asn	His	Ile	Pro	210	215	220	
Asp	Thr	Arg	Ala	Glu	Asn	Met	Ala	Arg	Gly	Gly	Ala	Ile	Cys	Ser	Arg	225	230	235	240
Lys	Ser	Ser	Cys	Ser	Ile	Ser	Asn	Asn	Leu	Gly	Pro	Ile	Ile	Phe	Asn	245	250	255	
Tyr	Asn	Gln	Gly	Gly	Lys	Gly	Gly	Ala	Ile	Ser	Ala	Thr	Gln	Cys	Val	260	265	270	
Ile	Ser	Asn	Asn	Glu	Glu	Arg	Ile	Val	Phe	Ser	Asn	Asn	Ser	Ser	Ile	275	280	285	
Gly	Trp	Asn	Lys	Ser	Thr	His	Ala	Ser	Asn	Gly	Gly	Ala	Ile	Gln	Thr	290	295	300	
Ala	Gln	Gly	Phe	Thr	Leu	Gln	Asn	Asn	Lys	Gly	Pro	Ile	Tyr	Phe	Asp	305	310	315	320
Ser	Asn	Thr	Ala	Ala	His	Ala	Gly	Gly	Ala	Ile	Asp	Cys	Gly	Tyr	Ile	325	330	335	
Asp	Ile	Arg	Asn	Asn	Gly	Pro	Ile	Tyr	Phe	Leu	Asn	Asn	Ser	Ala	Ala	340	345	350	
Trp	Gly	Ala	Ala	Phe	Asn	Leu	Ser	Lys	Leu	Arg	Pro	Ala	Thr	Asn	Tyr	355	360	365	
Ile	His	Thr	Gly	Thr	Gly	Asp	Ile	Val	Phe	Asn	Asn	Asn	Val	Val	Phe	370	375	380	
Lys	Phe	Asp	Ala	Asn	Leu	Leu	Gly	Met	Arg	Lys	Leu	Phe	His	Ile	Asn	385	390	395	400
Asn	Asn	Thr	Gln	Thr	Pro	Tyr	Thr	Leu	Ser	Leu	Gly	Ala	Lys	Glu	Asp	405	410	415	
Thr	Arg	Ile	Tyr	Phe	Tyr	Asp	Leu	Phe	Gln	Trp	Glu	Arg	Val	Arg	Glu				



			420					425					430				
Pro	Asn	Asn	Ala	Gln	Val	Ser	Pro	Ser	Ser	Arg	Asn	Val	Ile	Thr	Ile		
			435					440					445				
Asn	Pro	Ile	Glu	Glu	Phe	Ser	Gly	Ala	Val	Val	Phe	Ser	Tyr	Lys	Gln		
			450				455					460					
Met	Ser	Ser	Asp	Ile	Lys	Thr	Leu	Met	Gly	Thr	Glu	His	Asn	Tyr	Ile		
465						470				475					480		
Arg	Glu	Ala	Pro	Thr	Thr	Leu	Lys	Phe	Gly	Thr	Leu	Ala	Ile	Glu	Asp		
				485					490					495			
Gly	Ala	Glu	Leu	Glu	Phe	Phe	Asp	Ile	Pro	Phe	Thr	Gln	Asn	Pro	Thr		
			500					505					510				
Ser	Leu	Leu	Ala	Leu	Gly	Ser	Asp	Leu	Arg								
			515				520										

(2) INFORMATIONS POUR LA SEQ ID NO: 489:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 521 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 483402..484964

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 489:

Ser	Thr	Cys	Phe	Arg	Lys	Arg	Pro	Thr	Leu	Thr	Val	Gly	Lys	His	Gly		
1				5					10					15			
Lys	Leu	Asn	Ile	Thr	Asn	Leu	Gly	Val	Ile	Leu	Pro	Ile	Ile	Leu	Lys		
			20				25					30					
Glu	Gly	Lys	Ser	Pro	Pro	Cys	Ile	Arg	Val	Asn	Pro	Gln	Asp	Met	Thr		
		35				40				45							
Gln	Asn	Thr	Asp	Thr	Gly	Gln	Thr	Pro	Ser	Ser	Thr	Ser	Ser	Ile	Ser		
	50				55				60								
Thr	Pro	Met	Ile	Ile	Phe	Asn	Gly	Arg	Leu	Ser	Ile	Val	Asp	Glu	Asn		
65				70				75						80			
Tyr	Glu	Ser	Val	Tyr	Asp	Ser	Met	Asp	Leu	Ser	Arg	Gly	Lys	Ala	Glu		
			85					90					95				
Gln	Pro	Ile	Leu	Ser	Ile	Glu	Thr	Thr	Asn	Asp	Gly	Gln	Leu	Gly	Pro		
			100				105					110					
Asn	Trp	Gln	Asn	Ser	Leu	Asn	Thr	Ser	Leu	Leu	Ser	Pro	Pro	His	Tyr		
		115				120					125						
Gly	Tyr	Gln	Gly	Leu	Trp	Thr	Pro	Asn	Trp	Ile	Thr	Thr	Thr	Tyr	Thr		
	130					135				140							
Ile	Thr	Leu	Asn	Asn	Asn	Ser	Ser	Ala	Pro	Thr	Ser	Ala	Asn	Ser	Ile		
145					150				155						160		
Ala	Glu	Gln	Lys	Lys	Thr	Ser	Glu	Thr	Phe	Thr	Pro	Asn	Ser	Thr	Thr		
			165					170						175			
Thr	Ala	Gly	Ile	Pro	Ser	Ile	Lys	Ala	Ser	Ala	Gly	Ser	Gly	Ser	Gly		
			180				185					190					
Ser	Ser	Thr	Thr	Thr	Asp	Val	Gln	Val	Thr	Arg	His	Thr	Leu	Thr	Val		
		195				200						205					
Asn	Trp	Thr	Pro	Val	Gly	Tyr	Ile	Val	Asp	Pro	Ile	Arg	Arg	Gly	Asp		
	210				215					220							
Leu	Ile	Ala	Asn	Ser	Leu	Val	His	Ser	Gly	Arg	Asn	Met	Thr	Met	Gly		
225					230				235						240		

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Leu Arg Ser Leu Leu Pro Asp Asn Ser Trp Phe Ala Leu Gln Gly Ala
                245                250                255
Ala Thr Thr Leu Phe Thr Lys Gln Gln Lys Arg Leu Ser Tyr His Gly
                260                265                270
Tyr Ser Ser Ala Ser Lys Gly Tyr Thr Val Ser Ser Gln Ala Ser Gly
                275                280                285
Ala His Gly His Lys Phe Leu Leu Ser Phe Ser Gln Ser Ser Asp Lys
                290                295                300
Met Lys Glu Lys Glu Thr Asn Asn Arg Leu Ser Ser Arg Tyr Tyr Leu
305                310                315                320
Ser Ala Leu Cys Phe Glu His Pro Met Phe Asp Arg Ile Ala Leu Ile
                325                330                335
Gly Ala Ala Ala Cys Asn Tyr Gly Thr His Asn Met Arg Ser Phe Tyr
                340                345                350
Gly Thr Lys Arg Ser Ser Lys Gly Lys Phe His Ser Thr Thr Leu Gly
                355                360                365
Ala Ser Leu Arg Cys Glu Leu Arg Asp Ser Met Pro Leu Arg Ser Ile
370                375                380
Met Leu Thr Pro Phe Ala Gln Ala Leu Phe Ser Arg Thr Lys Pro Gly
385                390                395                400
Ala Ile Arg Glu Ser Gly Asp Leu Ala Arg Leu Phe Thr Leu Glu Gln
                405                410                415
Ala His Thr Ala Ile Val Ser Pro Ile Gly Ile Lys Gly Ala Tyr Ser
                420                425                430
Ser Asp Thr Trp Pro Thr Leu Ser Trp Glu Met Glu Leu Ala Tyr Gln
                435                440                445
Pro Thr Leu Tyr Trp Lys Arg Pro Leu Leu Asn Thr Leu Leu Ile Gln
450                455                460
Asn Asn Gly Ser Trp Val Thr Thr Asn Thr Pro Leu Ala Lys His Ser
465                470                475                480
Phe Tyr Gly Arg Gly Ser His Ser Leu Lys Phe Ser His Leu Lys Leu
                485                490                495
Phe Ala Asn Tyr Gln Ala Glu Val Ala Thr Ser Thr Val Ser His Tyr
                500                505                510
Ile Asn Ala Gly Gly Ala Leu Val Phe
                515                520

```

(2) INFORMATIONS POUR LA SEQ ID NO: 490:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 989 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 484898..487864

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 490:

```

Leu Ser Ser Arg Ser Gly Tyr Phe His Cys Leu Thr Leu His Gln Cys
1          5          10          15
Arg Arg Ser Ser Gly Leu Leu Thr Met Lys Lys Ala Phe Phe Phe
20          25          30
Leu Ile Gly Ser Ser Leu Ser Gly Leu Ala Arg Glu Val Pro Ser Arg
35          40          45
Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro Thr Lys Glu Ser Leu

```

50	55	60
Ser 65	Leu 70	Asn 75
Tyr 85	Arg 90	Leu 95
Asn 100	Ala 105	Leu 110
Thr 115	Phe 120	Leu 125
Gly 130	Ala 135	Pro 140
Arg 145	Val 150	Asn 155
Pro 165	Ala 170	Asn 175
Gly 180	Gln 185	Asn 190
Val 195	Phe 200	Arg 205
Ser 210	Val 215	Gln 220
Phe 225	Ile 230	Thr 235
Ala 245	Thr 250	Glu 255
Leu 260	Ala 265	Gly 270
Pro 275	Asn 280	Ile 285
Asn 290	Glu 295	Ala 300
Gly 305	Thr 310	Arg 315
Gly 325	Asn 330	Lys 335
Ile 340	Val 345	Asn 350
Ile 355	Lys 360	Ala 365
Thr 370	Ala 375	Arg 380
Glu 385	Val 390	Asn 395
Ala 405	Ala 410	Val 415
Glu 420	Gly 425	Asn 430
Pro 435	Gly 440	Val 445
Ala 450	Val 455	Gly 460
Ala 465	Leu 470	Thr 475
Thr 485	Cys 490	Glu 495
Val 500	Gly 505	Val 510
Ala 515	Gly 520	Asn 525

Ala	Ser	Ile	Thr	Leu	Lys	His	Ile	Gly	Leu	Asn	Leu	Ser	Ser	Ile	Leu
530						535					540				
Lys	Ser	Gly	Ala	Glu	Ile	Pro	Leu	Leu	Trp	Val	Glu	Pro	Thr	Asn	Asn
545					550					555					560
Ser	Asn	Asn	Tyr	Thr	Ala	Asp	Thr	Ala	Ala	Thr	Phe	Ser	Leu	Ser	Asp
				565					570					575	
Val	Lys	Leu	Ser	Leu	Ile	Asp	Asp	Tyr	Gly	Asn	Ser	Pro	Tyr	Glu	Ser
			580					585					590		
Thr	Asp	Leu	Thr	His	Ala	Leu	Ser	Ser	Gln	Pro	Met	Leu	Ser	Ile	Ser
		595					600					605			
Glu	Ala	Ser	Asp	Asn	Gln	Leu	Arg	Ser	Asp	Asp	Met	Asp	Phe	Ser	Gly
	610					615					620				
Leu	Asn	Val	Pro	His	Tyr	Gly	Trp	Gln	Gly	Leu	Trp	Ser	Trp	Gly	Trp
625					630					635					640
Ala	Lys	Thr	Gln	Asp	Pro	Glu	Pro	Ala	Ser	Ser	Ala	Thr	Ile	Thr	Asp
				645					650					655	
Pro	Lys	Lys	Ala	Asn	Arg	Phe	His	Arg	Thr	Leu	Leu	Leu	Thr	Trp	Leu
			660					665					670		
Pro	Ala	Gly	Tyr	Val	Pro	Ser	Pro	Lys	His	Arg	Ser	Pro	Leu	Ile	Ala
		675					680					685			
Asn	Thr	Leu	Trp	Gly	Asn	Met	Leu	Leu	Ala	Thr	Glu	Ser	Leu	Lys	Asn
	690				695						700				
Ser	Ala	Glu	Leu	Thr	Pro	Ser	Asp	His	Pro	Phe	Trp	Gly	Ile	Thr	Gly
705					710					715					720
Gly	Gly	Leu	Gly	Met	Met	Val	Tyr	Gln	Asp	Pro	Arg	Glu	Asn	His	Pro
				725					730					735	
Gly	Phe	His	Met	Arg	Ser	Ser	Gly	Tyr	Ser	Ala	Gly	Met	Ile	Ala	Gly
			740					745					750		
Gln	Thr	His	Thr	Phe	Ser	Leu	Lys	Phe	Ser	Gln	Thr	Tyr	Thr	Lys	Leu
		755					760					765			
Asn	Glu	Arg	Tyr	Ala	Lys	Asn	Asn	Val	Ser	Ser	Lys	Asn	Tyr	Ser	Cys
	770					775					780				
Gln	Gly	Glu	Met	Leu	Phe	Ser	Leu	Gln	Glu	Gly	Phe	Leu	Leu	Ala	Lys
785					790					795					800
Leu	Val	Gly	Leu	Tyr	Ser	Tyr	Gly	Asp	His	Asn	Cys	His	His	Phe	Tyr
				805					810					815	
Thr	Gln	Gly	Glu	Asn	Leu	Thr	Ser	Gln	Gly	Thr	Phe	Arg	Ser	Gln	Thr
			820					825					830		
Met	Gly	Gly	Ala	Val	Phe	Phe	Asp	Leu	Pro	Met	Lys	Pro	Phe	Gly	Ser
		835					840					845			
Thr	His	Ile	Leu	Thr	Ala	Pro	Phe	Leu	Gly	Ala	Leu	Gly	Ile	Tyr	Ser
		850				855					860				
Ser	Leu	Ser	His	Phe	Thr	Glu	Val	Gly	Ala	Tyr	Pro	Arg	Ser	Phe	Ser
865					870					875					880
Thr	Lys	Thr	Pro	Leu	Ile	Asn	Val	Leu	Val	Pro	Ile	Gly	Val	Lys	Gly
				885					890					895	
Ser	Phe	Met	Asn	Ala	Thr	Gln	Arg	Pro	Gln	Ala	Trp	Thr	Val	Glu	Leu
			900					905					910		
Ala	Tyr	Gln	Pro	Val	Leu	Tyr	Arg	Gln	Glu	Leu	Glu	Ile	Ala	Thr	Gln
		915					920					925			
Leu	Leu	Ala	Ser	Lys	Gly	Ile	Trp	Phe	Gly	Ser	Gly	Ser	Pro	Ser	Ser
		930				935					940				
Arg	His	Ala	Met	Ser	Tyr	Lys	Ile	Ser	Gln	Gln	Thr	Gln	Pro	Leu	Ser
945					950					955					960
Trp	Leu	Thr	Leu	His	Phe	Gln	Tyr	His	Gly	Phe	Tyr	Ser	Ser	Ser	Thr
				965					970					975	
Phe	Cys	Asn	Tyr	Leu	Asn	Gly	Glu	Ile	Ala	Leu	Arg	Phe			
			980					985							

(2) INFORMATIONS POUR LA SEQ ID NO: 491:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 168 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(485222..485725)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 491:

```

Arg Thr Asp Arg Gly Glu Asp Arg Ser Ser Cys Thr Thr Gly Val Ile
1      5      10      15
Asp Lys Glu Glu Ile Ala Val Ile Thr Leu Lys Arg Ile Ala Arg Ser
20      25      30
Ser Ile Asp Ser Ala Thr Phe Ser Cys Cys Ile Ser Leu Asn Thr Asp
35      40      45
Val Val His Lys Glu Lys Thr Arg Leu Ile Leu Ala His Asn Lys Gly
50      55      60
Ile Ser Gly Thr Asn Gly Ser Ser Ser Asp Ile Arg Lys Val Leu His
65      70      75      80
Lys Ser Asp His Ile Met Ile Val Ile Tyr Val Lys Ile Leu Ser Met
85      90      95
Asn Cys Ser Ala Phe Ser Tyr Phe Ile Asn Ser Cys Ile Arg Ile Thr
100     105     110
Arg Cys Lys Trp Ser Ala Thr Ser Ile Ile Phe Lys Asp Tyr Arg Thr
115     120     125
Tyr Cys Ile Thr Asn Leu His Gly Arg Arg Ile Gly Thr Arg Ile Thr
130     135     140
Asn Arg Thr Thr Thr Phe Arg Gly Glu Ile Phe Cys Lys Ile Asn Thr
145     150     155     160
Phe Phe Leu Cys Ile Lys Lys Ala
165

```

(2) INFORMATIONS POUR LA SEQ ID NO: 492:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 348 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 488204..489247

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 492:

```

Phe Ser Ser Phe Thr Pro Phe Leu Ile Tyr Asn Pro Ser Leu Gly Ala
1      5      10      15
Ala Lys His Thr Leu Leu Leu Arg Ser Asn Leu Pro Ser Leu Phe Gln
20      25      30
Tyr Leu Phe Arg Leu Leu Leu Leu Pro Tyr Arg Val Leu Ser Thr Pro
35      40      45

```

```

Pro Pro Pro Val Ile Ser Arg Pro Ser Thr Pro Ser Ala Pro Lys Pro
 50      55      60
Ser Thr Pro Pro Pro Leu Leu Pro Lys Ala Pro Lys Pro Val Lys Thr
65      70      75      80
Gln Glu Asp Leu Leu Pro Leu Val Pro Glu Gln Val Phe Val Glu Met
      85      90      95
Tyr Glu Asp Met Ala Arg Arg Gln Thr Ile Glu Ala Leu Val Pro Ala
      100      105      110
Trp Asp Ser Asp Ile Ile Phe Lys Cys Leu Cys Tyr Phe His Thr Leu
      115      120      125
Tyr Pro Gly Leu Ile Pro Leu Glu Thr Phe Pro Pro Ala Thr Ile Phe
      130      135      140
Asn Phe Lys Gln Lys Ile Ile Ser Ile Leu Glu Asp Lys Lys Ala Val
145      150      155      160
Leu Arg Gly Glu Pro Ile Lys Gly Pro Leu Pro Ile Trp Cys Ser Lys
      165      170      175
Glu Asn Tyr Arg Arg His Leu Gln Arg Thr Thr Leu Leu Pro Val Phe
      180      185      190
Met Trp Tyr His Pro Thr Pro Lys Thr Xaa Ser Asp Thr Met Gln Thr
      195      200      205
Met Lys Gln Leu Ala Ile Lys Gly Ser Val Gly Ala Ser His Trp Leu
      210      215      220
Leu Val Ile Val Asp Ile Gln Ala Arg Arg Leu Val Tyr Xaa Asp Ser
225      230      235      240
Leu Tyr Asn Tyr Val Met Pro Pro Glu Asn Met Lys Lys Glu Leu Gln
      245      250      255
Ser Phe Ala Gln Gln Leu Asp Gln Val Tyr Pro Ala Tyr Asp Ser Lys
      260      265      270
Lys Phe Ser Val Lys Ile Ala Ala Lys Glu Val Ile Gln Arg Gly Ser
      275      280      285
Gly Ser Ser Cys Gly Ala Trp Cys Cys Gln Phe Leu His Trp Tyr Leu
      290      295      300
Lys Asp Pro Leu Thr Asp Ala Leu Asn Asp Leu Pro Val Asp Ser Val
305      310      315      320
Glu Arg His Glu Asn Leu Ala Ser Phe Val Gln Ala Cys Glu Ala Ala
      325      330      335
Val Gln Asp Leu Pro Glu Leu Ser Trp Pro Glu Ala
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 493:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 113 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(488233..488571)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 493:

```

His Arg His Leu Lys Ile Met Ser Glu Ser Gln Ala Gly Thr Asn Ala
1      5      10      15
Ser Met Val Cys Arg Arg Ala Ile Ser Ser Tyr Ile Ser Thr Asn Thr
      20      25      30
Cys Ser Gly Thr Lys Gly Arg Arg Ser Ser Cys Val Leu Thr Gly Leu

```

Leu 1	Phe	Val	Cys	Leu 5	Ile	Asn	Glu	Gln	Phe 10	Ile	Met	Glu	Pro	Ile 15	His
Asn	Pro	Pro	Pro	Gln	Thr	Cys	Ser	Tyr	Ser	Arg	Pro	Ser	Thr	Thr	Tyr
			20					25					30		
Thr	Ser	Phe	Lys	Asp	Ala	Ser	Cys	Asp	Thr	Lys	Val	Thr	Arg	Ile	Ile
		35					40				45				
Ile	Ala	Leu	Phe	Leu	Ile	Val	Ile	Ser	Cys	Gly	Leu	Ile	Leu	Cys	Ala
	50					55				60					
Tyr	Thr	Phe	Arg	Asp	Leu	Leu	Asp	Ala	Asp	Tyr	Leu	Ala	Gln	Glu	Gly
65					70					75				80	
Pro	Gln	Gln	Ala	Thr	Lys	Leu	Leu	Gln	Gln	Leu	Asp	Asp	Val	Leu	Thr
				85					90					95	
Gly	Pro	Pro	Leu	Pro	Ile	Trp	Asp	Asn	Glu	His	Leu	Phe	Gln	Phe	Ser
			100					105					110		
Cys	Leu	Met	Gln	Asn	Lys	His	Arg	Arg	Val	Leu	Pro	Ile	Asp	Ile	Cys
		115					120				125				
Asn	Pro	Leu	Thr	Lys	Phe	Asn	Phe	Leu	Glu	Cys	Ile	Cys	Asn	Cys	Leu
		130				135					140				
Met	Thr	Lys	Gln	Ser	Val	Asn	Val	Asn	Glu	Thr	Asp	Met	Cys	Glu	Leu
145					150					155					160
Phe	Cys	Pro	Pro	Thr	Cys	Thr	Pro	Glu	Asn	Tyr	Arg	Arg	Leu	Leu	Cys
				165					170					175	
Thr	Ser	Ser	Val	Phe	Pro	Phe	Val	Met	Trp	His	Asp	Pro	Ser	Ala	Asp
			180					185					190		
Thr	Gln	Glu	Ala	Met	Leu	Thr	Lys	Met	Asp	Gln	Thr	Met	Ser	Ser	Gly
		195					200				205				
Arg	Val	Gly	Asn	Ser	His	Trp	Val	Leu	Val	Ile	Val	Asp	Ile	Glu	Tyr
	210					215					220				
Arg	Cys	Val	Thr	Phe	Phe	Asp	Ser	Leu	Cys	Asp	Tyr	Val	Ala	Ser	Pro
225					230					235					240
Gln	Gln	Met	Arg	Glu	Gln	Leu	Glu	Gly	Leu	Ala	Val	Ser	Leu	Gly	Ala
				245					250					255	

```

Ile Tyr Pro Lys Glu Gly Gly Ala Asp Ser Asp Gln Glu Glu Leu Leu
                260                265                270
Ser Pro Phe Gln Val Arg Ile Gly Ser Thr Val Lys Val Gln Ser Pro
                275                280                285
Gly Glu Phe Thr Cys Gly Ala Trp Cys Cys Gln Phe Leu Ala Trp Tyr
                290                295                300
Leu Glu Asn Pro Asp Phe Asp Leu Glu Glu Lys Val Pro Thr Asn Pro
305                310                315                320
Ser Glu Arg Arg Ala Leu Leu Ala Asp Phe Ile Ser Thr Thr Glu Gln
                325                330                335
Ala Met Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 495:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 753 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(490507..492765)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 495:

```

Pro Arg Ile Tyr Gly Thr Val Phe Val Asn Lys Cys Arg Lys Tyr Cys
1          5          10          15
Gly Pro Phe Phe Leu Asn Thr Gln His Val Glu Leu Leu Val Ser Gly
20          25          30
Lys Gln Ser Ser Pro Gln Asp Leu Leu Gly Ile Val Ser Glu Ser Leu
35          40          45
Asn Gln Asp Arg Ile Val Leu Phe Arg Pro Gly Ala Glu Thr Val Phe
50          55          60
Val Glu Leu Arg Gly Lys Ile Gln Gln Ala Glu Ser His His Ser Gly
65          70          75          80
Ile Phe Ser Leu Pro Val Met Lys Gly Ile Ser Pro Gln Asp Tyr Arg
85          90          95
Val Tyr His Gln Asn Gly Leu Leu Ala His Asp Pro Tyr Ala Phe Pro
100         105         110
Leu Leu Trp Gly Glu Ile Asp Ser Phe Leu Phe His Glu Gly Thr His
115         120         125
Gln Arg Ile Tyr Glu Arg Met Gly Ala Ile Pro Cys Glu Ile Asp Gly
130         135         140
Val Pro Gly Val Arg Phe Ile Val Trp Ala Pro His Ala Gln Arg Val
145         150         155         160
Ser Val Ile Gly Asp Phe Asn Gly Trp His Gly Leu Val Asn Pro Leu
165         170         175
His Lys Val Ser Asp Gln Gly Val Trp Glu Leu Phe Val Pro Gly Leu
180         185         190
Thr Ala Gly Ala Cys Tyr Lys Trp Glu Met Val Thr Glu Ser Gly Gln
195         200         205
Val Leu Ile Lys Ser Asp Pro Tyr Gly Lys Phe Phe Gly Pro Pro Pro
210         215         220
Arg Ser Val Ser Val Val Ile Asp Asp Ser Tyr Glu Trp Asn Asp Ser
225         230         235         240
Glu Trp Leu Glu Glu Arg Ile Lys Lys Thr Glu Gly Pro Met Asn Leu

```



				245					250					255			
Tyr	Glu	Val	His	Val	Gly	Ser	Trp	Gln	Trp	Gln	Glu	Gly	Gln	Pro	Leu		
			260					265					270				
Asn	Tyr	Lys	Glu	Leu	Ala	Asp	Gln	Leu	Ala	Leu	Tyr	Cys	Lys	Gln	Met		
		275					280					285					
His	Tyr	Thr	His	Val	Glu	Leu	Leu	Pro	Val	Thr	Glu	His	Pro	Leu	Asn		
	290					295					300						
Glu	Ser	Trp	Gly	Tyr	Gln	Thr	Thr	Gly	Tyr	Tyr	Ala	Pro	Thr	Ser	Arg		
305					310					315					320		
Tyr	Gly	Ser	Phe	Glu	Asp	Leu	Gln	Tyr	Phe	Ile	Asp	Thr	Met	His	Gln		
				325					330					335			
His	Gly	Ile	Gly	Val	Ile	Leu	Asp	Trp	Val	Pro	Gly	His	Phe	Pro	Ile		
			340				345						350				
Asp	Ser	Phe	Ala	Met	Ser	Gly	Phe	Asp	Gly	Thr	Pro	Leu	Tyr	Glu	Tyr		
		355					360					365					
Thr	Arg	Asn	Pro	Ser	Pro	Leu	His	Pro	His	Trp	His	Thr	Tyr	Thr	Phe		
	370					375					380						
Asp	Tyr	Ala	Lys	Pro	Glu	Val	Cys	Asn	Phe	Leu	Leu	Gly	Ser	Ala	Leu		
385					390					395					400		
Phe	Trp	Ile	Asp	Lys	Met	His	Val	Asp	Gly	Ile	Arg	Val	Asp	Ala	Val		
				405					410					415			
Ser	Ser	Met	Leu	Tyr	Leu	Asp	Tyr	Gly	Arg	Tyr	Ala	Gly	Glu	Trp	Val		
			420					425					430				
Pro	Asn	Arg	Tyr	Gly	Gly	Arg	Glu	Asn	Leu	Asp	Ala	Ile	Arg	Phe	Leu		
		435					440					445					
Gln	Gln	Phe	Asn	Thr	Val	Ile	His	Glu	Lys	Tyr	Pro	Gly	Val	Leu	Thr		
	450					455					460						
Phe	Ala	Glu	Glu	Ser	Thr	Thr	Phe	Pro	Lys	Ile	Thr	Val	Ser	Val	Glu		
465					470					475					480		
Glu	Gly	Gly	Leu	Gly	Phe	Asp	Tyr	Lys	Trp	Asn	Met	Gly	Trp	Met	His		
				485					490					495			
Asp	Thr	Leu	His	Tyr	Phe	Glu	Lys	Asp	Phe	Pro	Tyr	Arg	Pro	Tyr	His		
			500					505					510				
Gln	Ser	Asp	Leu	Thr	Phe	Pro	Gln	Trp	Tyr	Ala	Phe	Ser	Glu	Arg	Phe		
		515					520					525					
Leu	Leu	Pro	Phe	Ser	His	Asp	Glu	Val	Val	His	Gly	Lys	Arg	Ser	Leu		
	530					535					540						
Ile	Gly	Lys	Met	Pro	Gly	Asp	Ala	Trp	Arg	Gln	Phe	Ala	Gln	Leu	Arg		
545					550					555					560		
Leu	Leu	Leu	Gly	Tyr	Gln	Ile	Cys	Gln	Pro	Gly	Lys	Lys	Leu	Leu	Phe		
				565					570					575			
Met	Gly	Gly	Glu	Phe	Gly	Gln	Gly	Arg	Glu	Trp	Ser	Pro	Gly	Arg	Glu		
			580				585						590				
Leu	Asp	Trp	Glu	Leu	Leu	Asp	Ile	Ser	Tyr	His	Gln	Gly	Val	His	Leu		
		595					600					605					
Cys	Ser	Gln	Glu	Leu	Asn	Ala	Leu	Tyr	Val	Gln	Ser	Pro	Gln	Leu	Trp		
	610					615					620						
Gln	Ala	Asp	His	Leu	Pro	Ser	Ser	Phe	Arg	Trp	Val	Asp	Phe	Ser	Asp		
625					630					635					640		
Val	Arg	Asn	Gly	Val	Val	Ala	Tyr	Leu	Arg	Phe	Ala	Asp	Ala	Asp	Ala		
				645					650					655			
Lys	Lys	Ala	Leu	Leu	Cys	Val	His	His	Phe	Gly	Val	Gly	Tyr	Phe	Pro		
			660				665						670				
His	Tyr	Leu	Leu	Pro	Ile	Leu	Pro	Leu	Glu	Ser	Cys	Asp	Leu	Leu	Met		
		675					680					685					
Asn	Thr	Asp	Asn	Thr	Arg	Phe	Gly	Gly	Ser	Gly	Lys	Gly	Phe	Arg	Glu		
	690					695					700						
Pro	Glu	Ile	Leu	Thr	Pro	Glu	Ile	Ala	Arg	Gln	Glu	Arg	Glu	Ala	Ala		
705					710					715					720		

Gly Leu Ile Glu Ala Asp Asp Glu Ser Gly Pro Asp Cys Trp Gly Leu  
                               725                              730                              735  
 Asp Ile Glu Leu Pro Pro Ser Ala Thr Leu Ile Phe Ser Val Thr Leu  
                               740                              745                              750  
 Gln

(2) INFORMATIONS POUR LA SEQ ID NO: 496:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 179 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 492357..492893

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 496:

His Pro Cys Val His Arg Tyr Ala Asp Glu Ser Leu His Gly Ile Lys  
 1                              5                              10                              15  
 Lys Asn Arg Phe Pro Pro Lys Val Lys Gly Arg His Lys Asp His Glu  
                               20                              25                              30  
 Pro Ile Asn His Phe Asp Asp Arg Leu Asp Asn Leu Gly Glu Lys Phe  
                               35                              40                              45  
 Leu Ser Leu Gln Glu Glu Lys Lys Ser Leu Asn Gly Ala Thr Leu Pro  
                               50                              55                              60  
 Val Glu Ser Tyr Leu Ala Thr Gln Gln Lys Arg Ser Leu Pro Gln Gly  
 65                              70                              75                              80  
 Gly Lys Glu Leu Ser Asp Leu Asp Ser Asn Phe Gln Lys Gln Phe Pro  
                               85                              90                              95  
 Lys Asp Leu Val Asp Cys Ser Val Tyr Gln Lys Arg Glu Val Pro Arg  
                               100                              105                              110  
 Val Glu Tyr Leu Arg Lys Lys Asp His Asn Ile Phe Cys Ile Tyr Leu  
                               115                              120                              125  
 Gln Lys Arg Ser His Arg Tyr Val Val Pro Ala Phe Ile Ser Thr Phe  
                               130                              135                              140  
 Ser Lys Arg Phe Phe Ile Leu Gln Glu Ile Ile Leu Pro Cys Ser Ser  
 145                              150                              155                              160  
 Thr Arg Lys Arg Asp Glu Tyr Thr Pro Gly Leu Met Ile Ala Ser Ser  
                               165                              170                              175  
 Leu Glu Thr

(2) INFORMATIONS POUR LA SEQ ID NO: 497:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 336 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(492737..493744)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 497:

Tyr	Lys	Gly	Ala	Gly	Ser	Phe	Met	Ile	Lys	Ile	Ala	Gln	Ser	Phe	Lys	1	5	10	15
Pro	Tyr	Ile	Met	Glu	Pro	Gly	Ala	Lys	Ile	Pro	Ile	Pro	Gly	Ser	Thr	20	25	30	
Leu	Tyr	Ala	Gln	Val	Phe	Pro	Ser	Leu	Trp	Arg	Ile	Phe	Ser	Ser	Ser	35	40	45	
His	Glu	Leu	Val	Asn	Glu	Gly	Arg	Val	Pro	Ile	Gln	Gly	Pro	Leu	Gln	50	55	60	
Arg	Phe	Ala	Val	Phe	Gln	Asn	Leu	Asn	Arg	Gly	Gly	Val	Ala	Val	Met	65	70	75	80
Thr	Glu	Gln	Tyr	Lys	Tyr	Tyr	Leu	Ser	Pro	Asn	Gly	Cys	Tyr	Thr	Arg	85	90	95	
Ser	Ile	Ala	Asp	Leu	Pro	Ser	Ala	Ser	Phe	Tyr	Ser	Gly	Glu	Tyr	Val	100	105	110	
Ser	Phe	Gly	Val	His	Lys	His	Ala	Asp	Xaa	Glu	Lys	Ile	Arg	Arg	Arg	115	120	125	
Lys	Asp	Leu	Lys	Glu	Ile	Leu	Pro	Phe	Leu	Phe	Arg	His	Gly	Ala	Leu	130	135	140	
Leu	Gln	Asn	Gln	Pro	Asn	Leu	Ser	Met	Glu	Lys	Thr	Glu	Val	Ala	Leu	145	150	155	160
Leu	Leu	Asp	Thr	Leu	Asp	Ala	Ala	Ile	Ala	Glu	Pro	Asn	Lys	Glu	Arg	165	170	175	
Val	Phe	Ser	Leu	Leu	Glu	Arg	Phe	Val	Tyr	Ala	Gly	Leu	Ser	Lys	Thr	180	185	190	
Leu	Leu	Pro	Arg	Leu	Tyr	Asp	Glu	Glu	Tyr	Gln	Gly	Ile	Val	Ser	Glu	195	200	205	
Asp	Pro	Arg	Pro	Gly	Asn	Glu	Ala	Val	Pro	Phe	Ser	Leu	Leu	Arg	Ala	210	215	220	
Ala	Ala	Leu	Ser	Met	Arg	Arg	Ile	Phe	Ile	Gln	Glu	Ser	Asp	Gly	Val	225	230	235	240
Val	Thr	Leu	Leu	Pro	Ala	Leu	Pro	Pro	Glu	Phe	Pro	Cys	Gly	Arg	Trp	245	250	255	
Ile	Gly	Leu	Tyr	Phe	Glu	Asn	Ile	Gly	Glu	Ile	Ser	Phe	Glu	Trp	Ser	260	265	270	
Lys	Lys	Thr	Ile	Arg	Arg	Val	Ile	Leu	Lys	Ala	His	Val	Ser	Arg	Glu	275	280	285	
Leu	Ala	Ile	Ile	Ser	Pro	Gly	Val	Tyr	Ser	Ser	Arg	Phe	Arg	Val	Glu	290	295	300	
Glu	Gln	Gly	Arg	Ile	Ile	Ser	Cys	Lys	Ile	Lys	Asn	Leu	Leu	Glu	Lys	305	310	315	320
Val	Glu	Ile	Lys	Ala	Gly	Thr	Thr	Tyr	Leu	Trp	Asp	Arg	Phe	Cys	Lys	325	330	335	

## (2) INFORMATIONS POUR LA SEQ ID NO: 498:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 235 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: 493971..494675

Met 1	Thr	Pro	Ser	Ala 5	Leu	Phe	His	Lys	Arg 10	Leu	Ile	Glu	Gln	Phe 15	Thr
Ile	Phe	Leu	Ser 20	Val	Asp	Arg	Gly	Ile 25	Ser	Pro	Leu	Ser 30	Val	Gln	Ala
Tyr	Cys	Gln	Asp 35	Val	Leu	Leu	Phe 40	Leu	Gln	Arg	Ala	Ser 45	Ile	Glu	Ala
Thr	Asp 50	Arg	Ile	Asn	Gln	Glu 55	Ser	Val	Phe	Leu	Phe 60	Val	Glu	Lys	Cys
His 65	Lys	Ala	Lys	Glu	Ser 70	Glu	Thr	Thr	Leu	Ala 75	Arg	Arg	Leu	Ile 80	Ala
Leu	Lys	Val	Phe 85	Phe	His	Phe	Leu	Lys 90	Asp	Val	Lys	Met	Leu	Asp 95	Gln
Gln	Pro	Phe	Ile 100	Glu	His	Pro	Lys	Ile 105	Trp	Lys	Arg	Leu	Pro 110	Ser	Ile
Leu	Ser	Thr	Glu 115	Glu	Val	Asn	Ser	Leu 120	Leu	Asp	Gln	Pro 125	Leu	Asn	Ile
Pro	Asn 130	Leu	Asp	Thr	His	Ile 135	Ala	Ser	Arg	Asp	Ala 140	Ala	Ile	Leu	Tyr
Thr 145	Phe	Tyr	Ala	Thr	Gly 150	Ile	Arg	Val	Ser	Glu 155	Leu	Cys	Asp	Leu 160	Cys
Ile	Gly	Asp	Ile 165	Ser	Asp	Asp	Phe	Ile 170	Arg	Val	Thr	Gly	Lys 175	Gly	Arg
Lys	Thr	Arg	Leu 180	Val	Pro	Ile	Ser	Ile 185	Lys	Ala	Lys	Gln	Ala 190	Ile	Asp
Ala	Tyr	Leu	Ser 195	Ser	Phe	Arg	Asp 200	Glu	Leu	Gln	Lys	Lys 205	Ile	Pro	Leu
Lys	Asn 210	Met	Tyr	Phe	Cys	Leu 215	Ser	Glu	Gly	Lys	Asn 220	Ser	Ile	Val	Pro
Val 225	Tyr	Gly	Asn	Ala	Leu 230	Leu	Phe	Met	Gln	Asn 235					

Thr	Thr	Lys	Lys	Asn	Pro	Ser	Glu	Glu	His	Val	Phe	Leu	Ser	Ile	Arg
1				5					10					15	
Gly	Lys	Lys	Leu	Asp	Arg	Ser	Cys	Val	Trp	Lys	Arg	Ile	Thr	Phe	Tyr
			20					25					30		
Ala	Lys	Leu	Val	Thr	Thr	Lys	Arg	Ile	Ser	Pro	His	Ser	Leu	Arg	His
			35				40					45			
Pro	Phe	Ala	Thr	His	Leu	Leu	Asn	Asn	His	Ala	Asp	Leu	Arg	Ile	Ile
	50					55				60					
Gln	Glu	Met	Leu	Gly	His	Ser	Arg	Ile	Ser	Ser	Thr	Glu	Ile	Tyr	Thr
65					70					75					80
His	Val	Ala	Ser	Glu	Ser	Leu	Ile	Glu	Lys	Phe	His	Thr	Tyr	His	Pro

95

- (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 500:

Ala

- (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 501:

```

Met Lys Gln Leu Ser Ile Leu Leu Gly Met Val Ser Leu Ser Ser Ala
1      5      10      15
Val Phe Gly Ala Asp Ala Val Tyr Ser Gly Ser Leu Val Gln Pro Ser
      20      25      30
Glu Ser Val Leu Val Ala Gly Val Glu Phe Glu Glu Gln Glu Gly Glu
      35      40      45
Arg Ile Pro Tyr Ser Phe Tyr Tyr Pro Tyr Gln Tyr Asp Tyr Tyr Tyr
      50      55      60
Pro Asn Thr Gly Val Asp Glu Asp Thr Pro Glu Ser Phe Gln Glu Lys
65      70      75      80
His Glu Cys Pro Cys Lys Lys Pro Val Pro Glu Lys Lys Lys Lys Lys
      85      90      95
Pro Arg Arg Arg Ser
      100

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(2) INFORMATIONS POUR LA SEQ ID NO: 502:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 316 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 495687..496634

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 502:

```

Val Pro Ser Phe Leu Lys Gly Leu Asp Thr Leu Thr Ser Val Thr Met
1      5      10      15
Asp Thr Pro Thr Pro Leu Ser Ser Val Pro Thr Asn Ala Ser Leu Lys
      20      25      30
Gly Glu Pro Gly Ser Ser Ser Gln Phe Ser Ser Ala Glu Lys Gly Val
      35      40      45
Leu Lys Thr Ser Ile Gly Asp Val Val Leu Ser Gln Ser Ile Glu Asp
      50      55      60
Gly Gly Asn Glu Thr Gln Ile Ser Leu Val Gly Val Val Asn Ile Asn
65      70      75      80
Met Ala Gln Glu Glu Leu Pro Ala Leu Val Ser Pro Arg Thr Phe Ile
      85      90      95
Phe Leu Pro Pro Glu Thr Val Glu Leu Glu Ile Gln Ile Ala Glu Met
      100      105      110
Phe Gln Ala Leu Glu Glu Thr Pro Ser Ser Asp Ser Arg Ser Leu Gln
      115      120      125
Gln Lys Glu Thr Ser Ala Gln Thr Pro Pro Ala Pro Ser Gly Lys Val
      130      135      140
Ser Ile Phe Ser Leu Gln Ala Gln Gly Ser Ser Gln Thr Arg Ser Leu
145      150      155      160
Pro Ser Ser Gln Glu Ser Leu Ser Pro Gln Gln Pro Ala Arg Ala Ile
      165      170      175
Gln Gly Leu Asn Thr Pro Phe Ser Pro Ala Ala Arg Cys Thr Ile Arg
      180      185      190
Ala Val Pro Leu Ser Ile Val Pro His Arg Arg Ala Asn Pro Lys Pro
      195      200      205
Ser Gln Ser Val Leu Ile Ile Ala Leu Val Leu Thr Arg Gln Ala Ile
      210      215      220
Gln Gln Glu Arg Leu Asn Phe Leu Pro Arg Asn Gly Asn Phe Leu Leu

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225					230					235					240
Lys	Gln	Leu	Lys	Pro	Ala	Gln	Gln	Glu	Glu	Lys	Lys	Glu	Thr	Val	Asn
				245					250					255	
Lys	Lys	Asp	Ile	Leu	Ile	Lys	Asn	Arg	Ile	Val	Ile	Ile	Leu	Thr	Lys
			260					265					270		
Arg	Lys	Ile	Ser	Arg	Met	Ile	Cys	Lys	Cys	Leu	Leu	Leu	Lys	Asp	Pro
		275					280					285			
Leu	Ile	Arg	Lys	Met	Lys	Ile	Leu	Arg	Lys	Tyr	Phe	Leu	Ser	Leu	Thr
	290					295				300					
Leu	Leu	Ile	Met	Arg	Pro	Leu	Ile	Leu	Arg	Pro	Ile				
305					310				315						

(2) INFORMATIONS POUR LA SEQ ID NO: 503:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 294 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 496295..497176

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 503:

Ser	Lys	Ser	Lys	Thr	Phe	Ser	Lys	Cys	Ser	His	His	Ser	Ser	Arg	Thr
1				5					10					15	
Tyr	Gln	Thr	Gly	His	Ser	Thr	Gly	Thr	Ala	Gln	Leu	Ser	Ser	Gln	Glu
			20					25					30		
Trp	Glu	Phe	Ser	Ser	Gln	Thr	Val	Lys	Thr	Cys	Ser	Thr	Gly	Arg	Glu
		35					40					45			
Lys	Arg	Asp	Gly	Gln	Gln	Glu	Arg	His	Ser	Asp	Gln	Glu	Gln	Asn	Ser
	50					55				60					
Asp	His	Ser	Tyr	Gln	Glu	Glu	Asp	Leu	Ser	Asp	Asp	Met	Gln	Val	Ser
65				70					75					80	
Ser	Ser	Lys	Arg	Ser	Ser	His	Pro	Glu	Asp	Glu	Asn	Thr	Glu	Glu	Val
			85					90					95		
Phe	Ser	Val	Ser	His	Phe	Ala	Tyr	His	Ala	Ala	Pro	His	Pro	Ala	Ser
		100						105					110		
Asn	Leu	Asp	Gln	Glu	Ser	Asn	Gln	Ser	Thr	Phe	Gln	Lys	Arg	Pro	Pro
	115						120					125			
Ser	Pro	Met	Ser	Leu	Phe	Ser	Ser	Gln	Asn	Ala	Thr	Glu	Glu	Ala	Pro
	130					135				140					
Lys	Glu	Ala	Arg	Val	Glu	Asn	Val	Phe	Leu	Arg	Phe	Met	Arg	Leu	Met
145				150					155					160	
Ala	Arg	Ile	Leu	Gly	Gln	Ala	Glu	Ala	Glu	Ala	His	Glu	Leu	Tyr	Leu
			165				170						175		
Arg	Val	Lys	Glu	Arg	Thr	Asp	Ser	Val	Asp	Ala	Leu	Thr	Leu	Leu	Leu
		180					185						190		
Ser	Lys	Ile	Asn	Asn	Glu	Lys	Gly	Ala	Ile	Asp	Trp	Asn	Gln	Asp	Glu
	195						200					205			
Glu	Met	Arg	Ala	Leu	Val	Asp	Gln	Ala	Lys	Lys	Leu	Gly	Val	Pro	Ile
	210					215					220				
Gly	Asp	Ser	Tyr	Asp	Trp	Ser	Glu	Glu	Gly	Lys	Lys	Leu	Leu	Lys	Glu
225				230					235					240	
Asn	Ile	Gln	Met	Arg	Lys	Glu	Asn	Met	Glu	Lys	Ile	Thr	Gln	Leu	Glu
			245						250					255	

Arg Thr Asp Met Gln Arg His Leu Gln Glu Val Ser Gln Cys His Gln  
                   260                  265                  270  
 Ala Arg Ser Asn Val Leu Lys Leu Leu Lys Glu Leu Met Asp Thr Phe  
                   275                  280                  285  
 Ile Tyr Asn Met Arg Pro  
                   290

(2) INFORMATIONS POUR LA SEQ ID NO: 504:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 271 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 497703..498515

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 504:

Ile Thr Lys Asp Ser Tyr Tyr Tyr Val Ile Leu Val Cys Ser Arg Thr  
 1                  5                  10                  15  
 Asp Val Ala Leu Ser Gln Thr Leu Asp Leu Pro Asp Ala Ser Leu Ala  
                   20                  25                  30  
 Val Gln Thr Glu Lys Phe Pro Tyr Ser Cys Ser Ile Ser Lys Glu Ser  
                   35                  40                  45  
 Ala Pro Ser Cys Ile Arg Lys Ile Phe Ala His Leu Ala Ser Gln Lys  
                   50                  55                  60  
 Glu Ser Ala Pro Leu Ser Phe Ser Arg Leu Gln Pro Thr Thr Pro Lys  
 65                  70                  75                  80  
 Glu Arg Ile Leu Phe Phe Gly Ser Ser Pro Ser Ser Gln Leu Ser Ser  
                   85                  90                  95  
 Thr Val Arg Thr Thr Thr Ser Ser Pro Trp Asn Leu Phe Ser Asn Ser  
                   100                  105                  110  
 Gln Ala Arg Asn Ser Thr Arg Lys Leu Ser Glu Lys Leu His Leu Ser  
                   115                  120                  125  
 Ser Glu Leu Ser Ala Arg Asp Ser Thr Lys Pro Ser Ser Ser Glu Pro  
                   130                  135                  140  
 Val Lys Pro Ser Glu Asn Leu Leu His Thr Pro Glu His His Lys Glu  
 145                  150                  155                  160  
 Ser Phe Ser Ser Leu Lys Lys Asp Asn Leu Ser Pro Ile Met Glu Glu  
                   165                  170                  175  
 Ile Asp Ser Phe Ser Ala Glu Thr Glu Ser Leu Glu Glu Arg Leu Val  
                   180                  185                  190  
 Thr Gln Lys Lys Glu Glu Thr Val Ala Gln Glu Gln Lys His Pro Leu  
                   195                  200                  205  
 Leu Arg Thr Ser Thr Pro Pro Ser Lys Ala Ser Gly Glu Ser Gln Asp  
                   210                  215                  220  
 Ser Ser Glu His Ser Ser Lys Glu Asp Pro Tyr Ser Gln Gln Pro Ser  
 225                  230                  235                  240  
 His Lys Ile Gln Arg Arg Gly Thr Ser Gln Lys Ser Cys Ser Tyr His  
                   245                  250                  255  
 His Thr Thr Tyr Cys Arg Asp Leu Leu Phe Lys Leu Pro Ser His  
                   260                  265                  270

(2) INFORMATIONS POUR LA SEQ ID NO: 505:



## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 320 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 498280..499239

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 505:

His	Lys	Lys	Lys	Lys	Lys	Pro	Leu	His	Lys	Asn	Lys	Asn	Ile	Leu	Tyr	1	5	10	15
Leu	Glu	Pro	Pro	Pro	Leu	Leu	Pro	Lys	His	Gln	Glu	Lys	Val	Lys	Thr	20	25	30	
Arg	Pro	Ser	Thr	Leu	Arg	Lys	Lys	Thr	Leu	Ile	Leu	Ser	Asn	Leu	Leu	35	40	45	
Thr	Lys	Tyr	Lys	Glu	Glu	Glu	Arg	Ala	Lys	Arg	Val	Val	Pro	Ile	Ile	50	55	60	
Thr	Pro	Pro	Thr	Val	Gly	Ile	Phe	Ser	Leu	Ser	Tyr	Leu	Leu	Thr	Lys	65	70	75	80
Gln	Gly	Ile	Leu	Ala	Asp	Phe	Ser	Ala	Tyr	Ser	Ala	Tyr	Lys	Asp	Asn	85	90	95	
Leu	Glu	Thr	Thr	Gln	Gln	Glu	Leu	Thr	Met	Leu	His	Gln	Glu	Arg	Ile	100	105	110	
Glu	Gln	Val	Gln	Lys	Ile	Val	Asp	Lys	Ser	Lys	Thr	Met	Arg	Phe	Trp	115	120	125	
Asp	Ser	Leu	Ala	Ser	Ile	Val	Ala	Thr	Ile	Ile	Pro	Trp	Ile	Glu	Met	130	135	140	
Gly	Val	Ala	Val	Thr	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Ile	Leu	Ser	Trp	145	150	155	160
Cys	Ser	Leu	Phe	Ala	Ala	Leu	Ile	Met	Ile	Val	Ile	Ser	Leu	Leu	Glu	165	170	175	
Ala	Phe	Asp	Gly	Trp	Arg	Ala	Ile	Ala	Lys	His	Leu	Pro	Gly	Asn	Asp	180	185	190	
Leu	Glu	Lys	Lys	Met	Arg	Tyr	Leu	Gly	Tyr	Val	Lys	Leu	Ala	Leu	Thr	195	200	205	
Val	Phe	Ser	Cys	Leu	Leu	Ser	Leu	Ser	Ala	Leu	Tyr	Val	Ala	Lys	Leu	210	215	220	
Gly	Met	Ser	Pro	Leu	Leu	Gly	Gly	Val	Val	Lys	Ser	Ile	Ala	Pro	Ala	225	230	235	240
Leu	Ser	Gly	Met	Leu	Gly	Leu	Thr	Gln	Gly	Val	Ala	Leu	Tyr	Leu	Gln	245	250	255	
Ser	Ser	Ser	Gln	Lys	Ile	Arg	Ala	Arg	Cys	Thr	Gln	Ile	Asp	Ala	Arg	260	265	270	
Ile	Glu	Leu	Ile	Asn	Trp	Glu	Arg	Asp	Glu	Tyr	Phe	Leu	Arg	Ala	Glu	275	280	285	
Gln	Leu	Leu	Asp	Ser	Met	Gln	Thr	Ser	Phe	Glu	Gln	Leu	Thr	Glu	Thr	290	295	300	
Leu	Gln	Leu	Gln	Arg	Glu	Ile	Asp	Gln	Thr	Phe	Thr	Asp	Ala	Leu	Arg	305	310	315	320

(2) INFORMATIONS POUR LA SEQ ID NO: 506:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 506 acides aminés

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 506:

Pro 1	Asn	Val	Tyr	Arg 5	Arg	Leu	Thr	Ile	Ala 10	Ile	Leu	Pro	Met	Thr 15	Ile
Thr	Val	Pro	Gln 20	Glu	Thr	Leu	Pro	Ser 25	Leu	Gln	Thr	Ile 30	Ala	Thr	Gly
Glu	Gln	Thr 35	Glu	Thr	Ser	Cys	Glu 40	Glu	Ala	Ser	Ala	Leu 45	Ser	Asn	Glu
Ile	Gln 50	Leu	Leu	Glu	Pro	Gly 55	Gln	Ala	Ala	Ile	Leu 60	Arg	Ser	Leu	Ser
Asp 65	Leu	Cys	Leu	Ser	Val 70	Ile	Glu	Gln	Thr	Glu 75	Lys	Thr	Leu	Pro	His 80
Ser	Lys	His	Ser	Pro 85	Ser	Phe	Arg	Glu	Ser 90	Cys	Pro	Leu	Lys	Tyr 95	Leu
Ser	Gln	Gln	Thr 100	Ser	Ala	Ser	Ser	Arg 105	Thr	Gln	Glu	Ser	Ala	Thr	Ala
Glu	Gln	Gln 115	Ser	Leu	Thr	Pro	Thr 120	Pro	Thr	Pro	Gln	Lys 125	Thr	Pro	Thr
Gln	Thr 130	Leu	His	Asn	Lys	Pro 135	Ser	Thr	Pro	Ile	Ser	His 140	Lys	Ser	Ser
Val 145	Gln	Gly	Arg	Ile	Gln 150	Thr	Ser	Pro	Gln	His	Ser	Thr 155	Pro	Leu	Arg 160
Ser	Ile	Pro	Val 165	Ile	Ile	Ser	Leu	Pro	Asn 170	Thr	Gln	Gln	Ala	Leu	Thr 175
Asp	Arg	Glu	Pro 180	Ile	Gln	Asn	Ser	Asn 185	Cys	Ser	Pro	Thr	Leu	Ser	Val 190
Thr	Ile 195	Phe	Asn	Lys	Glu	Ser	Ser 200	Ser	Ser	Ser	Lys	Lys 205	Asp	Ser	Ala
Ala	Ser 210	Arg	Glu	Gln	Ser	Ser 215	Ser	His	Ser	Ser	Ser	Leu 220	Gln	Lys	Asn
Leu 225	Ser	Ser	Pro	Arg	Ala 230	Ala	Leu	Leu	Ser	Pro	Met	Ala	Leu	Phe	Glu 240
Thr	Thr	Ala	Gln 245	Lys	Glu	Thr	Leu	Ala	Arg 250	Glu	Gly	Leu	Leu	His	Glu 255
Arg	Glu	Asp	Leu 260	Ser	Gln	Glu	Gly	Asp 265	Arg	Asp	His	His	Gln	Ser	Asp 270
Gln	Gln 275	Gln	Glu	Glu	Lys	Glu	Asp 280	Leu	Ala	Ile	Ser	Ala 285	Ser	Phe	Leu
Ser	His 290	Ser	Lys	Lys	Arg	Arg 295	Glu	His	His	Phe	Asp	Pro	Glu	Tyr	Leu
Pro 305	Glu	Glu	Ile	Arg	Glu 310	Phe	Ala	Leu	Ser	Glu	Ala	Gln	Leu	Ser	Gln 320
Leu	Leu	His	Ile 325	Arg	Leu	Asn	His	Leu	Asp 330	Ile	Leu	Arg	Ile	Cys	Ala 335
Glu	Ile	Met	Lys 340	Leu	Met	Leu	Asn	Ser 345	Arg	Glu	Gln	Asp	Leu	Leu	Glu 350
Arg	Arg	Ser 355	Thr	Arg	Thr	His	Phe	Met 360	Gln	Glu	Ala	Lys	Lys	Ile	Ala
Asp	Ser 370	Phe	Ala	Lys	Gln	Ala 375	Arg	Ile	Thr	Lys	Trp	Leu	Gly	Ile	Ala
Thr	Ala	Thr	Leu	Gly	Ile	Phe	Gly	Gly	Ile	Ser	Pro	Ile	Ile	Gly	Glu

385					390					395					400
Val	Gly	Gly	Glu	Gly	Leu	Leu	Asn	Val	Ile	Arg	Lys	Ala	Thr	Gly	Gly
				405					410					415	
Trp	Gln	Gln	Ala	Ser	Ser	Lys	Thr	Phe	Phe	Glu	Gly	Trp	Gly	Lys	Cys
			420					425					430		
Val	Leu	Ser	Leu	Ser	Glu	Leu	Ala	Lys	Val	Ser	Ser	Thr	Val	Tyr	Asp
		435					440					445			
Leu	Arg	Pro	Lys	Pro	Val	Arg	Thr	Ile	Ala	Glu	Ser	Tyr	Lys	Glu	Leu
	450					455					460				
Phe	Arg	Leu	Glu	His	Asp	Glu	Met	Leu	Arg	Ser	Ile	Glu	Glu	Leu	Lys
465					470					475					480
Asp	His	Gly	Arg	Asn	Met	Asp	Ser	Phe	Leu	Leu	Gln	Ile	Leu	Gln	Thr
				485				490						495	
Gln	His	Asp	Ala	Val	Arg	Ser	Leu	Tyr	Gln						
			500					505							

(2) INFORMATIONS POUR LA SEQ ID NO: 507:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 307 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(500790..501710)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 507:

Met	Arg	Lys	Ile	Ile	Leu	Cys	Ser	Pro	Arg	Gly	Phe	Cys	Ala	Gly	Val
1				5					10					15	
Ile	Arg	Ala	Ile	Gln	Thr	Val	Glu	Val	Ala	Leu	Glu	Lys	Trp	Gly	Arg
			20					25					30		
Pro	Ile	Tyr	Val	Lys	His	Glu	Ile	Val	His	Asn	Arg	His	Val	Val	Asp
		35					40					45			
Lys	Leu	Arg	Glu	Lys	Gly	Ala	Ile	Phe	Ile	Glu	Asp	Leu	Gln	Glu	Val
	50					55				60					
Pro	Arg	Asn	Ser	Arg	Val	Ile	Phe	Ser	Ala	His	Gly	Val	Pro	Pro	Ser
65					70				75						80
Leu	Arg	Glu	Glu	Ala	Thr	Glu	Arg	Gly	Leu	Ile	Ala	Ile	Asp	Ala	Thr
				85				90					95		
Cys	Gly	Leu	Val	Thr	Lys	Val	His	Ser	Ala	Val	Lys	Met	Tyr	Ala	Lys
			100					105					110		
Lys	Gly	Tyr	His	Ile	Ile	Leu	Ile	Gly	Lys	Arg	Lys	His	Val	Glu	Ile
		115					120					125			
Ile	Gly	Ile	Arg	Gly	Glu	Ala	Pro	Asp	Gln	Ile	Thr	Val	Val	Glu	Asn
	130					135					140				
Ile	Ala	Glu	Val	Glu	Ala	Leu	Pro	Phe	Ser	Ala	Gln	Asp	Pro	Leu	Phe
145					150				155						160
Tyr	Val	Thr	Gln	Thr	Thr	Leu	Ser	Met	Asp	Asp	Ala	Ala	Asp	Ile	Val
				165				170						175	
Ala	Ala	Leu	Lys	Ala	Arg	Tyr	Pro	Arg	Ile	Phe	Thr	Leu	Pro	Ser	Ser
			180					185					190		
Ser	Ile	Cys	Tyr	Ala	Thr	Gln	Asn	Arg	Gln	Gly	Ala	Leu	Arg	Asn	Ile
		195					200					205			
Leu	Pro	Gln	Val	Asp	Phe	Val	Tyr	Val	Ile	Gly	Asp	Arg	Gln	Ser	Ser
	210					215					220				

Asn Ser Asn Arg Leu Arg Glu Val Ala Glu Arg Arg Gly Val Thr Ala  
 225 230 235 240  
 Arg Leu Val Asn His Pro Asp Glu Val Thr Glu Glu Ile Leu Gln Tyr  
 245 250 255  
 Ser Gly Asn Ile Gly Ile Thr Ala Gly Ala Ser Thr Pro Glu Asp Val  
 260 265 270  
 Val Gln Ala Cys Leu Met Lys Leu Gln Glu Leu Ile Pro Asp Leu Ser  
 275 280 285  
 Ile Glu Met Asp Leu Phe Val Glu Glu Asp Thr Val Phe Gln Leu Pro  
 290 295 300  
 Lys Glu Leu  
 305

(2) INFORMATIONS POUR LA SEQ ID NO: 508:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(501808..502863)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 508:

Phe Ala Ile Leu Leu Ser Asn Gly Ser Ala Phe Leu Gly Arg Ala Ser  
 1 5 10 15  
 Gln Ser Leu Cys Asn Glu Trp Phe Glu Lys Arg Val Gln Tyr Trp Glu  
 20 25 30  
 Tyr Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu  
 35 40 45  
 Gly Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys  
 50 55 60  
 Ser His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp  
 65 70 75 80  
 Met Glu Asp Phe Asp Pro Ser Gly Pro Pro Trp Glu Glu Phe Ala  
 85 90 95  
 Lys Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp  
 100 105 110  
 Gln Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu  
 115 120 125  
 Ser Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile  
 130 135 140  
 Leu Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu  
 145 150 155 160  
 Glu Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn  
 165 170 175  
 Met Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser  
 180 185 190  
 Phe Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu  
 195 200 205  
 Ser Thr Pro Ile Pro Leu Phe Gly Phe Glu Lys Ile His Pro His Pro  
 210 215 220  
 Arg Val Gln Tyr Ser Lys Pro Ile Cys Val Leu Ile Asn Glu Gln Asp  
 225 230 235 240  
 Phe Ser Cys Ala Asp Phe Phe Pro Val Val Leu Lys Asp Asn Asp Arg

				245					250					255			
Ala	Leu	Ile	Val	Gly	Thr	Arg	Thr	Ala	Gly	Ala	Gly	Gly	Phe	Val	Phe		
			260					265					270				
Asn	Val	Gln	Phe	Pro	Asn	Arg	Thr	Gly	Ile	Lys	Thr	Cys	Ser	Leu	Thr		
		275					280					285					
Gly	Ser	Leu	Ala	Val	Arg	Glu	His	Gly	Ala	Phe	Ile	Glu	Asn	Ile	Gly		
	290					295					300						
Val	Glu	Pro	His	Ile	Asp	Leu	Pro	Phe	Thr	Ala	Asn	Asp	Ile	Arg	Tyr		
305					310					315					320		
Lys	Gly	Tyr	Ser	Glu	Tyr	Leu	Asp	Lys	Val	Lys	Lys	Leu	Val	Cys	Gln		
			325						330					335			
Leu	Ile	Asn	Asn	Asp	Gly	Thr	Ile	Ile	Leu	Ala	Glu	Asp	Gly	Ser	Phe		
		340						345					350				

(2) INFORMATIONS POUR LA SEQ ID NO: 509:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 328 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(502692..503675)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 509:

Lys	Gly	Ser	Leu	Pro	Ile	Leu	Gly	Pro	Phe	Leu	Asn	Gly	Lys	Met	Gly		
1			5					10					15				
Phe	Trp	Arg	Thr	Ser	Ile	Met	Lys	Met	Asn	Arg	Ile	Trp	Leu	Leu	Leu		
		20					25					30					
Leu	Thr	Phe	Ser	Ser	Ala	Ile	His	Ser	Pro	Val	Arg	Gly	Glu	Ser	Leu		
	35					40					45						
Val	Cys	Lys	Asn	Ala	Leu	Gln	Asp	Leu	Ser	Phe	Leu	Glu	His	Leu	Leu		
50						55				60							
Gln	Val	Lys	Tyr	Ala	Pro	Lys	Thr	Trp	Lys	Glu	Gln	Tyr	Leu	Gly	Trp		
65					70				75					80			
Asp	Leu	Val	Gln	Ser	Val	Ser	Ala	Gln	Gln	Lys	Leu	Arg	Thr	Gln			
			85				90					95					
Glu	Asn	Pro	Ser	Thr	Ser	Phe	Cys	Gln	Gln	Val	Leu	Ala	Asp	Phe	Ile		
		100					105					110					
Gly	Gly	Leu	Asn	Asp	Phe	His	Ala	Gly	Val	Thr	Phe	Phe	Ala	Ile	Glu		
		115					120					125					
Ser	Ala	Tyr	Leu	Pro	Tyr	Thr	Val	Gln	Lys	Ser	Ser	Asp	Gly	Arg	Phe		
	130					135					140						
Tyr	Phe	Val	Asp	Ile	Met	Thr	Phe	Ser	Ser	Glu	Ile	Arg	Val	Gly	Asp		
145					150				155					160			
Glu	Leu	Leu	Glu	Val	Asp	Gly	Ala	Pro	Val	Gln	Asp	Val	Leu	Ala	Thr		
			165				170							175			
Leu	Tyr	Gly	Ser	Asn	His	Lys	Gly	Thr	Ala	Ala	Glu	Glu	Ser	Ala	Ala		
		180					185					190					
Leu	Arg	Thr	Leu	Phe	Ser	Arg	Met	Ala	Ser	Leu	Gly	His	Lys	Val	Pro		
		195					200					205					
Ser	Gly	Arg	Thr	Thr	Leu	Lys	Ile	Arg	Arg	Pro	Phe	Gly	Thr	Thr	Arg		
	210					215					220						
Glu	Val	Arg	Val	Lys	Trp	Arg	Tyr	Val	Pro	Glu	Gly	Val	Gly	Asp	Leu		
225					230				235						240		

Ala	Thr	Ile	Ala	Pro	Ser	Ile	Arg	Ala	Pro	Gln	Leu	Gln	Lys	Ser	Met
				245					250					255	
Arg	Ser	Phe	Phe	Pro	Lys	Lys	Asp	Asp	Ala	Phe	His	Arg	Ser	Ser	Ser
			260					265					270		
Leu	Phe	Tyr	Ser	Pro	Met	Val	Pro	His	Phe	Trp	Ala	Glu	Leu	Arg	Asn
		275					280					285			
His	Tyr	Ala	Thr	Ser	Gly	Leu	Lys	Ser	Gly	Tyr	Asn	Ile	Gly	Ser	Thr
	290					295					300				
Met	Gly	Phe	Ser	Leu	Ser	Leu	Gly	Leu	Leu	Tyr	Gly	Ser	Arg	Arg	Val
305					310					315					320
Phe	Ser	Ala	Leu	Ile	Phe	Leu	Arg								
				325											

(2) INFORMATIONS POUR LA SEQ ID NO: 510:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 421 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(503722..504984)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 510:

Met	Leu	Lys	Phe	Gln	Leu	Cys	Leu	Leu	Phe	Leu	Phe	Gly	Tyr	Leu	Ala
1				5					10					15	
Ile	Val	Phe	Glu	His	Ile	Val	Arg	Val	Asn	Lys	Ser	Ala	Val	Ser	Leu
			20					25					30		
Ala	Met	Gly	Gly	Leu	Met	Trp	Leu	Val	Cys	Phe	Ser	His	Ile	Pro	His
		35					40					45			
Ile	Asp	His	Val	Met	Met	Val	Glu	Glu	Ile	Ala	Asp	Met	Ala	Gln	Val
	50					55					60				
Ile	Phe	Phe	Leu	Phe	Ala	Ala	Met	Ala	Ile	Val	Glu	Leu	Ile	Asp	Ala
65					70					75					80
His	Arg	Gly	Phe	Ser	Ile	Val	Val	Arg	Cys	Cys	Asn	Val	Glu	Ser	Arg
				85					90					95	
Ser	Val	Leu	Leu	Trp	Val	Leu	Leu	Ile	Leu	Ser	Phe	Phe	Leu	Ser	Ala
			100					105					110		
Ala	Leu	Asp	Asn	Leu	Thr	Ser	Ile	Ile	Ile	Ile	Ile	Ser	Ile	Leu	Lys
		115					120					125			
Arg	Leu	Val	Lys	Ala	Arg	Glu	Asp	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Cys
	130					135					140				
Val	Ile	Gly	Val	Asn	Ala	Gly	Gly	Ala	Trp	Thr	Pro	Leu	Gly	Asp	Val
145					150					155					160
Thr	Thr	Thr	Met	Leu	Trp	Ile	Asn	Asp	Lys	Ile	Ser	Thr	Ser	Gly	Ile
				165					170					175	
Ile	Thr	Thr	Leu	Phe	Leu	Pro	Ser	Val	Val	Cys	Val	Val	Ile	Ala	Gly
			180					185					190		
Ile	Cys	Gly	Gln	Leu	Leu	Leu	Lys	Lys	Arg	Arg	Cys	Ser	Gly	Leu	Ser
		195					200					205			
Glu	Asp	Leu	Asp	Arg	Glu	Pro	Ala	Leu	Pro	Lys	Ser	Asn	Leu	Ile	Ala
	210					215					220				
Cys	Val	Gly	Phe	Gly	Ser	Leu	Leu	Met	Val	Pro	Met	Trp	Lys	Ala	Val
225					230					235					240
Leu	Gly	Val	Pro	Pro	Phe	Met	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Val

				245					250					255					
Trp	Leu	Val	Ser	Asp	Trp	Ile	His	Ser	Pro	His	Gly	Glu	Gly	Arg	Asn				
			260					265					270						
His	Leu	Arg	Met	Pro	His	Ile	Leu	Thr	Arg	Ile	Asp	Ile	Ser	Ser	Val				
		275					280					285							
Thr	Phe	Phe	Ile	Gly	Ile	Leu	Leu	Ala	Val	Asn	Ala	Leu	Thr	Tyr	Ser				
	290					295					300								
His	Val	Leu	Arg	Asp	Leu	Ser	Val	Ser	Met	Asp	Ala	Leu	Phe	Ser	Arg				
305					310					315					320				
Asn	Thr	Leu	Ala	Val	Leu	Leu	Gly	Leu	Val	Ser	Ser	Val	Leu	Asp	Asn				
			325						330					335					
Val	Pro	Leu	Val	Ala	Ala	Thr	Ile	Gly	Met	Tyr	Asp	Leu	Pro	Met	Asn				
		340						345					350						
Asp	Pro	Leu	Trp	Lys	Leu	Ile	Ala	Tyr	Thr	Ala	Gly	Thr	Gly	Gly	Ser				
	355					360						365							
Ile	Leu	Ile	Ile	Gly	Ser	Ala	Ala	Gly	Val	Ala	Tyr	Met	Gly	Met	Glu				
	370					375					380								
Lys	Val	Ser	Phe	Gly	Trp	Tyr	Val	Lys	His	Ala	Ser	Trp	Ile	Ala	Leu				
385					390					395					400				
Ala	Ser	Tyr	Phe	Gly	Leu	Ala	Val	Tyr	Phe	Leu	Met	Glu	Asn	Cys					
			405					410					415						
Val	Asn	Leu	Phe	Val															
			420																

(2) INFORMATIONS POUR LA SEQ ID NO: 511:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 408 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 505763..506986

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 511:

Lys	His	Leu	Ile	Pro	Lys	Leu	Val	Thr	Cys	Leu	Lys	Glu	Gly	Tyr	Ser				
1				5					10					15					
Phe	Asn	Thr	Leu	Lys	Lys	Asp	Phe	Thr	Ala	Gly	Ile	Thr	Ala	Gly	Ile				
		20						25					30						
Leu	Ala	Phe	Pro	Leu	Ala	Ile	Ala	Ile	Ala	Ile	Gly	Ile	Gly	Val	Ser				
		35				40						45							
Pro	Leu	Gln	Gly	Leu	Leu	Ala	Ser	Ile	Ile	Gly	Gly	Phe	Leu	Ala	Ser				
	50					55					60								
Ala	Leu	Gly	Gly	Ser	Arg	Val	Leu	Ile	Ser	Gly	Pro	Thr	Ser	Ser	Phe				
65				70					75					80					
Ile	Ser	Ile	Leu	Tyr	Cys	Ile	Gly	Val	Lys	Tyr	Gly	Glu	Asp	Gly	Leu				
			85					90					95						
Phe	Thr	Ile	Thr	Leu	Met	Ala	Gly	Ile	Phe	Leu	Val	Ile	Phe	Gly	Leu				
		100						105					110						
Ala	Gly	Leu	Gly	Thr	Phe	Ile	Lys	Tyr	Met	Pro	Tyr	Pro	Val	Val	Thr				
	115						120					125							
Gly	Leu	Thr	Thr	Gly	Ile	Ala	Val	Ile	Ile	Phe	Ser	Ser	Gln	Ile	Arg				
	130				135						140								
Asp	Phe	Leu	Gly	Leu	Gln	Met	Gly	Asp	Gly	Val	Pro	Leu	Asp	Phe	Ile				
145					150					155					160				

Gly	Lys	Trp	Ala	Ala	Tyr	Trp	Asp	Tyr	Leu	Trp	Thr	Trp	Asp	Ser	Lys
				165					170					175	
Thr	Phe	Ala	Val	Gly	Leu	Phe	Thr	Leu	Leu	Leu	Met	Ile	Tyr	Phe	Arg
			180					185					190		
Asn	Tyr	Lys	Pro	Arg	Tyr	Pro	Gly	Val	Met	Ile	Ser	Ile	Ile	Ile	Ala
		195					200					205			
Ser	Thr	Leu	Val	Trp	Ile	Leu	Lys	Ile	Asp	Ile	Pro	Thr	Ile	Gly	Ser
	210					215					220				
Arg	Tyr	Gly	Thr	Leu	Pro	Ser	Ser	Leu	Pro	Gly	Pro	Val	Phe	Pro	His
225					230					235					240
Ile	Ser	Ile	Thr	Lys	Met	Leu	Gln	Leu	Met	Pro	Asp	Ala	Leu	Thr	Ile
				245					250						255
Ser	Val	Leu	Ser	Gly	Ile	Glu	Thr	Leu	Leu	Ala	Ala	Val	Val	Ala	Asp
			260					265					270		
Gly	Met	Thr	Gly	Trp	Arg	His	Gln	Ser	Asn	Cys	Gln	Leu	Ile	Gly	Gln
		275					280					285			
Gly	Ile	Ala	Asn	Ile	Gly	Thr	Ser	Leu	Phe	Ala	Gly	Met	Pro	Val	Thr
	290					295					300				
Gly	Ser	Leu	Ser	Arg	Thr	Thr	Ala	Ser	Ile	Lys	Cys	Gly	Ala	Ser	Thr
305					310					315					320
Pro	Ile	Ala	Gly	Ile	Ile	His	Ala	Ile	Cys	Leu	Ser	Phe	Ile	Leu	Leu
				325					330						335
Leu	Leu	Ala	Pro	Leu	Thr	Ile	Lys	Ile	Pro	Leu	Thr	Cys	Leu	Ala	Ala
			340					345					350		
Val	Leu	Ile	Leu	Ile	Ala	Trp	Asn	Met	Ser	Glu	Ile	His	His	Phe	Ile
			355				360					365			
His	Leu	Phe	Thr	Ala	Pro	Lys	Lys	Asp	Val	Leu	Val	Leu	Leu	Thr	Val
	370					375					380				
Phe	Ile	Leu	Thr	Val	Met	Thr	Thr	Ile	Thr	Ser	Ala	Val	Gln	Val	Gly
385					390					395					400
Met	Ile	Leu	Gln	Pro	Phe	Tyr	Ser								
				405											

(2) INFORMATIONS POUR LA SEQ ID NO: 512:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 147 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 506999..507439

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 512:

Ala	Ile	Tyr	Leu	Met	Leu	Ser	Pro	Gln	Gln	Asn	Ile	Leu	Met	Asn	Pro
1				5					10					15	
Asn	Asn	Leu	Lys	Met	Thr	Cys	Tyr	Phe	Ser	Lys	Asn	Glu	Val	Pro	Pro
			20					25					30		
Phe	Thr	Glu	Ile	Tyr	Glu	Ile	Asn	Gly	Pro	Phe	Phe	Phe	Gly	Ile	Ala
		35					40					45			
Asp	Arg	Leu	Lys	Asn	Leu	Leu	Asn	Glu	Ile	Glu	Lys	Pro	Pro	Lys	Ile
	50					55				60					
Phe	Ile	Leu	Cys	Met	Thr	Arg	Val	Pro	Thr	Ile	Asp	Ala	Ser	Ala	Met
65					70					75					80
His	Ala	Leu	Glu	Glu	Phe	Phe	Leu	Glu	Cys	Asp	Arg	Gln	Gly	Thr	Leu



(2) INFORMATION POUR LA SEQ ID NO: 513:

(A) LONGUEUR: 252 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(507649..508404)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 513:

Ser 1	Phe	Arg	Val	Cys 5	Ser	Arg	Tyr	Lys	Asn 10	Trp	Lys	Asn	Ala	Phe 15	Asp
Gly	Cys	Ser	Ser 20	Asn	Asp	Ser	Trp	Ala 25	Lys	Glu	Phe	Ser	Gly 30	Tyr	Ser
Cys	Gln	Leu	His 35	Asn	Cys	Leu	Glu 40	Arg	Ile	Gly	Phe	Ser 45	Leu	Thr	His
Leu	Tyr 50	Glu	Leu	Ala	Ile	Gly 55	Gly	Thr	Ala	Ile	Gly 60	Thr	Gly	Leu	Asn
Val 65	Pro	Glu	Gly	Phe	Val 70	Glu	Lys	Val	Ile	Gln 75	Tyr	Leu	Arg	Arg	Glu 80
Thr	Gly	Glu	Pro	Phe 85	Val	Pro	Ala	Ser	Asn 90	Tyr	Phe	Ala	Ala	Leu 95	Ser
Asn	His	Asp	Ala 100	Leu	Val	Gln	Ala	His 105	Gly	Ser	Leu	Thr	Val	Leu	Ala
Cys	Ala	Leu	Val 115	Lys	Ile	Ala	Thr	Asp 120	Leu	Ser	Xaa	Leu	Gly	Ser	Gly
Pro	Arg 130	Cys	Gly	Leu	Gly	Glu 135	Ile	Phe	Phe	Pro	Glu 140	Asn	Glu	Pro	Gly
Ser 145	Ser	Ile	Met	Pro	Gly 150	Lys	Ile	Asn	Pro	Thr	Gln 155	Ser	Glu	Ala	Leu 160
Gln	Met	Val	Cys	Ser 165	Gln	Val	Ile	Gly	Asn 170	Asn	Gln	Ser	Ile	Ile	Phe
Ser	Gly	Thr	Lys 180	Gly	Asn	Phe	Glu	Leu 185	Asn	Val	Met	Lys	Pro	Val	Ile
Ile	Tyr 195	Asp	Phe	Leu	Gln	Ser	Val 200	Asn	Leu	Leu	Ala	Gly	Ala	Met	Arg
Ser	Phe 210	Ala	Asp	Cys	Phe	Val 215	Cys	Gly	Leu	Lys	Val 220	Asn	Lys	Gly	Gln
Leu 225	Gln	Gln	Asn	Val	Glu 230	Arg	Ser	Leu	Met	Leu 235	Val	Thr	Ala	Leu	Val 240
Pro	Phe	Trp	Gly	Thr 245	Ile	Asn	Val	Gln	Arg 250	Leu	Leu				

(2) INFORMATIONS POUR LA SEQ ID NO: 514:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 100 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 508291..508590

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 514:

Thr	Ile	Met	Gln	Leu	Thr	Thr	Ile	Pro	Arg	Lys	Leu	Phe	Cys	Pro	Arg
1				5					10					15	
Val	Ile	Gly	Thr	Thr	Ser	Ile	Lys	Cys	Val	Leu	Pro	Ile	Phe	Ile	Ser
			20				25						30		
Arg	Ala	Asn	Ser	Lys	Ala	Leu	Ala	Ser	Thr	Thr	Phe	Phe	Lys	Cys	Ser
		35				40						45			
Asn	Thr	Gly	Ile	Lys	Asp	Pro	Phe	Ile	Leu	Cys	Thr	Ala	Ala	Ile	Cys
	50				55					60					
Ile	Ala	Val	Gly	Lys	Thr	Ser	Phe	Glu	Asp	Trp	Val	Tyr	Ser	Arg	Asp
65				70					75					80	
His	Trp	Asp	Ala	Arg	Asp	Val	Tyr	Phe	Gln	Ala	Leu	Pro	His	Asp	Ala
			85					90					95		
Glu	Leu	Leu	Asn												
			100												

(2) INFORMATIONS POUR LA SEQ ID NO: 515:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(508478..508915)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 515:

Met	Xaa	Gln	Glu	Asn	Asp	Ser	Leu	Gly	Ile	Val	Leu	Val	Pro	Glu	Asp
1				5					10					15	
Lys	Leu	Phe	Gly	Ala	Gln	Thr	Gly	Xaa	Ser	Gln	Glu	Phe	Phe	Ser	Tyr
			20				25						30		
Gly	Lys	Glu	Ser	Met	Pro	Leu	Glu	Ile	Ile	His	Ala	Leu	Val	Lys	Ile
		35				40						45			
Lys	Lys	Cys	Ala	Ala	Lys	Ala	Asn	Gly	Asp	Leu	Gly	Cys	Leu	Asp	Ala
	50				55					60					
Lys	Arg	Arg	Asp	Met	Ile	Val	Ala	Ala	Thr	Asp	Glu	Ile	Leu	Ser	Gly
65				70					75					80	
Glu	Phe	Asp	Glu	His	Phe	Pro	Leu	Lys	Val	Trp	Gln	Thr	Gly	Ser	Gly
			85				90						95		
Thr	Gln	Ser	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ala	Asn	Leu	Ala	Ile
			100				105					110			
Gln	Arg	His	Gly	Gly	Glu	Leu	Gly	Ser	Lys	His	Pro	Val	His	Pro	Asn

		115				120				125			
Asp	His	Val	Asn	Lys	Pro	Ser	Pro	Gln	Met	Met	Phe	Ser	Gln
	130					135					140		
Cys	Ile												
145													

(2) INFORMATIONS POUR LA SEQ ID NO: 516:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 313 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 509753..510691

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 516:

Ile	Pro	Ile	Thr	Val	Leu	Pro	Cys	Leu	Phe	Tyr	Leu	Lys	Asp	Asp	Pro
1				5					10					15	
Lys	Leu	Ala	Ala	Pro	Val	Pro	Thr	Lys	Ser	Phe	Thr	Leu	Leu	Leu	Asp
		20						25					30		
Trp	Thr	Pro	Asn	Pro	Asn	His	Ile	Pro	Leu	Tyr	Val	Gly	Val	Glu	Lys
		35				40						45			
Gly	Phe	Phe	Val	Asp	Glu	Gly	Ile	Ser	Leu	Thr	Leu	Gln	Lys	Asn	Thr
	50				55						60				
Asp	Thr	Cys	Ser	Ser	Ile	Pro	His	Leu	Leu	Leu	Glu	Lys	Val	Asp	Tyr
65					70					75				80	
Thr	Leu	Tyr	His	Ser	Leu	Gly	Val	Leu	Lys	Thr	Ala	Val	Arg	Gly	Ala
			85						90				95		
Pro	Val	Gln	Val	Ala	Gly	Arg	Leu	Ile	Asp	Ser	Ser	Leu	Gln	Gly	Leu
		100					105						110		
Ile	Tyr	Arg	Lys	Asn	Glu	Gly	Val	Glu	Lys	Leu	Glu	Asp	Leu	Asn	Gly
	115					120						125			
Arg	Val	Leu	Gly	Phe	Cys	Leu	Asn	Asp	Ser	Lys	Asn	Leu	Pro	Asn	Leu
	130				135						140				
Leu	Glu	Ala	Leu	Arg	Lys	His	His	Val	Val	Pro	Ser	Glu	Ile	Lys	Asn
145					150					155				160	
Val	Ser	Ala	Asp	Met	Ile	Ser	Pro	Met	Leu	Thr	Tyr	Gln	Ile	Asp	Phe
			165						170				175		
Leu	Tyr	Gly	Gly	Phe	Tyr	Asn	Val	Glu	Gly	Val	Thr	Ile	Ala	Leu	Lys
		180					185					190			
Gly	Thr	Pro	Thr	Gly	Cys	Phe	Leu	Ser	Asp	Thr	Tyr	Gly	Ser	Pro	Thr
	195					200						205			
Gly	Pro	Gln	Leu	Leu	Ile	Cys	Gly	Lys	Lys	Gly	Ser	Pro	Ala	Met	Thr
	210				215						220				
Pro	Gln	Thr	Leu	Gln	Ser	Leu	Gln	Lys	Ala	Leu	Ser	Arg	Ser	Leu	Asp
225				230						235				240	
Phe	Cys	Arg	Glu	Tyr	Pro	Gln	Glu	Ala	Phe	Ala	Ile	Tyr	Val	Glu	Ala
			245						250				255		
Thr	Lys	Asp	Ser	Pro	Lys	Val	Leu	Ser	Asp	Glu	Gln	Ala	Gln	Trp	Glu
		260					265					270			
Val	Thr	Leu	Pro	Leu	Leu	Ala	Lys	Thr	Gln	Glu	Pro	Leu	Ser	Arg	Glu
	275					280						285			
Leu	Leu	Glu	Ser	Leu	Leu	Val	Thr	Leu	Ser	Thr	Thr	Cys	Pro	Asp	Leu
	290					295					300				

Gln Ala Ser Ile Asp Thr Phe Phe Tyr  
305 310

(2) INFORMATIONS POUR LA SEQ ID NO: 517:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 511039..511527

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 517:

Lys	Lys	Gln	Ser	Ala	Ala	Ser	Leu	Glu	Gly	Lys	Ser	Phe	Cys	Ser	Ser	1	5	10	15
Arg	Val	Phe	Cys	Ser	Leu	Ser	Ser	Ile	Ile	Arg	Ala	Pro	Leu	Leu	Phe	20	25	30	
Ala	Asn	Thr	Ser	Met	Arg	Ser	Thr	Val	Val	Gly	Gly	Cys	Gly	Val	Met	35	40	45	
Phe	Thr	Gly	Met	Arg	Ala	Ile	Leu	Arg	Asn	Thr	Gln	Ala	Ser	Leu	Trp	50	55	60	
Ser	Lys	Ile	Pro	Ser	Leu	Ser	Gln	Ser	Pro	Lys	Val	Ala	Pro	Ile	Ala	65	70	75	80
Leu	Pro	Leu	Met	Ile	Gly	Pro	Ser	Trp	Leu	Cys	Ala	Cys	Ala	Pro	Leu	85	90	95	
Ala	Met	Gln	Gln	Leu	Pro	Phe	Ser	Ile	Val	Cys	Ala	Leu	Leu	Cys	Leu	100	105	110	
Ser	Trp	Leu	Met	Met	Thr	Ile	Thr	Thr	Ile	Val	Leu	Gln	Thr	Ala	Asn	115	120	125	
Lys	Ala	Gly	Ser	Gln	Thr	Ile	Ile	Ala	Thr	Gln	Thr	Ile	Leu	Gly	Leu	130	135	140	
Ala	Val	Val	Ile	Val	Gly	Ala	Gln	Leu	Leu	Val	Ser	Gly	Leu	Gln	Gln	145	150	155	160
Thr	Phe	Leu																	

(2) INFORMATIONS POUR LA SEQ ID NO: 518:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 213 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 511547..512185

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 518:

Met	Leu	His	Ser	Leu	Phe	Arg	Leu	Thr	Leu	Leu	Phe	Tyr	Ala	Leu	Phe	1	5	10	15
Asn	Ala	Leu	Gly	Ser	Leu	Pro	Val	Phe	Ile	Ala	Leu	Leu	Lys	Asn	Phe				

20												25				30			
Ser	Phe	Lys	Lys	Gln	Gln	Arg	Ile	Ile	Leu	Arg	Glu	Ser	Ile	Phe	Ala				
		35					40					45							
Leu	Leu	Leu	Leu	Leu	Leu	Phe	Val	Thr	Phe	Gly	Arg	Gly	Phe	Phe	Arg				
	50					55					60								
Leu	Leu	Gly	Ile	Thr	Leu	Pro	Ala	Phe	Gln	Phe	Thr	Gly	Gly	Leu	Leu				
65					70					75					80				
Leu	Gly	Ser	Ile	Ala	Ile	Asp	Met	Met	Lys	Ala	Leu	Pro	Ser	Gln	Ser				
				85					90					95					
Glu	Thr	Leu	Glu	Lys	Asp	Lys	Asp	Glu	Pro	Val	Phe	Phe	Pro	Leu	Ala				
			100					105						110					
Phe	Pro	Val	Ile	Thr	Gly	Pro	Ala	Met	Ile	Thr	Ser	Thr	Leu	Gly	His				
		115					120					125							
Met	Glu	Glu	Gly	Ile	Phe	Pro	Lys	Glu	Ile	Val	Leu	Gly	Ala	Ile	Val				
	130					135					140								
Xaa	Ala	Trp	Leu	Phe	Ser	Leu	Ile	Thr	Leu	Leu	Phe	Ser	Ser	Ser	Ile				
145					150					155					160				
Asn	Arg	Leu	Phe	Gly	Gln	Met	Gly	Leu	Leu	Ala	Leu	Glu	Arg	Leu	Phe				
				165					170					175					
Gly	Ile	Ser	Leu	Ala	Leu	Met	Ala	Gly	Asn	Leu	Met	Leu	Lys	Ala	Leu				
			180					185					190						
Ser	Thr	Ala	Phe	Asn	Ile	Gly	Tyr	Tyr	Met	Leu	His	Leu	Lys	Ala	Leu				
		195					200					205							
Leu	Tyr	Val	Lys	Arg															
	210																		

(2) INFORMATIONS POUR LA SEQ ID NO: 519:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 237 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 512382..513092

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 519:

Ser	Leu	Pro	Ser	Tyr	Ser	Ser	Tyr	Ser	Arg	Cys	Phe	Met	Arg	Xaa	Ala
1				5					10					15	
Lys	Glu	Gly	Val	Thr	Thr	Asn	Glu	Leu	Asp	Leu	Leu	Ser	Arg	Glu	Leu
			20				25						30		
His	Lys	Arg	His	Asn	Ala	Ile	Pro	Ala	Pro	Leu	Asn	Tyr	Gly	His	Pro
		35				40						45			
Pro	Phe	Pro	Lys	Thr	Ile	Cys	Thr	Ser	Leu	Asn	Glu	Val	Ile	Cys	His
	50					55					60				
Gly	Ile	Pro	Asn	Asp	Ile	Pro	Leu	Gln	Asn	Gly	Asp	Ile	Met	Asn	Ile
65				70						75				80	
Asp	Val	Ser	Cys	Ile	Val	Asp	Gly	Phe	Tyr	Gly	Asp	Cys	Ser	Arg	Met
			85						90					95	
Val	Met	Ile	Gly	Glu	Val	Ser	Glu	Ile	Lys	Arg	Lys	Val	Cys	Glu	Ala
			100				105						110		
Ser	Leu	Glu	Ala	Leu	Asn	Ala	Ile	Ser	Ile	Leu	Glu	Pro	Asn	Leu	
		115				120						125			
Pro	Leu	Tyr	Glu	Ile	Gly	Glu	Val	Ile	Glu	Asn	Cys	Ala	Ala	Lys	Tyr
	130					135					140				

Gly	Phe	Ser	Val	Val	Asp	Gln	Phe	Val	Gly	His	Gly	Val	Gly	Val	Lys
145					150				155						160
Phe	His	Glu	Asn	Pro	Phe	Val	Ala	His	His	Arg	Asn	Ser	Cys	Lys	Ile
			165						170					175	
Pro	Leu	Ala	Pro	Gly	Met	Ile	Phe	Thr	Ile	Glu	Pro	Met	Ile	Asn	Val
			180					185					190		
Gly	Lys	Lys	Glu	Gly	Phe	Ile	Asp	Pro	Ile	Asn	His	Trp	Glu	Ala	Arg
		195					200					205			
Thr	Cys	Asp	His	Gln	Pro	Ser	Ala	Gln	Trp	Glu	His	Ala	Ile	Leu	Ile
	210					215					220				
Thr	Asp	Ser	Gly	Cys	Glu	Val	Leu	Thr	Leu	Leu	Asp	Lys			
225					230					235					

(2) INFORMATIONS POUR LA SEQ ID NO: 520:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 411 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(513055..514287)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 520:

Thr	Lys	Lys	Arg	Val	Leu	Met	Gly	Phe	Gly	Thr	Val	Arg	Gly	Lys	Gly
1				5					10					15	
Lys	Ala	Val	Lys	Ser	Phe	Phe	Leu	Arg	Pro	Leu	Gln	Asn	Leu	Glu	Val
			20					25					30		
Gly	Leu	Phe	Ser	Leu	Pro	Ile	Val	Leu	Leu	Leu	Gly	Glu	Ile	Gly	Cys
		35					40					45			
Val	Ser	Ser	Ile	Ser	Ser	Val	Ser	Leu	Val	Ala	Val	Leu	Ser	Ile	Val
	50					55					60				
Gly	Val	Phe	Val	Ala	Leu	Val	Ser	Phe	Phe	Arg	Ser	Trp	Gly	Tyr	Gly
65					70					75					80
Leu	Ser	Val	Val	Gly	Ala	Ile	Phe	Phe	Gly	Leu	Ala	Leu	Cys	Asn	Asn
				85					90					95	
Phe	Pro	Val	Ser	Val	Phe	Trp	Gly	Gly	Leu	Leu	Thr	Val	Ser	Phe	Ile
			100					105					110		
Ile	Ser	Tyr	Gly	Ile	Leu	Leu	Leu	Ser	Val	Ser	Leu	Val	Glu	Gly	His
		115					120					125			
Ile	Lys	Glu	Lys	Ala	Val	Ser	Leu	Ser	Glu	Leu	Thr	Ala	Ser	His	Asn
	130					135					140				
Ser	Leu	Gln	Asp	Ser	Tyr	Asn	Arg	Glu	Val	Gln	Glu	Arg	Lys	Glu	Lys
145					150					155					160
Glu	Leu	Leu	Ala	Gln	Ser	Lys	Ile	Thr	Ala	Leu	Glu	Gln	Glu	Leu	Ser
				165					170					175	
Val	Ser	His	Glu	Gln	Leu	Gln	Glu	Val	Ser	Arg	Lys	Tyr	Thr	His	Thr
		180						185					190		
Ser	Glu	Asp	Leu	Gln	Ile	Leu	Ile	Asp	Gln	Arg	Asp	Ser	Trp	Leu	Lys
		195					200					205			
Asp	Tyr	Met	Thr	Leu	His	Gln	Glu	Tyr	Val	Arg	Val	Val	Ala	Gly	Asp
	210					215					220				
Glu	Glu	Asn	Val	Ile	Phe	Pro	Trp	Lys	Val	Phe	Gln	Gly	Asn	Ser	Glu
225						230					235				240
Lys	Asp	Ser	Gly	Tyr	Gln	Gln	Arg	Val	Gln	Asp	Ala	Glu	His	Lys	Ile

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 522:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 514994..515269

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 522:

Thr	Lys	Lys	Arg	Ile	Lys	Ser	Asn	Thr	Leu	Ser	Leu	Ala	Leu	Glu	Leu
1				5					10					15	
Lys	Lys	Thr	Lys	Ile	Thr	Arg	Val	Gln	Asn	Gln	Asn	Gln	Asn	Tyr	Ser
			20					25					30		
Ala	Gln	Arg	Ser	Asn	Ile	Gln	Asp	Gln	Leu	Val	Thr	Ala	Arg	Gln	Asn
		35					40					45			
Gly	Gln	Ile	Ile	Leu	Ser	His	Ala	Ser	Thr	Asn	Ile	Asn	Ile	Met	Gln
	50					55					60				
Gln	Ile	Ala	Gln	Gln	Asn	Ser	Ser	Phe	Ile	Lys	Thr	Leu	Asn	Ser	Val
65					70					75					80
Gly	Ser	Thr	Val	Asn	Gln	Leu	Asn	Lys	Pro	Leu	Ser				
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 523:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 84 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 515553..515804

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 523:

Ile	Tyr	Thr	Thr	Ile	Pro	Lys	Asn	Gln	Val	Asn	Ser	Gln	Asn	Ser	Ser
1				5					10					15	
Tyr	Leu	Gln	Asn	Val	Gln	Ser	Val	Asn	Gln	Ala	Val	Gly	Ala	Ser	Arg
			20					25					30		
Gln	Ala	Ile	Gln	Asn	Gln	Ile	Ser	Gly	Leu	Gly	Asn	Ala	Ser	Gln	Val
		35					40					45			
Ile	Ser	Ser	Asn	Leu	Asn	Thr	Asn	Asn	Asn	Ile	Ile	Gln	Gln	Ser	Leu
	50					55					60				
Gln	Val	Gly	Gln	Ala	Leu	Ile	Gln	Thr	Phe	Ser	Gln	Ile	Val	Ser	Leu
65					70					75					80
Ile	Ala	Asn	Ile												

(2) INFORMATIONS POUR LA SEQ ID NO: 524:

(i) CARACTERISTIQUES DE LA SEQUENCE:



(A) LONGUEUR: 205 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 515808..516422

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 524:

Arg	Gly	Tyr	Pro	Met	Ser	Ser	Ala	Ile	Ile	Pro	Thr	Leu	Pro	Glu	Lys
1				5					10					15	
Asn	Thr	Val	Ile	Pro	Asp	Ser	Thr	Leu	Ile	Glu	Pro	Thr	Ser	Ile	Glu
			20					25					30		
Ile	Asn	Lys	Lys	Ser	Ala	Met	Tyr	Phe	Cys	Ile	Ala	Val	Met	Leu	Lys
		35					40					45			
Leu	Ser	Val	Ala	Thr	Thr	Asp	Tyr	Ser	His	Ala	Ile	Met	Ala	Val	Leu
	50					55					60				
Gln	Glu	Asn	Thr	Leu	Glu	Gln	Gln	Arg	Lys	Thr	Lys	Glu	Leu	Ile	Asn
65					70				75					80	
Ile	Pro	Leu	Leu	Tyr	Val	Pro	Asp	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Asp
				85					90					95	
Asp	Glu	Tyr	Thr	Asn	His	Ser	Thr	Ile	Gln	Ala	Phe	Gln	Thr	Ser	Asn
			100					105					110		
Gln	Gln	Ile	Thr	Ala	Asn	Arg	Glu	Leu	Ile	Gln	Gln	Glu	Leu	Ser	Ala
		115					120					125			
Ala	Gln	Gln	Arg	Ala	Gln	Ala	Asn	Gln	Lys	Ser	Val	Asn	Ala	Thr	Ser
	130					135					140				
Thr	Glu	Ser	Met	Lys	Ile	Leu	Gln	Ala	Val	Ser	Ala	Leu	Leu	Thr	Ser
145					150					155				160	
Leu	Ile	Asp	Leu	Thr	Ile	Lys	Ala	Asn	Leu	Thr	Thr	Ser	Leu	Arg	Thr
				165					170					175	
Asn	Ile	Leu	Gly	Cys	Thr	Gly	Phe	Pro	Met	His	Pro	Asn	Asn	Lys	Pro
			180					185					190		
Cys	Glu	Thr	Lys	Gly	Arg	Leu	Thr	Ala	Lys	Asn	Arg	Ala			
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 525:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 232 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 516476..517171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 525:

Glu	Leu	Ser	Ser	Pro	Ile	Ser	Thr	Asn	Lys	Leu	Pro	Phe	Gly	Glu	Ser
1				5					10					15	
Pro	Lys	Thr	Ala	Ser	Leu	Leu	Val	Leu	Val	Thr	Ser	Cys	Ser	Ala	Pro
			20					25					30		
Ser	Ile	Ala	Phe	Phe	Leu	Gln	Tyr	Phe	Phe	Gln	Val	Arg	Gly	Pro	Ile
		35					40					45			

```

Glu Trp Leu Ala Leu Ser Val Lys Gly Ile His Gln His Tyr Phe Trp
 50                      55                      60
Gln Trp Leu Thr Tyr Pro Leu Val Thr Ala Asp Thr Leu Lys Leu Gly
65                      70                      75                      80
Asp Leu Arg Ser Leu Glu Ile Thr Gln Arg Leu Leu Met Arg Asn Val
                      85                      90                      95
Leu Asp Phe Ile Leu Phe Tyr Lys Ala Thr Asp Val Ile Ile Arg Lys
                      100                     105                     110
Leu Gly Thr Gly Ser Phe Val Phe Leu Leu Thr Thr Gln Val Ser Ile
                      115                     120                     125
Ala Gly Ile Ser Ile Trp Ala Phe Leu Trp Leu Ile Gly Ser Thr Gln
                      130                     135                     140
Ala Phe Phe Gly Pro Glu Ser Leu Ile Cys Ala Leu Leu Ile Val Arg
145                      150                      155                      160
Val Phe Leu Asp Pro Glu Lys Arg Leu Thr Leu Pro Leu Phe Pro Ile
                      165                      170                      175
Ser Leu Ser Arg Lys Trp Ser Phe Val Leu Leu Leu His Phe Tyr Phe
                      180                      185                      190
Leu Ile Leu Ile Leu Ser Gly Ala Tyr Ala Ile Leu Leu Gly Ser Val
                      195                     200                     205
Leu Ser Met Ala Leu Ala Ile Cys Phe Cys Tyr Lys Glu Asn Ile Pro
210                      215                      220
Asn Pro Tyr Arg Gly Ser Tyr Arg
225                      230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 526:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(517400..517888)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 526:

```

Met Cys Ile Glu Lys Asp Leu Phe Phe Met Lys Lys Ala Leu Asp Glu
 1                      5                      10                      15
Ala Arg Lys Ala Tyr Glu Gln Asp Glu Val Pro Val Gly Cys Ile Ile
                      20                      25                      30
Val His Gly Asp Lys Ile Ile Ala Arg Gly His Asn Ser Val Glu Gln
                      35                      40                      45
Leu Lys Asp Pro Thr Ala His Ala Glu Met Ile Cys Ile Ser Ala Ala
50                      55                      60
Ala Glu Tyr Leu Glu Asn Trp Arg Leu Lys Asp Thr Ile Leu Tyr Cys
65                      70                      75                      80
Thr Leu Glu Pro Cys Leu Met Cys Ala Gly Ala Ile Gln Leu Ala Arg
                      85                      90                      95
Ile Pro Arg Ile Val Trp Gly Ala Pro Asp Leu Arg Leu Gly Ala Gly
                      100                     105                     110
Gly Ser Trp Leu Asn Val Phe Leu Glu Lys His Pro Phe His Gln Val
                      115                     120                     125
Glu Cys Cys Ser Gly Val Cys Tyr Gln Glu Ser Glu Gln Leu Met Lys
130                      135                      140
Asn Phe Phe Leu Glu Lys Arg Lys Ala Lys Asp Glu Gly Arg Asn Ser

```

160

Asp 1	Asn	Ser	Met	Ala 5	Phe	Glu	Thr	Phe	Ser 10	Val	Ala	Leu	Asp	Lys 15	Asp
Lys	Thr	Leu	Ile 20	Phe	Glu	Thr	Gly	Lys 25	Ile	Ala	Arg	Gln	Ala	Ser	Gly
Ala	Val	Leu 35	Val	Lys	Met	Asn	Glu 40	Thr	Trp	Val	Phe	Ser	Ser	Ala	Cys
Ala	Ala 50	Ser	Leu	Ser	Glu	Ala 55	Val	Gly	Phe	Leu	Pro 60	Phe	Arg	Val	Asp
Tyr 65	Gln	Glu	Lys	Phe	Ser 70	Ser	Ala	Gly	Arg	Thr 75	Ser	Gly	Gly	Phe	Leu 80
Lys	Arg	Glu	Gly	Arg 85	Pro	Ser	Glu	Arg	Glu 90	Ile	Leu	Val	Ser	Arg 95	Leu

```

Ile Asp Arg Ser Leu Arg Pro Ser Phe Pro Asn Arg Leu Met Gln Asp
      100                      105                      110
Ile Gln Val Leu Ser Tyr Val Trp Ser Tyr Asp Gly Lys Thr Leu Pro
      115                      120                      125
Asp Pro Pro Ser Leu Phe Ala Glu Leu Leu Pro Leu
      130                      135                      140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 529:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 518923..519516

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 529:

```

Val Pro Pro Ser Leu Asp Leu Val Met Ala Gly Thr Ala Ser Ala Val
1      5      10      15
Leu Met Ile Glu Gly His Cys Asp Phe Leu Thr Glu Glu Gln Val Leu
      20      25      30
Glu Ala Ile Ala Phe Gly Gln Thr Tyr Ile Ala Lys Ile Cys Asp Ala
      35      40      45
Ile Glu Ala Trp Gln Lys Ala Ile Gly Lys Gln Lys Asn Phe Ser Ala
      50      55      60
Val Leu Asp Met Pro Glu Asp Val Gln Asn Val Val Ser Asp Phe Ile
65      70      75      80
Arg Glu Lys Phe Glu Lys Ala Leu Ser Phe Arg Asp Lys Glu Ala Leu
      85      90      95
Glu Gln Ala Ser Lys Glu Leu Glu Glu Ser Val Ile Ala Asn Leu Val
      100     105     110
Gln Glu Glu Asn Ser Asp Phe Ser Leu Leu Asn Val Lys Ala Ala Phe
      115     120     125
Lys Thr Ala Lys Ser Asn Gln Met Arg Ala Leu Ile Gln Asp Leu Gly
      130     135     140
Ile Arg Val Asp Gly Arg Thr Thr Thr Glu Ile Arg Pro Ile Ser Ile
145     150     155     160
Glu Thr Pro Leu Leu Pro Arg Thr His Gly Ser Cys Leu Phe Thr Arg
      165     170     175
Gly Glu Thr Gln Ser Met Ala Val Cys Thr Leu Gly Gly Glu Asn Met
      180     185     190
Ala Gln Asp Ser Lys Ile
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 530:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 307 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 519577..520497

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 530:

```

Lys Val Gly Arg Ile Gly Ser Pro Gly Arg Arg Glu Ile Gly His Gly
1      5      10      15
Lys Leu Ala Glu Xaa Ala Leu Ser His Val Leu Pro Glu Thr Ser Arg
20      25      30
Phe Pro Tyr Ile Ile Arg Leu Glu Ser Asn Ile Thr Glu Ser Asn Gly
35      40      45
Ser Ser Ser Met Ala Ser Val Cys Gly Gly Cys Leu Ala Leu Met Asp
50      55      60
Ala Gly Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu
65      70      75      80
Ile Leu Asp Arg Asp Gln Ala Ile Ile Leu Ser Asp Ile Ser Gly Ile
85      90      95
Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Lys
100     105     110
Gly Ile Thr Ala Phe Gln Met Asp Ile Lys Ile Glu Gly Ile Thr His
115     120     125
Lys Ile Met Glu Gln Ala Leu Ala Gln Ala Lys Gln Gly Arg Ser His
130     135     140
Ile Leu Asn Leu Met Thr Gln Val Leu Ala Ser Pro Lys Gly Thr Val
145     150     155     160
Ser Lys Tyr Ala Pro Arg Ile Glu Thr Met Gln Ile Asn Thr Ser Lys
165     170     175
Ile Ala Thr Val Ile Gly Pro Gly Gly Lys Gln Ile Arg Gln Ile Ile
180     185     190
Glu Arg Ser Gly Ala Gln Val Asp Ile Asn Asp Asp Gly Val Ile Asn
195     200     205
Ile Ala Ala Ser Thr Gln Glu Ser Ile Asn Lys Ala Lys Glu Leu Ile
210     215     220
Glu Gly Leu Thr Gly Glu Val Glu Val Gly Lys Val Tyr Asn Gly Arg
225     230     235     240
Val Thr Ser Ile Ala Thr Phe Gly Val Phe Val Glu Val Leu Pro Gly
245     250     255
Lys Glu Gly Leu Cys His Ile Ser Glu Leu Ser Lys Gln Lys Val Asp
260     265     270
Asn Ile Ser Asp Phe Val Lys Glu Gly Asp Lys Leu Ala Val Lys Leu
275     280     285
Leu Ser Ile Asn Glu Lys Gly Gln Leu Lys Leu Ser His Lys Ala Thr
290     295     300
Leu Glu Asp
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 531:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(520718..521986)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 531:

Pro	Val	Leu	Ile	Ser	Leu	Lys	Cys	Leu	Leu	Gly	Leu	Glu	Gln	Val	Glu	1	5	10	15
Ser	Glu	Ile	Cys	Ser	Ser	Arg	Arg	Ser	Val	Met	Leu	Leu	Gly	Ile	Ile	20	25	30	
Phe	Ile	Asp	Glu	Ile	Asp	Ala	Val	Gly	Arg	His	Arg	Gly	Ala	Gly	Ile	35	40	45	
Gly	Gly	Gly	His	Asp	Glu	Arg	Glu	Gln	Thr	Leu	Asn	Gln	Leu	Leu	Val	50	55	60	
Glu	Met	Asp	Gly	Phe	Gly	Thr	Asn	Glu	Gly	Val	Ile	Leu	Met	Ala	Ala	65	70	75	80
Thr	Asn	Arg	Pro	Asp	Val	Leu	Asp	Lys	Ala	Leu	Leu	Arg	Pro	Gly	Arg	85	90	95	
Phe	Asp	Arg	Arg	Val	Val	Val	Asn	Leu	Pro	Asp	Ile	Lys	Gly	Arg	Phe	100	105	110	
Glu	Ile	Leu	Ala	Val	His	Ala	Lys	Arg	Ile	Lys	Leu	Asp	Pro	Thr	Val	115	120	125	
Asp	Leu	Met	Ala	Val	Ala	Arg	Ser	Thr	Pro	Gly	Ala	Ser	Gly	Ala	Asp	130	135	140	
Leu	Glu	Asn	Leu	Leu	Asn	Glu	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Lys	Asp	145	150	155	160
Arg	Thr	Ala	Val	Thr	Ala	Val	Glu	Val	Ala	Glu	Ala	Arg	Asp	Lys	Val	165	170	175	
Leu	Tyr	Gly	Lys	Glu	Arg	Arg	Ser	Leu	Glu	Met	Asp	Ala	Gln	Glu	Lys	180	185	190	
Lys	Thr	Thr	Ala	Tyr	His	Glu	Ser	Gly	His	Ala	Ile	Val	Gly	Leu	Cys	195	200	205	
Val	Glu	His	Ser	Asp	Pro	Val	Asp	Lys	Val	Thr	Ile	Ile	Pro	Arg	Gly	210	215	220	
Leu	Ser	Leu	Gly	Ala	Thr	His	Phe	Leu	Pro	Glu	Lys	Asn	Lys	Leu	Ser	225	230	235	240
Tyr	Trp	Lys	Lys	Glu	Leu	Tyr	Asp	Gln	Leu	Ala	Val	Leu	Met	Gly	Gly	245	250	255	
Arg	Ala	Ala	Glu	Gln	Ile	Phe	Leu	Gly	Asp	Val	Ser	Ser	Gly	Ala	Gln	260	265	270	
Gln	Asp	Ile	Ala	Gln	Ala	Thr	Lys	Ile	Val	Arg	Ser	Met	Ile	Cys	Glu	275	280	285	
Trp	Gly	Met	Ser	Asp	His	Leu	Gly	Thr	Val	Ala	Tyr	Asp	Glu	His	Ser	290	295	300	
Glu	Ala	Ala	Pro	Thr	Gly	Tyr	Gly	Ser	Tyr	His	Glu	Lys	Asn	Tyr	Ser	305	310	315	320
Glu	Glu	Thr	Ala	Lys	Val	Ile	Asp	Asn	Glu	Leu	Lys	Thr	Leu	Leu	Asp	325	330	335	
Ala	Ala	Tyr	Gln	Arg	Ala	Leu	Asp	Ile	Ile	Asn	Ser	His	Lys	Glu	Glu	340	345	350	
Leu	Glu	Leu	Met	Thr	Gln	Met	Leu	Ile	Glu	Phe	Glu	Thr	Leu	Asp	Ser	355	360	365	
Lys	Asp	Val	Lys	Glu	Ile	Met	Asp	His	Ser	Trp	Asp	Ala	Asp	Lys	Lys	370	375	380	
Arg	Ala	Arg	Met	Lys	Glu	Gly	Met	Leu	Tyr	Lys	Lys	Ile	Ser	Asp		385	390	395	400
Asp	Leu	Pro	Pro	Pro	Pro	Pro	Gln	Glu	Asn	Val	Gln	Asp	Gly	Thr	Ser	405	410	415	
Leu	Lys	Phe	Asn	Thr	Ser	Thr										420			

## (2) INFORMATIONS POUR LA SEQ ID NO: 532:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 82 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(521886..522131)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 532:

```

Ile Ser Leu Lys Asn Pro Thr Lys Phe Thr Ser Leu Gly Gly Arg Ile
1      5      10      15
Pro Lys Gly Ile Leu Leu Ile Gly Ala Pro Gly Thr Gly Lys Thr Leu
      20      25      30
Ile Ala Lys Ala Val Ala Gly Glu Ala Asp Arg Pro Phe Phe Ser Ile
      35      40      45
Ala Gly Ser Asp Phe Val Glu Met Phe Val Gly Val Gly Ala Ser Arg
      50      55      60
Ile Arg Asp Met Phe Glu Gln Ala Lys Arg Asn Ala Pro Trp His Tyr
65      70      75      80
Leu His

```

(2) INFORMATIONS POUR LA SEQ ID NO: 533:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 451 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(522143..523495)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 533:

```

Leu Ser Ala Cys Leu Ile Ser Ile Val Val Ser Phe Met Ala Lys Asp
1      5      10      15
Lys Lys Thr Asn Pro Glu Ser Lys Lys Ser Phe Pro Thr Ala Phe Phe
      20      25      30
Phe Leu Leu Phe Gly Val Ile Phe Gly Val Val Thr Val Gln Asn Phe
      35      40      45
Phe Ser Ala Lys Lys Ala Ser Val Gly Phe Ser His Gln Leu Glu His
      50      55      60
Leu Val Asn Leu Lys Leu Leu Ile Pro Glu Glu Ser Arg Lys Thr Ala
65      70      75      80
Leu Asn Asp Asn Leu Val Ser Phe Ser Gly Arg Phe Arg Glu Val Val
      85      90      95
Pro Ala Glu Gly Gln Val Arg Tyr Gln Tyr Leu Asp Leu Ile Glu Arg
      100      105      110
Lys His Gln Ile Asp Phe Glu Leu Glu Glu Ala Ser Lys Ser Leu Thr
      115      120      125
Val Leu Ser Lys Glu Val Arg Asn Ala Ile Thr Trp Phe Ser Ala Ile
130      135      140

```

```

Ser Gly Met Pro Ile Pro Glu Ala Gly Tyr Thr Ile Ser Pro Arg Thr
145          150          155          160
Asp Val Gly Leu Ser Val Leu Glu Pro Leu Val Val Tyr Gly Pro Val
          165          170          175
Asp Ala Gln Ile Val Asn Leu Ala Ala Leu Glu Asn Arg Val Arg Ser
          180          185          190
Leu Pro Lys Ser Thr Glu Ser Leu Arg Val Phe Gly Ser Asp Leu Tyr
          195          200          205
Ala Leu Ile Gly Lys Tyr Leu Ser Pro Ala Leu Gly Ile Gly Ser Glu
          210          215          220
Ser Leu Lys Lys Glu Ile Lys Asp Leu His Gln Gln Val Glu Asn Ser
225          230          235          240
Leu Thr Gln Val Ile Glu Gly Asp Gln Ala Val Ala Leu Tyr Lys Thr
          245          250          255
Val Leu Glu Thr Leu His Arg Ile Ser Leu Ala Leu Val Ser Pro Glu
          260          265          270
Glu Gly Thr Arg Phe His Gln Leu Arg Ser Val Arg Leu Tyr Arg Glu
          275          280          285
Asp Phe Asn Arg Cys Val Lys Leu Leu Arg Glu Ser Asp Glu Thr Gln
          290          295          300
Val Gln Leu Asp Lys Leu Arg Gly Glu Leu Val Gln Ala Val Trp Tyr
305          310          315          320
Phe Asn Asn Gln Glu Leu Ser Ser Arg Ala Leu Glu Lys Gln Asp Pro
          325          330          335
Glu Val Phe Ser Arg Trp Phe Glu Gly Ala Lys Gln Glu Trp Ala Ala
          340          345          350
Phe Ser Ser Asn Lys Ser Leu Ser Phe Arg Ala Pro Asp Gln Pro Arg
          355          360          365
Asn Leu Val Leu Glu Lys Thr Phe Arg Ser Glu Glu Pro Thr Pro His
          370          375          380
Tyr Ser Gly Tyr Leu Phe Thr Phe Met Pro Ile Ile Leu Val Leu Leu
385          390          395          400
Phe Ile Tyr Phe Ile Phe Ser Arg Gln Val Lys Gly Met Asn Gly Ser
          405          410          415
Ala Met Ser Phe Gly Lys Ser Pro Ala Arg Leu Leu Ala Lys Gly Gln
          420          425          430
Lys Gln Ser Asn Phe Cys Gly Cys Ser Arg Asp Arg Gly Ser Gln Arg
          435          440          445
Arg Thr Arg
          450

```

(2) INFORMATIONS POUR LA SEQ ID NO: 534:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 323 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(523623..524591)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 534:

```

Cys Tyr Asp Asn Pro Phe Ile Phe Glu Asn Asp Lys Gln Leu Glu Gly
1          5          10          15
Phe Phe Ser Ser Leu Asp Lys Lys Lys Tyr Leu Leu Ala Leu Ser

```



[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 535:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 524652..525746

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 535:

Asn Val Gln Leu Ile Phe Tyr Tyr Gly Ile Ile Met Pro Ile Leu Trp  
1 5 10 15  
Lys Val Leu Ile Phe Arg Tyr Leu Lys Thr Thr Val Phe Cys Thr Leu  
20 25 30

Ser	Leu	Ile	Cys	Ile	Ser	Ile	Ile	Ser	Ser	Leu	Gln	Glu	Ile	Val	Ser
		35					40					45			
Tyr	Ile	Ala	Lys	Asp	Val	Pro	Tyr	Ala	Thr	Val	Phe	Lys	Val	Thr	Ala
	50					55					60				
Tyr	Gln	Ile	Pro	Tyr	Leu	Leu	Pro	Phe	Ile	Leu	Pro	Ala	Ser	Cys	Phe
65					70					75					80
Ile	Ser	Ala	Phe	Thr	Leu	Phe	Arg	Lys	Leu	Ser	Asp	Asn	Asn	Gln	Ile
				85					90					95	
Thr	Phe	Leu	Lys	Ala	Ser	Gly	Ala	Ser	Gln	Gly	Met	Ile	Ile	Phe	Pro
			100					105					110		
Val	Leu	Ile	Ala	Ser	Gly	Val	Leu	Cys	Cys	Phe	Asn	Phe	Tyr	Thr	Cys
		115					120					125			
Ser	Glu	Leu	Ala	Ser	Ile	Cys	Arg	Phe	Gln	Thr	Gly	Lys	Ala	Ile	Ala
	130					135					140				
Asn	Ile	Ala	Met	Thr	Ser	Pro	Ala	Leu	Leu	Leu	Gln	Thr	Leu	Gln	Lys
145					150					155					160
Lys	Glu	Asn	Asp	Arg	Ile	Phe	Ile	Ala	Ile	Asp	His	Cys	Gly	Lys	Ser
				165						170					175
Lys	Phe	Asp	Asn	Val	Ile	Ile	Ala	Leu	Lys	His	Asn	Gln	Glu	Ile	Ser
			180					185					190		
Asn	Ile	Gly	Phe	Ile	Glu	Thr	Ile	Ile	Pro	Asp	Val	Asn	Lys	Asp	Ser
		195					200					205			
Val	Gln	Ala	Lys	Asn	Val	Leu	Val	Ile	Ser	Lys	Ile	Pro	Leu	Phe	Ser
	210					215					220				
Glu	Ala	Arg	Thr	Ser	Asn	Pro	Asn	Glu	Phe	Tyr	Leu	Glu	Thr	Leu	Asp
225					230					235					240
Glu	Phe	Leu	Ile	Pro	Lys	Ile	Thr	Ala	Thr	Leu	Phe	Ala	Gly	Lys	Ser
				245					250					255	
Tyr	Met	Lys	Thr	Arg	Thr	Asp	Tyr	Leu	Pro	Trp	Lys	Gln	Leu	Ile	Gln
			260					265					270		
Asp	Ala	Arg	Leu	His	Leu	Ala	Glu	Ile	Leu	Arg	Arg	Ile	Ala	Ile	Gly
		275					280					285			
Leu	Leu	Cys	Ser	Thr	Met	Thr	Phe	Ser	Gly	Leu	Ala	Leu	Gly	Thr	Tyr
	290					295					300				
Lys	Pro	Arg	Phe	Arg	Lys	Pro	Val	Leu	Ile	Tyr	Ala	Leu	Phe	Pro	Ile
305					310					315					320
Leu	Asn	Leu	Ile	Phe	Leu	Ile	Val	Gly	Lys	Asn	Thr	Ile	His	Pro	Ile
				325					330					335	
Ser	Ala	Val	Met	Leu	Phe	Leu	Phe	Pro	Gln	Leu	Leu	Ser	Trp	Leu	Ile
			340					345					350		
Phe	Ser	Trp	Arg	Ile	Tyr	Thr	Glu	Asn	Gln	Gly	His	Ala			
		355					360					365			

(2) INFORMATIONS POUR LA SEQ ID NO: 536:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 116 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 525731..526078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 536:

Lys Ser Arg Ala Cys Ile Asp Met Val Ile Trp Lys Arg Tyr Leu Leu

```

1           5           10           15
Ser Arg Phe Trp Ile Ser Leu Ser Ser Leu Phe Phe Leu Ala Val Ile
                20           25           30
Phe Tyr Ala Ser Ile His His Ser Leu His Ala Phe Arg Glu Gly Lys
                35           40           45
Thr Ala Ile Ala Gly Ala Pro Leu Gln Leu Ser Leu Leu Tyr Tyr Leu
                50           55           60
Ser Gln Ile Ser Leu Lys Ala Glu Phe Ile Leu Pro Thr Thr Arg Cys
65           70           75           80
Asn Cys Phe Asp Asn Tyr Thr Ile Phe His Ala Glu Gln Lys Arg Asn
                85           90           95
Ser Ile Thr Ala Gly Phe Arg Ala Phe Pro Glu Asn Phe Xaa Thr Ser
                100           105           110
Thr Ser Tyr Ile
                115

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 537:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 525939..526400

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 537:

```

Lys Gln Asn Ser Phe Ser Leu Gln Leu Val Ala Ile Ala Ser Thr Ile
1           5           10           15
Thr Leu Phe Ser Met Gln Ser Lys Arg Glu Ile Leu Leu Leu Gln Ala
                20           25           30
Ser Gly Leu Ser Leu Lys Thr Leu Xaa Arg Pro Leu Val Ile Ser Ser
                35           40           45
Ser Leu Ile Thr Leu Leu Leu Tyr Ala Asn Phe Gln Trp Leu His Pro
50           55           60
Ile Cys Glu Lys Ile Ser Val Thr Lys Glu His Met Asp Lys Gly Thr
65           70           75           80
Leu Glu Lys Ala Gln Glu Lys Ile Pro Ala Leu Tyr Leu Lys Asp Gln
                85           90           95
Thr Val Leu Ile Phe Ser Ser Ile Asn Arg Arg Ala Ala Thr Leu Asn
                100           105           110
Asn Val Phe Trp Ile Lys Gly Pro Lys Thr Ile Tyr Ala Ile Lys Lys
                115           120           125
Leu Ala Phe Thr Thr Pro Ser Leu Leu Ser Gly Leu Lys Cys Pro Ile
130           135           140
Phe Pro Lys Met Lys Ile Thr Lys Cys Leu
145           150

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 538:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 526301..526735

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 538:

```

Asn Asp Leu Cys Asn Gln Lys Thr Cys Ile Tyr Tyr Ser Ile Ala Pro
1      5      10      15
Ile Gly Leu Glu Val Ser Tyr Phe Ser Glu Asp Glu Asn His Glu Val
      20      25      30
Ser Leu Thr Gln Phe Phe Asp Met Lys Glu Phe Pro Glu Leu Glu Phe
      35      40      45
Ser Tyr Tyr Asp Asn Pro Phe Ser Lys Ile Phe Ile Thr Gly Arg Asp
      50      55      60
Cys Ser Phe Ser Ala Phe Leu Gln Ala Ile Pro Trp His Ala Ala Lys
65      70      75      80
Phe Gly Leu Leu Thr Thr Val Pro Gln Arg Ile Leu Ser Leu Leu Thr
      85      90      95
Leu Phe Tyr Tyr Met Leu Ile Ser Pro Leu Leu Cys Ile Ala Ala Val
      100      105      110
Ile Leu Ser Ala His Leu Cys Leu Arg Phe His Arg Leu Pro Lys Ile
      115      120      125
Thr Trp Ala Tyr Leu Val Leu Trp Glu Pro Leu Ile Phe Ser Leu Leu
      130      135      140
Phe
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 539:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 491 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(526851..528323)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 539:

```

Arg Lys Leu Ser Ile Ser Xaa Gly Lys Ile His Glu Ser Met His Glu
1      5      10      15
Asn Asp Pro Leu Thr Lys Thr Ile Val Trp Asn Ser Asp Glu Ile Thr
      20      25      30
Lys Leu Ala Ser Ser Leu Val Tyr Thr Asn Asp Met Pro Ile Arg Leu
      35      40      45
Phe Tyr Gln Lys Ala Leu Thr Asn Met Ser Ala Glu Leu Thr Val Asn
      50      55      60
Val His Asn Ala Leu Met Ala Leu Phe Leu Ala Arg Tyr Glu Ala Thr
65      70      75      80
Ala Val Ser Gln Gln Pro Arg Lys Glu Asn Leu Ser Tyr Phe Asn Asp
      85      90      95
Phe Leu His Phe Leu Arg Lys Ala Ala Leu Leu Asn Glu Lys Asp
      100      105      110
Leu Leu Asp Leu Gln Glu Lys His Ser Lys Ser Leu Val Ser Ser Leu

```

(2) INFORMATION POUR LA SEQ ID NO: 540:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(528292..528861)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 540:

Lys	Asp	Tyr	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Gly	Met	Glu	Lys	Thr	Arg
1				5					10					15	
Lys	Phe	Glu	Lys	Ala	Leu	Glu	Asn	Leu	Glu	Gln	Leu	Lys	Lys	Ile	Ser
			20					25					30		
Tyr	Asp	Tyr	Ser	Ser	Gly	Asn	Ala	Glu	Ala	Ser	Ser	His	Asn	Lys	Ala
			35				40					45			
Leu	Ser	Glu	Met	Lys	Lys	Ala	Met	His	Tyr	Ile	Asp	His	Tyr	Phe	Lys
	50					55					60				
Gln	Ala	Gly	Ala	Leu	Ser	Gln	Lys	Asp	Val	Asp	Lys	Val	Ile	Lys	Glu
65					70				75						80
Thr	Asp	Phe	Leu	Ile	Ala	Gly	Val	Gln	Asp	Val	Phe	Ser	Phe	Leu	Glu
				85					90					95	
Asp	Arg	Lys	Glu	Glu	Val	Tyr	Arg	Ser	Leu	Ser	Gln	Asp	Tyr	Arg	His
			100					105					110		
Leu	Asn	His	Thr	Tyr	Asp	Val	Thr	Arg	Glu	His	Leu	Asn	Asn	Lys	Met
			115				120					125			
Val	Glu	Pro	Lys	Glu	Ile	Leu	Asn	Gly	Ser	Leu	Glu	Asn	Cys	Gln	Asp
	130					135					140				
Arg	Glu	Glu	Phe	Leu	Asn	Asn	Leu	Val	Glu	Val	Lys	Arg	Asp	Arg	Ser
145					150					155					160
Tyr	Glu	Leu	Phe	Tyr	Met	Ala	Asn	Glu	Asp	Asn	Lys	Arg	Phe	Tyr	Thr
				165					170					175	
Asp	Ala	Leu	Ala	Gln	Ile	Ile	Tyr	Lys	Xaa	Arg	Glu	Asp	Pro		
			180					185					190		

(2) INFORMATIONS POUR LA SEQ ID NO: 541:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(529142..529723)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 541:

Phe	Arg	Arg	Arg	Ser	Ser	Cys	Ser	Thr	Asp	Ala	Gly	Tyr	Phe	Leu	Phe
1				5					10					15	
Gly	Ser	His	His	Gly	Leu	Gly	Ser	Ala	Pro	Leu	Asp	Phe	Ala	Ser	Arg
			20					25					30		
Glu	Leu	Ala	Arg	Asn	Lys	Pro	Pro	Val	Arg	Ile	Val	Ala	Pro	Gly	Glu
		35				40						45			
Cys	Phe	Arg	Asn	Glu	Asp	Val	Ser	Ala	Arg	Ser	His	Val	Ile	Phe	His
	50					55					60				
Gln	Val	Glu	Ala	Phe	Cys	Val	Asp	Lys	Asp	Ile	Ser	Phe	Ser	Asp	Leu
65					70					75					80
Thr	Ser	Met	Leu	Ala	Gly	Phe	Tyr	His	Ile	Phe	Phe	Gly	Arg	Lys	Val
				85					90					95	
Glu	Leu	Arg	Phe	Arg	His	Ser	Tyr	Phe	Pro	Phe	Val	Glu	Pro	Gly	Ile
			100					105					110		
Glu	Val	Asp	Ile	Ser	Cys	Glu	Cys	His	Gly	Ala	Gly	Cys	Ser	Leu	Cys

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 542:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire.

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(529624..530166)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 542:

[illegible]

(2) INFORMATIONN POUR LA SEQ ID NO: 543:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(530223..530543)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 543:

```

Met Val Arg Ala Thr Gly Ser Val Ala Ser Arg Ser Arg Arg Lys Arg
1          5          10          15
Val Leu Lys Gln Ala Lys Gly Phe Trp Gly Asp Arg Lys Gly His Phe
          20          25          30
Arg Gln Ser Arg Ser Ser Val Met Arg Ala Met Ala Phe Asn Tyr Met
          35          40          45
His Arg Lys Asp Arg Lys Gly Asp Phe Arg Ser Leu Trp Ile Thr Arg
          50          55          60
Leu Asn Val Ala Ser Arg Ile His Gly Leu Ser Tyr Ser Arg Leu Ile
65          70          75          80
Asn Gly Leu Lys Gln Ala Gly Ile His Leu Xaa Glu Lys Cys Cys Leu
          85          90          95
Arg Trp Leu Phe Met Thr Leu Lys Gly Leu Leu
          100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 544:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(530737..531378)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 544:

```

Glu Lys Ser Leu Phe Leu Gly Lys Gly Gly Leu Trp Phe Phe Leu Gly
1          5          10          15
Ser Pro Ser Ala Ile Thr Asn Phe Ser Arg Val Asp Val Ala Leu Asn
          20          25          30
Leu Arg Ile Asn Arg Gln Ile Arg Ala Pro Arg Val Arg Val Ile Gly
          35          40          45
Ser Ala Gly Glu Gln Leu Gly Ile Leu Ser Ile Lys Glu Ala Leu Asp
          50          55          60
Leu Ala Lys Glu Ala Asp Leu Asp Leu Val Glu Val Ala Ser Asn Ser
65          70          75          80
Glu Pro Pro Val Cys Lys Ile Met Asp Tyr Gly Lys Tyr Arg Tyr Asp
          85          90          95
Ile Thr Lys Lys Glu Lys Asp Ser Lys Lys Ala Gln His Gln Val Arg
          100          105          110
Ile Lys Glu Val Lys Leu Lys Pro Asn Ile Asp Asp Asn Asp Xaa Leu
          115          120          125
Thr Lys Ala Lys Gln Ala Arg Ala Phe Ile Glu Lys Gly Asn Lys Val
          130          135          140
Lys Val Ser Cys Met Phe Arg Gly Arg Glu Leu Ala Tyr Pro Glu His
145          150          155          160
Gly His Lys Val Val Gln Arg Met Cys Gln Gly Leu Glu Asp Ile Gly

```



```

                165                170                175
Phe Val Glu Ser Glu Pro Lys Leu Asn Gly Arg Ser Leu Ile Cys Val
                180                185                190
Ile Ala Pro Gly Thr Leu Lys Thr Lys Lys Lys Gln Glu Lys Val His
                195                200                205
Ala Gln Asp Glu Lys Gln
                210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 545:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 301 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 532370..533272

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 545:

```

Met Thr Asp Ser Phe Pro Phe Ser Val Gln Glu Ser Val Pro Leu Ser
1      5      10      15
Arg Phe Ser Thr Phe Arg Ile Gly Gly Pro Ala Arg Tyr Phe Lys Glu
      20      25      30
Leu Thr Ser Leu Ser Glu Ala Leu Thr Val Phe Ser Tyr Leu His Thr
      35      40      45
His Pro Leu Pro Tyr Ile Ile Gly Lys Gly Ser Asn Cys Leu Phe
      50      55      60
Asp Asp Gln Gly Phe Asp Gly Leu Val Leu Tyr Asn Asn Ile Gln Gly
65      70      75      80
Gln Glu Phe Leu Ser Asp Thr Gln Ile Lys Val Leu Ser Gly Ser Ser
      85      90      95
Phe Ala Leu Leu Gly Lys Arg Leu Ser Ser Gln Gly Phe Ser Gly Leu
      100     105     110
Glu Phe Ala Val Gly Ile Pro Gly Thr Val Gly Gly Ala Val Phe Met
      115     120     125
Asn Ala Gly Thr Thr Leu Ala Asn Thr Ala Ser Ser Leu Ile Asn Val
      130     135     140
Glu Ile Ile Asp His Ser Gly Ile Leu Leu Ser Ile Pro Arg Glu Lys
145     150     155     160
Leu Leu Phe Ser Tyr Arg Thr Ser Pro Phe Gln Lys Lys Pro Ala Phe
      165     170     175
Ile Ala Ser Ala Thr Phe Gln Leu Thr Lys Asp Pro Gln Ala Ala Lys
      180     185     190
Arg Ala Lys Ala Leu Ile Glu Glu Arg Ile Leu Lys Gln Pro Tyr Glu
      195     200     205
Tyr Pro Ser Ala Gly Cys Ile Phe Arg Asn Pro Glu Gly Leu Ser Ala
      210     215     220
Gly Ala Leu Ile Asp Arg Ala Gly Leu Lys Gly Leu Lys Ile Gly Gly
225     230     235     240
Gly Gln Ile Ser Glu Lys His Gly Asn Phe Ile Ile Asn Thr Gly Asn
      245     250     255
Ala Cys Thr Ala Asp Ile Leu Glu Leu Ile Glu Ile Ile Gln Lys Ile
      260     265     270
Leu Lys Asn Lys Val Phe Pro Tyr Ile Lys Lys Ser Val Ser Ser Pro
      275     280     285

```

Phe Ala Ser Ser Leu Val Val Cys Glu Lys Glu Ile Thr  
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 546:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 187 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(533244..533804)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 546:

Ile	Leu	Phe	Ser	Asn	Ile	Ile	Lys	Leu	Ser	His	Ser	Ile	Phe	Arg	Gln
1				5					10					15	
Val	Val	Glu	Pro	Gly	Asp	Thr	Ile	Val	Asp	Ala	Thr	Cys	Gly	Asn	Gly
			20					25					30		
Lys	Asp	Ala	Leu	Phe	Leu	Ala	Gln	Leu	Leu	Arg	Gly	Lys	Gly	Arg	Leu
		35					40					45			
Val	Val	Tyr	Asp	Ile	Gln	Gln	Glu	Ala	Leu	Asp	Arg	Ala	Thr	Ala	Asn
	50					55				60					
Phe	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Glu	Arg	Ala	Ile	Ile	Glu	Met	Lys
65					70				75					80	
Leu	Cys	Ser	His	Glu	Tyr	Leu	Gln	Glu	Gln	Gly	Ala	Lys	Leu	Phe	His
			85						90				95		
Tyr	Asn	Leu	Gly	Tyr	Leu	Pro	Ser	Gly	Asp	Lys	Gln	Ile	Thr	Thr	Cys
		100						105					110		
Ser	Glu	Ser	Thr	Val	Thr	Ser	Ile	Tyr	Lys	Ala	Leu	Glu	Leu	Val	Ala
		115					120					125			
Pro	Ser	Gly	Ile	Val	Ser	Val	Val	Cys	Tyr	Pro	Gly	His	Gln	Glu	Gly
	130					135					140				
Ala	Ala	Glu	Leu	Cys	Cys	Val	Glu	Gln	Val	Ala	Thr	Glu	Leu	Asp	Pro
145					150					155				160	
Ser	Met	Trp	Glu	Val	Cys	Thr	His	Tyr	Ser	Val	Asn	Arg	Arg	Asn	Ala
			165						170					175	
Pro	Arg	Leu	Phe	Leu	Phe	Arg	Arg	Arg	Gln	Gly					
		180						185							

(2) INFORMATIONS POUR LA SEQ ID NO: 547:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 243 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(533944..534672)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 547:

Ser Gly Glu Val Trp Gly Trp Ser Arg Cys Ser Leu Ser His Thr Lys

1				5					10					15			
Tyr	Phe	Pro	Val	Lys	Pro	Gln	Asp	Leu	Lys	Leu	Pro	Tyr	Phe	Trp	Glu		
			20					25					30				
Glu	Arg	Ser	Pro	Gln	Ile	Ala	Asn	His	Val	Phe	Tyr	Val	Pro	Asn	Tyr		
		35					40					45					
Tyr	Ser	Arg	Tyr	Glu	Glu	Phe	Val	Ile	Pro	Thr	Trp	Gln	Glu	Leu	Phe		
	50					55				60							
Ala	Asn	Asn	Gly	Pro	Ile	Cys	Cys	Glu	Leu	Cys	Ser	Gly	Asn	Gly	Asp		
65					70					75					80		
Trp	Val	Val	Glu	Gln	Ala	Leu	Lys	Asp	Ala	Ser	Val	Asn	Trp	Ile	Ala		
			85						90					95			
Val	Glu	Lys	Arg	Phe	Asp	Arg	Val	Arg	Lys	Ile	Trp	Ser	Lys	Met	Gly		
		100						105					110				
Thr	Tyr	Arg	Val	Asn	Asn	Leu	Leu	Ile	Val	Cys	Gly	Glu	Ala	Gln	Thr		
		115						120				125					
Phe	Phe	Ser	His	Tyr	Val	Ser	Asp	Ala	Ser	Phe	Gln	Lys	Ile	Val	Val		
	130					135				140							
Asn	Phe	Pro	Asp	Pro	Trp	Pro	Lys	Phe	Arg	His	Arg	Lys	His	Arg	Leu		
145					150					155					160		
Phe	Gln	Asp	Leu	Phe	Val	Gln	Asp	Met	Met	Arg	Thr	Leu	Val	Val	Gly		
			165						170					175			
Gly	Gln	Leu	Thr	Leu	Ala	Thr	Asp	Asp	Tyr	Asn	Tyr	Leu	Val	Asn	Ala		
		180						185				190					
Ile	Thr	Val	Met	Leu	Lys	Tyr	Leu	Ser	Pro	Gly	Leu	Lys	Ser	Pro	His		
	195							200				205					
Tyr	Ile	Asn	Val	Lys	Asp	Asn	Tyr	Gly	Gly	Ser	Trp	Phe	Glu	Asn	Leu		
	210					215				220							
Trp	Arg	Ser	Lys	Gly	Gln	Glu	Ile	Phe	Cys	Thr	Glu	Phe	Ile	Lys	Arg		
225					230					235					240		
Val	Gly	Ile															

(2) INFORMATIONS POUR LA SEQ ID NO: 548:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(534878..535915)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 548:

Met	Gln	Ala	Asp	Ile	Leu	Asp	Gly	Lys	Gln	Lys	Arg	Val	Asn	Leu	Asn		
1				5				10					15				
Ser	Lys	Arg	Leu	Val	Asn	Cys	Asn	Gln	Val	Asp	Val	Asn	Gln	Leu	Val		
		20						25					30				
Pro	Ile	Lys	Tyr	Lys	Trp	Ala	Trp	Glu	His	Tyr	Leu	Asn	Gly	Cys	Ala		
		35					40					45					
Asn	Asn	Trp	Leu	Pro	Thr	Glu	Ile	Pro	Met	Gly	Lys	Asp	Ile	Glu	Leu		
	50					55				60							
Trp	Lys	Ser	Asp	Arg	Leu	Ser	Glu	Asp	Glu	Arg	Arg	Val	Ile	Leu	Leu		
65					70					75					80		
Asn	Leu	Gly	Phe	Phe	Ser	Thr	Ala	Glu	Ser	Leu	Val	Gly	Asn	Asn	Ile		
			85					90					95				

Val	Leu	Ala	Ile	Phe	Lys	His	Val	Thr	Asn	Pro	Glu	Ala	Arg	Gln	Tyr
			100					105					110		
Leu	Leu	Arg	Gln	Ala	Phe	Glu	Glu	Ala	Val	His	Thr	His	Thr	Phe	Leu
		115					120					125			
Tyr	Ile	Cys	Glu	Ser	Leu	Gly	Leu	Asp	Glu	Lys	Glu	Ile	Phe	Asn	Ala
	130					135					140				
Tyr	Asn	Glu	Arg	Ala	Ala	Ile	Lys	Ala	Lys	Asp	Asp	Phe	Gln	Met	Glu
145					150					155					160
Ile	Thr	Gly	Lys	Val	Leu	Asp	Pro	Asn	Phe	Arg	Thr	Asp	Ser	Val	Glu
				165					170					175	
Gly	Leu	Gln	Glu	Phe	Val	Lys	Asn	Leu	Val	Gly	Tyr	Tyr	Ile	Ile	Met
		180						185					190		
Glu	Gly	Ile	Phe	Phe	Tyr	Ser	Gly	Phe	Val	Met	Ile	Leu	Ser	Phe	His
	195						200					205			
Arg	Gln	Asn	Lys	Met	Ile	Gly	Ile	Gly	Glu	Gln	Tyr	Gln	Tyr	Ile	Leu
	210					215					220				
Arg	Asp	Glu	Thr	Ile	His	Leu	Asn	Phe	Gly	Ile	Asp	Leu	Ile	Asn	Gly
225					230					235					240
Ile	Lys	Glu	Glu	Asn	Pro	Glu	Ile	Trp	Thr	Pro	Glu	Leu	Gln	Gln	Glu
				245					250					255	
Ile	Val	Glu	Leu	Ile	Lys	Arg	Ala	Val	Asp	Leu	Glu	Ile	Glu	Tyr	Ala
		260						265					270		
Gln	Asp	Cys	Leu	Pro	Arg	Gly	Ile	Leu	Gly	Leu	Arg	Ala	Ser	Met	Phe
	275					280						285			
Ile	Asp	Tyr	Val	Gln	His	Ile	Ala	Asp	Arg	Arg	Leu	Glu	Arg	Ile	Gly
	290					295					300				
Leu	Lys	Pro	Ile	Tyr	His	Thr	Lys	Asn	Pro	Phe	Pro	Trp	Met	Ser	Glu
305					310					315					320
Thr	Ile	Asp	Leu	Asn	Lys	Glu	Lys	Asn	Phe	Phe	Glu	Thr	Arg	Asp	Thr
			325						330					335	
Glu	Tyr	Gln	His	Ala	Ala	Ser	Leu	Thr	Trp						
		340						345							

(2) INFORMATIONS POUR LA SEQ ID NO: 549:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1066 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(535956..539153)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 549:

Arg	Arg	Leu	Cys	Phe	Lys	Ile	Glu	Asn	Asn	Ala	Tyr	Ser	Met	Phe	Thr
1			5					10					15		
Arg	Ile	Val	Met	Val	Asp	Leu	Gln	Glu	Lys	Gln	Cys	Thr	Ile	Val	Lys
		20						25					30		
Arg	Asn	Gly	Met	Phe	Val	Pro	Phe	Asp	Arg	Asn	Arg	Ile	Phe	Gln	Ala
	35						40					45			
Leu	Glu	Ala	Ala	Phe	Arg	Asp	Thr	Arg	Arg	Ile	Asp	Asp	His	Met	Pro
	50					55					60				
Leu	Pro	Glu	Asp	Leu	Glu	Ser	Ser	Ile	Arg	Ser	Ile	Thr	His	Gln	Val
65					70					75				80	
Val	Lys	Glu	Val	Val	Gln	Lys	Ile	Thr	Asp	Gly	Gln	Val	Val	Thr	Val

				85					90					95		
Glu	Arg	Ile	Gln	Asp	Met	Val	Glu	Ser	Gln	Leu	Tyr	Val	Asn	Gly	Leu	
			100					105					110			
Gln	Asp	Val	Ala	Arg	Asp	Tyr	Ile	Val	Tyr	Arg	Asp	Asp	Arg	Lys	Ala	
		115					120					125				
His	Arg	Lys	Lys	Ser	Trp	Gln	Ser	Leu	Ser	Val	Val	Arg	Arg	Cys	Gly	
	130					135					140					
Thr	Val	Val	His	Phe	Asn	Pro	Met	Lys	Ile	Ser	Ala	Ala	Leu	Glu	Lys	
145				150						155					160	
Ala	Phe	Arg	Ala	Thr	Asp	Lys	Thr	Glu	Gly	Met	Thr	Pro	Ser	Ser	Val	
			165						170						175	
Arg	Glu	Glu	Ile	Asn	Ala	Leu	Thr	Gln	Asn	Ile	Val	Ala	Glu	Ile	Glu	
			180					185					190			
Glu	Cys	Cys	Ser	Gln	Gln	Asp	Arg	Arg	Ile	Asp	Ile	Glu	Lys	Ile	Gln	
	195						200					205				
Asp	Ile	Val	Glu	Gln	Gln	Leu	Met	Val	Val	Gly	His	Tyr	Ala	Ile	Ala	
	210					215					220					
Lys	Asn	Tyr	Ile	Leu	Tyr	Arg	Glu	Ala	Arg	Ala	Arg	Val	Arg	Asp	Asn	
225				230						235					240	
Arg	Glu	Glu	Asp	Gly	Ser	Thr	Glu	Lys	Thr	Ile	Ala	Glu	Glu	Ala	Phe	
			245						250					255		
Glu	Val	Leu	Ser	Lys	Asp	Gly	Ser	Thr	Tyr	Thr	Met	Thr	His	Ser	Gln	
			260					265					270			
Leu	Leu	Ala	His	Leu	Ala	Arg	Ala	Cys	Ser	Arg	Phe	Pro	Glu	Thr	Thr	
		275					280					285				
Asp	Ala	Ala	Leu	Leu	Thr	Asp	Met	Ala	Phe	Ala	Asn	Phe	Tyr	Ser	Gly	
	290				295						300					
Ile	Lys	Glu	Ser	Glu	Val	Val	Leu	Ala	Cys	Ile	Met	Ala	Ala	Arg	Ala	
305				310						315					320	
Asn	Ile	Glu	Lys	Glu	Pro	Asp	Tyr	Ala	Leu	Val	Ala	Ala	Glu	Leu	Leu	
			325						330					335		
Leu	Asp	Val	Val	Tyr	Lys	Glu	Ala	Leu	Gly	Lys	Ser	Lys	Tyr	Ala	Glu	
		340						345					350			
Asp	Leu	Glu	Gln	Ala	His	Arg	Asp	His	Phe	Lys	Arg	Tyr	Ile	Ala	Glu	
	355						360					365				
Gly	Asp	Thr	Tyr	Arg	Leu	Asn	Ala	Glu	Leu	Lys	His	Leu	Phe	Asp	Leu	
	370				375						380					
Asp	Ala	Leu	Ala	Asp	Ala	Met	Asp	Leu	Ser	Arg	Asp	Leu	Gln	Phe	Ser	
385				390						395					400	
Tyr	Met	Gly	Ile	Gln	Asn	Leu	Tyr	Asp	Arg	Tyr	Phe	Asn	His	His	Glu	
			405						410							

Trp	His	Leu	Asp	Tyr	Glu	Asp	Phe	Leu	Glu	Leu	Arg	Lys	Asn	Thr	Gly
				565					570					575	
Asp	Glu	Arg	Arg	Arg	Ala	His	Asp	Val	Asn	Thr	Ala	Ser	Trp	Ile	Pro
			580					585					590		
Asp	Leu	Phe	Phe	Lys	Arg	Leu	Gln	Gln	Lys	Gly	Thr	Trp	Thr	Leu	Phe
		595					600					605			
Ser	Pro	Asp	Asp	Val	Pro	Gly	Leu	His	Asp	Ala	Tyr	Gly	Glu	Glu	Phe
	610					615					620				
Glu	Arg	Leu	Tyr	Glu	Glu	Tyr	Glu	Arg	Lys	Val	Asp	Thr	Gly	Glu	Ile
625					630					635					640
Arg	Leu	Phe	Lys	Lys	Val	Glu	Ala	Glu	Asp	Leu	Trp	Arg	Lys	Met	Leu
				645					650					655	
Ser	Met	Val	Phe	Glu	Thr	Gly	His	Pro	Trp	Met	Thr	Phe	Lys	Asp	Pro
			660					665					670		
Ser	Asn	Ile	Arg	Ser	Ala	Gln	Asp	His	Lys	Gly	Val	Val	Arg	Cys	Ser
		675					680					685			
Asn	Leu	Cys	Thr	Glu	Ile	Leu	Leu	Asn	Cys	Ser	Glu	Thr	Glu	Thr	Ala
	690					695					700				
Val	Cys	Asn	Leu	Gly	Ser	Ile	Asn	Leu	Val	Gln	His	Ile	Val	Gly	Asp
705					710					715					720
Gly	Leu	Asp	Glu	Glu	Lys	Leu	Ser	Glu	Thr	Ile	Ser	Ile	Ala	Val	Arg
				725					730					735	
Met	Leu	Asp	Asn	Val	Ile	Asp	Ile	Asn	Phe	Tyr	Pro	Thr	Lys	Glu	Ala
			740					745					750		
Lys	Glu	Ala	Asn	Phe	Ala	His	Arg	Ala	Ile	Gly	Leu	Gly	Val	Met	Gly
		755					760					765			
Phe	Gln	Asp	Ala	Leu	Tyr	Lys	Leu	Asp	Ile	Ser	Tyr	Ala	Ser	Gln	Glu
	770					775					780				
Ala	Val	Glu	Phe	Ala	Asp	Tyr	Ser	Ser	Glu	Leu	Ile	Ser	Tyr	Tyr	Ala
785					790					795					800
Ile	Gln	Ala	Ser	Cys	Leu	Leu	Ala	Lys	Glu	Arg	Gly	Thr	Tyr	Ser	Ser
				805					810					815	
Tyr	Lys	Gly	Ser	Lys	Trp	Asp	Arg	Gly	Leu	Leu	Pro	Ile	Asp	Thr	Ile
			820					825					830		
Gln	Leu	Leu	Ala	Asn	Tyr	Arg	Gly	Glu	Ala	Asn	Leu	Gln	Met	Asp	Thr
		835					840					845			
Ser	Ser	Arg	Lys	Asp	Trp	Glu	Pro	Ile	Arg	Ser	Leu	Val	Lys	Glu	His
	850					855					860				
Gly	Met	Arg	His	Cys	Gln	Leu	Met	Ala	Ile	Ala	Pro	Thr	Ala	Thr	Ile
865					870					875					880
Ser	Asn	Ile	Ile	Gly	Val	Thr	Gln	Ser	Ile	Glu	Pro	Thr	Tyr	Lys	His
				885					890					895	
Leu	Phe	Val	Lys	Ser	Asn	Leu	Ser	Gly	Glu	Phe	Thr	Ile	Pro	Asn	Val
			900					905					910		
Tyr	Leu	Ile	Glu	Lys	Leu	Lys	Lys	Leu	Gly	Ile	Trp	Asp	Ala	Asp	Met
		915					920					925			
Leu	Asp	Asp	Leu	Lys	Tyr	Phe	Asp	Gly	Ser	Leu	Leu	Glu	Ile	Glu	Arg
	930					935					940				
Ile	Pro	Asp	His	Leu	Lys	His	Ile	Phe	Leu	Thr	Ala	Phe	Glu	Ile	Glu
945					950					955					960
Pro	Glu	Trp	Ile	Ile	Glu	Cys	Ala	Ser	Arg	Arg	Gln	Lys	Trp	Ile	Asp
				965					970					975	
Met	Gly	Gln	Ser	Leu	Asn	Leu	Tyr	Leu	Ala	Gln	Pro	Asp	Gly	Lys	Lys
			980					985					990		
Leu	Ser	Asn	Met	Tyr	Leu	Thr	Ala	Trp	Lys	Lys	Gly	Leu	Lys	Thr	Thr
		995					1000					1005			
Tyr	Tyr	Leu	Arg	Ser	Ser	Ser	Ala	Thr	Thr	Val	Glu	Lys	Ser	Phe	Val
	1010					1015					1020				
Asp	Ile	Asn	Lys	Arg	Gly	Ile	Gln	Pro	Arg	Trp	Met	Lys	Asn	Lys	Ser

```

1025          1030          1035          1040
Ala Ser Ala Gly Ile Val Glu Arg Ala Lys Lys Ala Pro Val Cys
          1045          1050          1055
Ser Leu Glu Glu Gly Cys Glu Ala Cys Gln
          1060          1065

```

(2) INFORMATIONS POUR LA SEQ ID NO: 550:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 247 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 539779..540519

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 550:

```

Pro Asn Ala Ile Thr Ala Phe Gly Leu Cys Cys Gly Leu Phe Ile Ile
1          5          10          15
Phe Lys Ser Val Leu Lys Thr Ser Ser Ser Leu Glu Leu Met His Arg
          20          25          30
Leu Gln Gly Leu Ser Leu Leu Leu Ile Ser Ala Met Ile Ala Asp Phe
          35          40          45
Ser Asp Gly Ala Val Ala Arg Ile Met Lys Ala Glu Ser Ala Phe Gly
50          55          60
Ala His Phe Asp Ser Leu Ser Asp Ala Ile Thr Phe Gly Ile Ala Pro
65          70          75          80
Pro Leu Ile Ala Ile Lys Ser Leu Asn Gly Glu Tyr Gly Gly Thr Phe
          85          90          95
Cys Ser Ser Phe Leu Leu Val Thr Cys Ile Ile Tyr Ser Leu Cys Gly
          100          105          110
Val Leu Arg Leu Val Arg Tyr Asn Leu Phe Ala Ala Thr Gly Glu Lys
          115          120          125
Ala Thr Thr Phe Thr Gly Leu Pro Ile Pro Ala Ala Ala Ala Cys Val
130          135          140
Val Ser Leu Gly Val Leu Leu Ala Ser Asp Thr Leu Asn Ser Leu Pro
145          150          155          160
Glu Arg Ala Arg Val Leu Leu Val Ser Leu Gly Leu Leu Leu Ser Gly
          165          170          175
Cys Leu Met Ile Ser Thr Trp Arg Phe Pro Gly Leu Lys His Phe His
          180          185          190
Phe Arg Val Ser Ser Ser Leu Leu Val Leu Gly Ile Gly Leu Val Ala
          195          200          205
Cys Leu Phe Phe Ser Gly Leu Val Asp His Phe Thr Gln Val Phe Xaa
210          215          220
Leu Val Ser Trp Leu Tyr Val Leu Val Val Ala Pro Val Phe Pro Phe
225          230          235          240
Ile Asn Lys Arg Ser Ser Ser
          245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 551:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 149 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 540523..540969

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 551:

```

Tyr Met Gly Val Phe Ala Ile Ser Leu Leu Ser Gln Thr Val Cys Leu
1      5      10      15
Tyr Phe Thr Phe Phe Ser Leu Gly Ile Ala Leu Gly Val Leu Phe Ser
20      25      30
Phe Lys Ile Phe Thr Lys Lys Leu Ser Arg Gln Tyr Glu Ile Ile Arg
35      40      45
Asp Leu Glu His Ser Lys Ala Ile Leu Gln Met Ser Leu Asp Thr Arg
50      55      60
Arg Ser Gln Glu Gln Ile Met Glu Glu Phe Ser His Lys Leu Thr Ser
65      70      75      80
Val Ser Gln Ala Phe Ala Arg Asp Met Lys Thr Glu Ser Gln Glu Phe
85      90      95
Phe Ser Glu Lys Thr Gln Ala Ile Thr Ser Val Leu Ala Pro Val His
100     105     110
Asn Thr Leu Ser Ala Phe Lys Gln Asn Leu Glu Asn Phe Glu Thr Lys
115     120     125
Gln Ala Glu Asp Arg Gly Val Ser Lys Asn Asn Ser Leu Asn Tyr Ser
130     135     140
Leu Gln Asn Arg Ser
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 552:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 300 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 540906..541805

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 552:

```

Ala Ser Arg Arg Pro Arg Ser Leu Lys Glu Gln Leu Ser Gln Leu Leu
1      5      10      15
Thr Ala Glu Gln Lys Leu Glu Arg Glu Thr Gln Ala Leu Thr Asn Ile
20      25      30
Leu Lys His Pro Gly Ser Arg Gly Arg Trp Gly Glu Ile Gln Leu Glu
35      40      45
Arg Ile Leu Glu Ile Ser Gly Met Leu Lys Tyr Cys Asp Tyr Ser Thr
50      55      60
Gln Thr Val Asp Ser Ser Glu Ser Ser Ser Arg Ala Asp Ile Val Ile
65      70      75      80
Arg Leu Pro Gln Asn Arg Ser Leu Val Ile Asp Ala Lys Thr Pro Phe
85      90      95
Ser Glu Glu Tyr Leu Thr Asp Asn His Ala Asp Pro Thr Asp Leu Val

```



			100					105					110			
Lys	Lys	Ile	Lys	Asp	His	Ile	Lys	Thr	Leu	Lys	Thr	Lys	Ser	Tyr	Trp	
		115					120					125				
Asp	Lys	Phe	Glu	Gln	Ser	Pro	Glu	Phe	Val	Ile	Leu	Phe	Leu	Pro	Gly	
	130					135					140					
Glu	Ser	Leu	Phe	Asn	Asp	Ala	Ile	Arg	Cys	Ala	Pro	Glu	Leu	Met	Asp	
145					150				155						160	
Tyr	Ala	Gly	Gln	Ser	Asn	Val	Ile	Leu	Ser	Ser	Pro	Val	Thr	Leu	Met	
			165					170						175		
Ala	Leu	Leu	Lys	Thr	Val	Thr	His	Val	Trp	Lys	Gln	Glu	Asn	Leu	Gln	
		180					185						190			
Asn	Gln	Ile	Arg	Glu	Ile	Gly	Gln	Leu	Gly	Lys	Asp	Leu	Tyr	Gln	Arg	
	195					200					205					
Met	His	Lys	Leu	Phe	Asp	His	Phe	His	Lys	Val	Gly	Lys	His	Leu	Gly	
	210				215						220					
Gln	Ala	Val	His	Ser	Tyr	Asn	Asp	Met	Ser	Ser	Ser	Leu	Ser	Ala	Arg	
225					230					235					240	
Val	Leu	Pro	Ile	Leu	Arg	Thr	Phe	Asp	Lys	Leu	Glu	Leu	Ser	Ser	Ser	
			245					250						255		
His	Asn	Lys	Ile	Glu	Ala	Leu	Ser	Gln	Val	Ser	Thr	Leu	Pro	His	Ser	
		260					265						270			
Pro	Lys	Val	Pro	Cys	Pro	Glu	Ser	Asp	Leu	Ala	Glu	Cys	Leu	Ser	Pro	
	275					280						285				
Glu	Ala	Ser	Tyr	Leu	Lys	Pro	Pro	Ser	Ser	Asn	Gln					
	290					295					300					

(2) INFORMATIONS POUR LA SEQ ID NO: 553:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 477 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(541825..543255)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 553:

Ala	Phe	Arg	Ser	Ile	Ser	Val	Ala	Arg	Arg	Arg	Leu	Asn	Lys	Val	Leu	
1				5				10						15		
Pro	Leu	Phe	Ala	Leu	Asp	Lys	Val	Pro	Ser	Leu	Gly	Lys	Glu	Phe	Val	
		20					25						30			
Leu	Glu	Lys	Glu	Val	Phe	Ala	Glu	Gly	Glu	Val	Leu	His	His	Asp	Cys	
	35					40						45				
Phe	Thr	Asn	Asp	Ile	Ile	Phe	Val	Glu	Leu	Val	Phe	Asp	Leu	Pro	Ala	
	50				55						60					
Leu	Ser	Ala	Glu	Glu	Leu	Pro	Trp	Leu	Arg	Leu	Leu	Val	Phe	Val	Leu	
65					70				75						80	
Leu	Gln	Leu	Gly	Ser	Gly	Asn	Arg	Ser	Tyr	Lys	Glu	His	Leu	Glu	Phe	
			85					90					95			
Leu	Leu	Glu	His	Thr	Gly	Gly	Val	Asp	Val	Leu	Tyr	Glu	Phe	Ser	Ser	
		100					105						110			
Gln	Ala	Thr	Asp	Thr	Asp	Arg	Leu	Ser	Pro	Ser	Ile	Ser	Ile	Arg	Gly	
	115					120						125				
Lys	Ala	Leu	Ile	Ser	Lys	Ala	Glu	Tyr	Leu	Phe	Gln	Val	Ile	Arg	Glu	
	130					135						140				

Thr	Leu	Thr	Thr	Val	Asp	Phe	Ser	Asp	Ile	Ala	Arg	Leu	Lys	Glu	Leu
145					150					155					160
Leu	Met	Gln	His	Ala	Glu	Ser	Leu	Thr	Asn	Ser	Val	Arg	Asn	Ser	Pro
				165					170					175	
Met	Gly	Tyr	Ala	Val	Ser	Leu	Ala	Cys	Cys	Asn	Lys	Ser	Ile	Ala	Gly
			180					185					190		
Gly	Leu	Ala	Tyr	Gln	Met	Ala	Gly	Leu	Pro	Tyr	Val	Lys	Tyr	Ile	Arg
		195					200					205			
Glu	Leu	Leu	Ser	Asn	Phe	Asp	Ser	Gln	Ala	Gln	Glu	Ile	Ile	Asp	Arg
	210					215					220				
Leu	Gln	Thr	Leu	Tyr	Lys	Lys	Cys	Phe	Val	Gly	Arg	Arg	Gln	Leu	Val
225					230					235					240
Ile	Ser	Ser	Ser	Lys	Ala	Asn	Tyr	Gln	Val	Leu	His	Asp	Gln	Arg	Phe
				245					250					255	
Phe	Gly	Leu	Leu	Asp	Glu	Arg	Leu	Glu	Gly	Gly	Glu	Leu	Trp	Lys	Asn
			260					265					270		
Pro	Val	Leu	Asp	Val	Val	Lys	Asp	Ser	Arg	Gly	Ile	Val	Ile	Pro	Ala
		275					280					285			
Arg	Gly	Ala	Tyr	Asn	Val	Leu	Ala	Phe	Pro	Leu	Gly	Ser	Leu	Ala	Tyr
	290				295						300				
Asp	His	Pro	Asp	Ala	Ala	Val	Leu	Ser	Val	Ala	Ala	Glu	Val	Leu	Gly
305					310					315					320
Asn	Val	Ile	Leu	His	Ala	Lys	Ile	Arg	Glu	Gln	Gly	Gly	Ala	Tyr	Gly
				325					330					335	
Ser	Gly	Ala	Ser	Ala	Asn	Leu	Gly	Arg	Gly	Ala	Phe	Tyr	Cys	Tyr	Ser
			340					345					350		
Tyr	Arg	Asp	Pro	Glu	Val	Ala	Thr	Thr	Tyr	Gln	Val	Leu	Leu	Gln	Gly
		355					360					365			
Ile	Arg	Asp	Met	Ala	Ala	Gly	Asp	Phe	Ser	Glu	Glu	Asp	Val	His	Glu
	370					375					380				
Gly	Ile	Leu	Gly	Val	Ile	Gln	Asn	Leu	Asp	Asp	Pro	Ile	Ser	Pro	Gly
385					390					395					400
Ser	Arg	Gly	Ser	Ala	Ser	Tyr	Tyr	Arg	Ser	Arg	Ser	Gly	Lys	Val	Pro
				405					410					415	
Phe	Val	Arg	Gln	Ala	Phe	Arg	Gln	Ala	Val	Leu	Ser	Thr	Thr	Lys	Ala
			420					425					430		
Gln	Ile	Cys	Glu	Val	Val	Arg	Asn	Arg	Leu	Glu	Gly	Cys	Leu	Ser	Glu
		435					440					445			
Ala	Ser	Phe	Val	Ser	Phe	Ala	Gly	Glu	Glu	Met	Leu	Gln	Lys	Ser	Ala
	450					455					460				
Lys	Glu	Leu	Asn	Glu	Ala	Phe	Gln	Ile	Glu	Ala	Ala	Phe			
465					470					475					

(2) INFORMATIONS POUR LA SEQ ID NO: 554:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 304 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(543222..544133)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 554:

Lys Arg Ser Ala Leu Phe Met Lys Val Ser Ile Arg Ser Val Val Val

1				5				10					15				
Phe	Phe	Ile	Phe	Met	Gly	Ile	Leu	Asn	Leu	Gly	Arg	His	Leu	Asp	Phe		
			20					25					30				
Leu	Glu	Glu	Lys	Leu	Leu	Arg	Arg	Val	Gly	Lys	Val	Glu	Lys	Gln	Ser		
		35					40					45					
Val	Thr	Leu	Pro	Leu	Gln	Lys	Arg	Phe	Lys	Glu	Pro	Val	Arg	Val	Ile		
	50					55					60						
Glu	Arg	Tyr	Pro	Ser	Asp	Gly	Ala	Asp	Glu	Asp	Lys	Val	Leu	Phe	Gly		
65					70					75					80		
Leu	Ala	Trp	Leu	Thr	Cys	Ser	Ile	Phe	Asp	Gln	Gln	Asp	Leu	Leu	Ala		
			85						90					95			
Leu	His	Val	Leu	Asp	Leu	Val	Leu	Met	Gly	Thr	Asp	Ala	Ala	Pro	Leu		
			100					105					110				
Lys	Ser	Arg	Leu	Leu	Lys	Ser	Gly	Leu	Cys	Lys	Gln	Val	Asp	Met	Ser		
		115					120					125					
Ile	Asp	Ser	Glu	Leu	His	Glu	Ile	Pro	Val	Tyr	Ile	Val	Cys	Lys	Gly		
	130					135					140						
Cys	Ser	His	Ser	Gly	Ser	Gln	Lys	Leu	Glu	Ser	Leu	Ile	Leu	Ala	Ser		
145					150					155					160		
Leu	Glu	Glu	Ile	Leu	Gln	Glu	Gly	Ile	Pro	Met	His	Leu	Val	Glu	Gly		
			165						170					175			
Ala	Val	His	Gln	Leu	Glu	Leu	Ala	Arg	Lys	Glu	Ile	Ala	Gly	Tyr	Ser		
			180					185					190				
Ile	Pro	Tyr	Gly	Leu	Ser	Leu	Phe	Phe	Arg	Ala	Gly	Leu	Leu	Arg	Gln		
		195					200					205					
His	Gly	Gly	Lys	Ala	Glu	Asp	Gly	Leu	Arg	Ile	His	Thr	Leu	Phe	Ala		
	210					215				220							
Asn	Leu	Arg	Glu	Asn	Ile	Gln	Lys	Pro	Asp	Tyr	Leu	Pro	Arg	Leu	Val		
225				230						235					240		
Arg	Lys	Tyr	Phe	Leu	Asp	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Phe	Leu		
			245						250					255			
Pro	Asp	Ser	Gln	Leu	Ile	Ala	Gln	Glu	Asn	Lys	Glu	Glu	Arg	Asn	Val		
			260					265					270				
Leu	His	Thr	Ile	Gln	Met	Gln	Met	Ser	Glu	Glu	Glu	Leu	Glu	Arg	Val		
		275					280					285					
Glu	Ala	Val	Ser	Lys	Arg	Leu	Glu	Ala	Tyr	Gln	Ser	Gln	Glu	Glu	Asp		
	290					295					300						

(2) INFORMATIONS POUR LA SEQ ID NO: 555:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544179..544565)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 555:

Trp	Ser	Gly	Ser	Arg	Thr	Arg	Ala	Tyr	Gly	Leu	Met	Xaa	Xaa	Ser	Glu		
1				5					10					15			
Ser	Tyr	Pro	Ile	Arg	Asp	Pro	Phe	Phe	Ser	Met	Thr	Arg	Arg	Ser	Leu		
		20					25					30					
Asn	Thr	Phe	Met	Asn	Ala	Phe	Thr	Gly	Ala	Asp	Phe	Thr	Cys	Tyr	Pro		
		35					40					45					

Ala	Ala	Ser	Gln	Ile	Pro	Glu	Asp	Phe	Tyr	Asn	Leu	Leu	Ser	Val	Tyr
50						55				60					
Ile	Asp	Ala	Val	Phe	His	Pro	Leu	Leu	Thr	Glu	Asn	Ser	Phe	Leu	Gln
65					70					75					80
Glu	Ala	Trp	Arg	Tyr	Glu	Arg	Thr	Glu	Glu	Gly	Asn	Leu	Ser	Tyr	Thr
				85					90					95	
Gly	Ile	Val	Phe	Asn	Glu	Met	Lys	Gly	Ala	Leu	Met	Ser	Gly	Glu	Ser
			100					105					110		
Arg	Leu	Ser	Glu	Val	Arg	Met	Pro	His	Cys	Ser	Leu	Arg	Ser	Leu	Thr
		115					120					125			
Val															

(2) INFORMATIONS POUR LA SEQ ID NO: 556:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544487..544762)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 556:

Lys	Ile	Glu	Trp	Asp	Met	Lys	Thr	Gly	Asp	Thr	Tyr	Arg	Asn	Phe	Val
1				5				10						15	
Val	Lys	Leu	Ser	Gln	Asp	Leu	Pro	Glu	Ile	Glu	Ser	Lys	Leu	Ile	Glu
			20					25					30		
Val	Glu	His	Thr	Pro	Thr	Gly	Ala	Thr	Ile	Met	Met	Ile	Val	Asn	Asp
		35					40					45			
Asp	Asp	Glu	Asn	Val	Phe	Asn	Ile	Ser	Phe	Arg	Thr	Cys	Pro	Gln	Asp
	50					55				60					
Ser	Ser	Gly	Val	Ala	His	Val	Leu	Glu	His	Met	Ala	Leu	Cys	Xaa	Gly
65					70					75					80
Leu	Arg	Val	Thr	Gln	Phe	Gly	Ile	Leu	Phe	Ser	Gln				
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 557:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 440 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544951..546270)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 557:

Ser	Arg	Val	Ala	Ala	Lys	Ala	Thr	Pro	Gly	Val	Val	Tyr	Ile	Glu	Asn
1					5				10					15	
Phe	Pro	Lys	Thr	Gly	Asn	Gln	Ala	Ile	Ala	Ser	Pro	Gly	Asn	Lys	Arg

			20					25				30			
Gly	Phe	Gln	Glu	Asn	Pro	Phe	Asp	Tyr	Phe	Asn	Asp	Glu	Phe	Phe	Asn
		35					40					45			
Arg	Phe	Phe	Gly	Leu	Pro	Ser	Tyr	Arg	Glu	Gln	Gln	Arg	Pro	Gln	Gln
	50					55					60				
Arg	Asp	Ala	Val	Arg	Gly	Thr	Gly	Phe	Ile	Val	Ser	Glu	Asp	Gly	Tyr
65					70					75					80
Val	Val	Thr	Asn	His	His	Val	Val	Glu	Asp	Ala	Gly	Lys	Ile	His	Val
			85						90					95	
Thr	Leu	His	Asp	Gly	Gln	Lys	Tyr	Thr	Ala	Lys	Ile	Val	Gly	Leu	Asp
			100					105					110		
Pro	Lys	Thr	Asp	Leu	Ala	Val	Ile	Lys	Ile	Gln	Ala	Glu	Lys	Leu	Pro
		115						120				125			
Phe	Leu	Thr	Phe	Gly	Asn	Ser	Asp	Gln	Leu	Gln	Ile	Gly	Asp	Trp	Ala
	130					135					140				
Ile	Ala	Ile	Gly	Asn	Pro	Phe	Gly	Leu	Gln	Ala	Thr	Val	Thr	Val	Gly
145					150					155					160
Val	Val	Ser	Ala	Lys	Gly	Arg	Asn	Gln	Leu	His	Ile	Val	Asp	Phe	Glu
			165					170						175	
Asp	Phe	Ile	Gln	Thr	Asp	Ala	Ala	Ile	Asn	Pro	Gly	Asn	Ser	Gly	Gly
			180					185					190		
Pro	Leu	Leu	Asn	Ile	Asn	Gly	Gln	Val	Ile	Gly	Val	Asn	Thr	Ala	Ile
		195					200					205			
Val	Ser	Gly	Ser	Gly	Gly	Tyr	Ile	Gly	Ile	Gly	Phe	Ala	Ile	Pro	Ser
	210					215					220				
Leu	Met	Ala	Lys	Arg	Val	Ile	Asp	Gln	Leu	Ile	Ser	Asp	Gly	Gln	Val
225					230					235					240
Thr	Arg	Gly	Phe	Leu	Gly	Val	Thr	Leu	Gln	Pro	Ile	Asp	Ser	Glu	Leu
			245						250					255	
Ala	Thr	Cys	Tyr	Lys	Leu	Glu	Lys	Val	Tyr	Gly	Ala	Leu	Val	Thr	Asp
			260					265					270		
Val	Val	Lys	Gly	Ser	Pro	Ala	Glu	Lys	Ala	Gly	Leu	Xaa	Gln	Glu	Asp
		275					280				285				
Val	Ile	Val	Ala	Tyr	Asn	Gly	Lys	Glu	Val	Glu	Ser	Leu	Ser	Ala	Leu
	290					295					300				
Arg	Asn	Ala	Ile	Ser	Leu	Met	Met	Pro	Gly	Thr	Arg	Val	Ile	Leu	Lys
305					310					315					320
Ile	Val	Arg	Glu	Gly	Lys	Thr	Ile	Glu	Ile	Pro	Val	Thr	Val	Thr	Gln
			325						330					335	
Ile	Pro	Thr	Glu	Asp	Gly	Val	Ser	Ala	Leu	Gln	Lys	Met	Gly	Val	Arg
			340					345					350		
Val	Gln	Asn	Ile	Thr	Pro	Glu	Ile	Cys	Lys	Lys	Leu	Gly	Leu	Ala	Ala
		355					360					365			
Asp	Thr	Arg	Gly	Ile	Leu	Val	Val	Ala	Val	Glu	Ala	Gly	Ser	Pro	Ala
	370					375					380				
Ala	Ser	Ala	Gly	Val	Ala	Pro	Gly	Gln	Leu	Ile	Leu	Ala	Val	Asn	Arg
385					390					395					400
Gln	Arg	Val	Ala	Ser	Val	Glu	Glu	Leu	Asn	Gln	Val	Leu	Lys	Asn	Ser
			405						410					415	
Lys	Gly	Glu	Asn	Val	Leu	Leu	Met	Val	Ser	Gln	Gly	Asp	Val	Val	Arg
			420					425					430		
Phe	Ile	Val	Leu	Lys	Ser	Asp	Glu								
		435					440								

(2) INFORMATIONS POUR LA SEQ ID NO: 558:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 299 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(546584..547480)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 558:

Val	Val	Ser	Trp	Glu	Arg	Asn	Cys	Val	Arg	Ile	Ile	Lys	Gln	Gly	Phe	1	5	10	15
Thr	Asp	Tyr	Tyr	Thr	Gly	Tyr	Tyr	Arg	Glu	Ser	Arg	Val	Phe	Ser	His	20	25	30	
Tyr	Thr	Met	Cys	Arg	Phe	Thr	Asp	Leu	Thr	Phe	Val	Gly	Gly	Val	Thr	35	40	45	
Pro	Gly	Lys	Gly	Gly	Ser	Gln	Phe	Leu	Asp	Leu	Pro	Ile	Phe	Asp	Ser	50	55	60	
Val	Leu	Glu	Ala	Lys	Arg	Ala	Thr	Gly	Cys	Arg	Ala	Ser	Met	Ile	Phe	65	70	75	80
Val	Pro	Pro	Pro	Phe	Ala	Ala	Glu	Ala	Ile	Phe	Glu	Ala	Glu	Asp	Xaa	85	90	95	
Gly	Ile	Glu	Leu	Ile	Val	Cys	Ile	Thr	Glu	Gly	Ile	Pro	Ile	Lys	Asp	100	105	110	
Met	Leu	Glu	Val	Ala	Ser	Leu	Met	Glu	Lys	Ser	Ala	Ser	Ser	Leu	Ile	115	120	125	
Gly	Pro	Asn	Cys	Pro	Gly	Val	Ile	Lys	Pro	Gly	Val	Cys	Lys	Ile	Gly	130	135	140	
Ile	Met	Pro	Gly	Tyr	Ile	His	Leu	Pro	Gly	Lys	Val	Gly	Val	Val	Ser	145	150	155	160
Xaa	Ser	Gly	Thr	Leu	Thr	Tyr	Glu	Ala	Val	Trp	Gln	Leu	Thr	Gln	Arg	165	170	175	
Lys	Ile	Gly	Gln	Ser	Val	Cys	Ile	Gly	Ile	Gly	Gly	Asp	Pro	Leu	Asn	180	185	190	
Gly	Thr	Ser	Phe	Ile	Asp	Ala	Leu	Gln	Glu	Phe	Glu	Lys	Asp	Ser	Gln	195	200	205	
Thr	Glu	Ala	Val	Leu	Met	Ile	Gly	Glu	Ile	Gly	Gly	Ser	Ala	Glu	Glu	210	215	220	
Glu	Ala	Ala	Asp	Trp	Ile	Arg	Gln	His	Ser	Ser	Lys	Pro	Val	Ile	Ala	225	230	235	240
Phe	Ile	Ala	Gly	Ala	Thr	Ala	Pro	Lys	Gly	Lys	Arg	Met	Gly	His	Ala	245	250	255	
Gly	Ala	Ile	Ile	Ser	Gly	Lys	Ser	Gly	Asp	Ala	Phe	Ser	Lys	Gln	Glu	260	265	270	
Ala	Leu	Arg	Gln	Ala	Gly	Val	Thr	Val	Val	Glu	Phe	Pro	Ala	Leu	Ile	275	280	285	
Gly	Glu	Ala	Val	Ala	Ser	Val	Leu	Lys	Pro	Arg						290	295		

(2) INFORMATIONS POUR LA SEQ ID NO: 559:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 546789..547382

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 559:

```

Arg Ile Gln Ser Ala Ala Ser Ser Ser Ala Leu Pro Pro Ile Ser Pro
1      5      10      15
Ile Ile Arg Thr Ala Ser Val Trp Leu Ser Phe Ser Asn Ser Trp Arg
      20      25      30
Ala Ser Ile Lys Asp Val Pro Phe Lys Gly Ser Pro Pro Ile Pro Ile
      35      40      45
His Thr Leu Cys Pro Ile Phe Leu Cys Val Ser Cys Gln Thr Ala Ser
      50      55      60
Tyr Val Ser Val Pro Asp Xaa Glu Thr Thr Pro Thr Phe Pro Gly Arg
65      70      75      80
Trp Ile Tyr Pro Gly Met Met Pro Ile Leu Gln Thr Pro Gly Leu Ile
      85      90      95
Thr Pro Gly Gln Phe Gly Pro Ile Lys Glu Leu Ala Leu Phe Ser Ile
      100     105     110
Arg Glu Ala Thr Ser Ser Ile Ser Leu Ile Gly Ile Pro Ser Val Ile
      115     120     125
Gln Thr Ile Ser Ser Ile Pro Xaa Ser Ser Ala Ser Lys Met Ala Ser
      130     135     140
Ala Ala Asn Gly Gly Gly Thr Lys Ile Ile Glu Ala Arg Gln Pro Val
145      150     155     160
Ala Arg Leu Ala Ser Lys Thr Glu Ser Lys Met Gly Lys Ser Lys Asn
      165     170     175
Trp Leu Pro Pro Phe Pro Gly Val Thr Pro Pro Thr Lys Val Arg Ser
      180     185     190
Val Lys Arg His Ile Val
      195

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(2) INFORMATIONS POUR LA SEQ ID NO: 560:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 142 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(547476..547901)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 560:

```

Pro Lys Gln Leu Gly Leu Ser Tyr Ile Ala Leu Asp Gly Thr Ile Gly
1      5      10      15
Cys Leu Val Asn Gly Ala Gly Leu Ala Met Ser Thr Leu Asp Ile Leu
      20      25      30
Lys Leu Tyr Gly Gly Ser Ala Ala Asn Phe Leu Asp Val Gly Gly Ser
      35      40      45
Ala Ser Glu Lys Gln Ile Gln Glu Ala Ile Ser Leu Val Leu Ser Asp
      50      55      60
Lys Ser Val Arg Val Leu Phe Ile His Ile Phe Gly Gly Ile Met Asp
65      70      75      80
Cys Ala Val Val Ala Ser Gly Leu Val Ser Ala Met Gln Gly Gln Lys
      85      90      95

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Glu	Thr	Ile	Pro	Thr	Val	Ile	Arg	Leu	Glu	Gly	Thr	Asn	Val	Asp	Lys
			100					105					110		
Gly	Lys	Gly	Met	Ile	Ile	Asn	Ala	Gly	Ile	Pro	Cys	Glu	Phe	Val	Thr
		115				120						125			
Ser	Met	Ser	Glu	Gly	Ala	Glu	Leu	Ala	Val	Gln	Leu	Ser	Arg		
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 561:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(547900..548634)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 561:

Met	His	Leu	His	Glu	Tyr	Gln	Ala	Lys	Asp	Leu	Leu	Thr	Ala	Tyr	Gln
1				5					10					15	
Leu	Pro	Ile	Pro	Pro	Tyr	His	Val	Ala	Thr	Ser	Val	Pro	Glu	Val	Glu
			20					25					30		
Ala	Ala	Ile	Gln	Xaa	Glu	Gln	Trp	Lys	Ala	Gly	Val	Val	Lys	Ala	Gln
		35					40					45			
Val	His	Ala	Gly	Gly	Arg	Gly	Lys	Asn	Gly	Gly	Val	Val	Ile	Ala	His
	50					55					60				
Ser	Pro	Glu	Asp	Leu	Leu	Ala	Ala	Ala	Asp	Lys	Leu	Leu	His	Met	Gln
65				70						75					80
Phe	Ser	Ser	Asn	Gln	Thr	Ala	Gly	Leu	Ser	Leu	Pro	Val	Asn	Lys	Val
			85						90					95	
Leu	Ile	Ser	Pro	Leu	Val	Glu	Ile	Ala	Ser	Glu	Tyr	Tyr	Leu	Ala	Ile
			100					105					110		
Val	Ile	Asp	Arg	Lys	His	Arg	Cys	Pro	Val	Ile	Met	Leu	Ser	Lys	Ala
		115					120					125			
Gly	Gly	Val	Asp	Ile	Glu	Glu	Val	Ala	Glu	Lys	Gln	Pro	Asp	Gln	Leu
	130					135					140				
Leu	Lys	Met	Thr	Leu	Pro	Ser	Ser	Gly	Lys	Ile	Tyr	Gly	Tyr	Gln	Leu
145					150					155					160
Arg	Arg	Ile	Ala	Lys	Phe	Met	Glu	Trp	Asp	Gln	Pro	Ile	Ala	Asp	Gln
			165						170					175	
Gly	Asn	Arg	Ile	Ile	Arg	Gln	Leu	Leu	Gln	Cys	Phe	Tyr	Glu	Lys	Asp
		180					185						190		
Ala	Ser	Leu	Leu	Glu	Ile	Asn	Pro	Leu	Val	Leu	Thr	Lys	Asp	Gly	Ser
		195					200					205			
Leu	Val	Ile	Leu	Asp	Ala	Lys	Met	Thr	Ile	Asp	Asp	Asn	Ala	Leu	Tyr
	210					215					220				
Arg	His	Pro	Glu	Leu	Ala	Asp	Cys	Tyr	Asp	Pro	Ser	Gln	Glu	Asn	Ile
225					230					235					240
Arg	Asp	Val	Leu	Ala											
				245											

(2) INFORMATIONS POUR LA SEQ ID NO: 562:

(i) CARACTERISTIQUES DE LA SEQUENCE:



(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 548692..549459

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 562:

Phe 1	Asp	Tyr	Ser	Val 5	Phe	Lys	Phe	Phe	Gly 10	Asn	Lys	Leu	Arg	Ser 15	Leu
Phe	Lys	Arg	Thr 20	Leu	Ser	Ser	Asp	Leu 25	Leu	Glu	Tyr	Ala 30	Glu	Val	Leu
Leu	Tyr	Glu	Gly 35	Asp	Phe	Gly	Pro 40	Lys	Leu	Thr	Glu	Ala 45	Phe	Cys	Glu
Glu	Leu	Arg	Arg	Cys	Lys	Asn 55	Pro	Asp	Glu	Arg	Ala 60	Val	Lys	Glu	Leu
Ile 65	Arg	Ser	Phe	Leu 70	Ser	Lys	Ile	Ile	Ser	Lys 75	Leu	Pro	Gln	Arg	Glu
Pro	Leu	Ser	Val 85	Arg	Pro	Phe	Ser	Thr	Leu 90	Val	Leu	Gly	Thr	Asn 95	Gly
Ser	Gly	Lys	Thr 100	Thr	Thr	Val	Ala	Lys 105	Leu	Ala	His	Tyr	Tyr	Leu	Ser
Gln	Asn	Gln	Lys 115	Val	Leu	Ile	Val	Ala 120	Thr	Asp	Thr	Phe	Arg	Ser	Ala
Gly	Met	Asp	Gln	Met	Arg	Cys 135	Trp	Ala	Glu	Thr	Leu 140	Asn	Cys	Gly	Phe
Ile 145	Ser	Gly	Lys	Pro 150	Gly	Asp	Ala	Ala	Ala	Ile	Ala	Phe	Asp	Gly	160
Ile	Ser	Ala	Ala	Val 165	Ala	Arg	Asp	Tyr	Asp 170	His	Val	Ile	Ile	Asp	Thr
Ser	Gly	Arg	Leu 180	His	Thr	His	Thr	Asn 185	Leu	Leu	Lys	Glu	Leu	Gln	Lys
Ile	Ala	Thr	Val 195	Cys	Asn	Lys	Ala 200	Phe	Pro	Gly	Ala	Pro	His	Glu	Thr
Leu	Met	Thr	Ile 210	Asp	Ala	Thr 215	Leu	Gly	Ser	Asn	Thr 220	Ile	Glu	Ser	Gly
Cys 225	Asn	Tyr	Ser	Met 230	Lys	Pro	Tyr	Leu	Ser	Lys 235	Trp	Thr	Tyr	Phe	His
Lys	Ser	Gly	Arg	Phe 245	Cys	Gln	Arg	Arg	Leu 250	Ser	Leu	Pro	Tyr	Arg	Arg

(2) INFORMATION POUR LA SEQ ID NO: 563:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 241 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(549663..550385)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 563:

```

Glu Ile Ser Met Gly Leu Tyr Asp Arg Asp Tyr Ala Gln Asp Ser Arg
1      5      10
Leu Pro Gly Thr Phe Ser Ser Arg Val Tyr Gly Trp Met Thr Ala Gly
      20      25      30
Leu Ala Val Thr Ala Leu Thr Ser Leu Gly Leu Tyr Ala Thr Gly Ala
      35      40      45
Tyr Arg Ala Leu Phe Pro Met Trp Trp Ile Trp Cys Phe Ala Thr Leu
      50      55      60
Gly Val Ser Phe Tyr Ile Gln Ala Gln Ile Gln Lys Leu Ser Val Pro
65      70      75      80
Ala Val Met Gly Leu Phe Leu Ala Tyr Ser Ile Leu Glu Gly Met Phe
      85      90      95
Phe Gly Thr Leu Val Pro Val Tyr Ala Ala Gln Phe Gly Gly Gly Val
      100      105      110
Val Trp Ala Ala Phe Gly Ser Ala Gly Ile Ile Phe Gly Leu Ser Ala
      115      120      125
Ala Tyr Gly Ala Phe Thr Lys Asn Asp Leu Thr Gln Ile His Arg Ile
      130      135      140
Leu Met Leu Ala Leu Val Gly Leu Val Val Ile Ser Leu Ala Phe Leu
      145      150      155      160
Ile Val Ser Leu Phe Thr Pro Met Pro Leu Leu Tyr Leu Leu Ile Cys
      165      170      175
Tyr Leu Gly Leu Ile Ile Phe Val Gly Leu Thr Val Val Asp Ala Gln
      180      185      190
Ser Ile Arg Arg Val Ala Arg Ser Val Gly Asp His Gly Asp Leu Ser
      195      200      205
Tyr Lys Leu Ser Leu Ile Met Ala Leu Gln Met Tyr Cys Asn Val Ile
      210      215      220
Met Ile Phe Trp Tyr Leu Leu Gln Ile Phe Ala Ser Ser Asp Lys Arg
225      230      235      240
Arg

```

(2) INFORMATIONS POUR LA SEQ ID NO: 564:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 395 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(550421..551605)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 564:

```

Met Arg Asn Lys Cys Val Gly Gly Ile Leu Ile Val Ala Gly Thr Val
1      5      10      15
Ile Gly Ala Gly Val Leu Ala Val Pro Ile Leu Thr Ala Val Glu Gly
      20      25      30
Phe Phe Pro Ala Val Val Leu Tyr Val Leu Ala Trp Leu Val Ser Leu
      35      40      45
Ala Ser Gly Tyr Gly Tyr Leu Glu Val Leu Thr Trp Cys Lys Gly Asn
      50      55      60
Arg Gln Ala Asn Leu Cys Ser Met Ala Glu Glu Thr Leu Gly Arg Val
      65      70      75      80
Gly Arg Ile Val Leu Cys Leu Val Tyr Leu Phe Leu Phe Tyr Ser Leu

```

				85					90					95			
Leu	Val	Ala	Tyr	Phe	Cys	Asp	Gly	Gly	Asn	Ile	Leu	Ser	Arg	Val	Ile		
			100					105					110				
Gly	Glu	Ser	Phe	Phe	Ser	Tyr	Pro	Trp	Met	Arg	His	Val	Met	Pro	Leu		
		115					120					125					
Leu	Phe	Phe	Ser	Leu	Phe	Ala	Pro	Leu	Leu	Met	Ala	Asn	Thr	Ser	Val		
	130					135					140						
Ile	Asp	Tyr	Cys	Asn	Arg	Gly	Phe	Val	Phe	Gly	Leu	Ile	Phe	Val	Phe		
145				150					155						160		
Gly	Leu	Phe	Cys	Val	Leu	Gly	Val	Pro	Arg	Ile	Gln	Gly	Glu	Leu	Leu		
			165						170					175			
Leu	Arg	Ala	Ser	Trp	Phe	Ser	Ser	Leu	Asn	Ser	Leu	Pro	Ile	Phe	Phe		
		180						185					190				
Leu	Ala	Phe	Gly	Phe	Gln	Asn	Val	Val	Pro	Ser	Leu	Tyr	His	Tyr	Leu		
	195						200					205					
Asp	Gly	Asn	Ile	Arg	Glu	Val	Lys	Arg	Ala	Ile	Leu	Ile	Gly	Ser	Leu		
	210					215					220						
Ile	Pro	Leu	Ile	Leu	Tyr	Ile	Ala	Trp	Glu	Ala	Leu	Val	Leu	Gly	Thr		
225				230					235						240		
Val	Pro	Leu	Val	Asp	Leu	Leu	Lys	Ala	Lys	Asp	Leu	Gly	Trp	Thr	Ala		
			245						250					255			
Ala	Gly	Ala	Leu	Gln	Gly	Ser	Leu	Lys	Asn	Ser	Ala	Phe	Tyr	Ile	Ala		
		260						265					270				
Gly	Glu	Leu	Phe	Gly	Phe	Phe	Ala	Leu	Val	Thr	Ser	Phe	Ile	Gly	Thr		
	275						280					285					
Ala	Leu	Ala	Leu	Lys	Asp	Phe	Tyr	Ile	Asp	Ile	Phe	Lys	Trp	Asp	Ala		
	290					295					300						
Arg	Lys	Lys	Arg	Val	Ser	Leu	Phe	Phe	Leu	Val	Gln	Val	Phe	Pro	Leu		
305				310					315						320		
Val	Trp	Ala	Ile	Phe	Tyr	Pro	Glu	Ile	Val	Leu	Ser	Cys	Leu	Arg	Tyr		
			325						330					335			
Ala	Gly	Gly	Ile	Gly	Gly	Ala	Cys	Ile	Val	Val	Leu	Phe	Pro	Val	Ala		
		340						345					350				
Met	Leu	Trp	Asn	Gly	Arg	Tyr	Gly	Lys	Arg	Arg	Cys	Phe	Gly	Lys	Arg		
	355						360					365					
Ile	Leu	Pro	Gly	Gly	Lys	Thr	Val	Leu	Leu	Ile	Leu	Thr	Gly	Tyr	Thr		
	370				375						380						
Val	Leu	Asn	Xaa	Ala	Thr	Leu	Tyr	Tyr	Ala	Phe							
385					390					395							

(2) INFORMATIONS POUR LA SEQ ID NO: 565:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 398 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(551797..552990)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 565:

Met	Ile	Asn	Lys	Met	Leu	Gly	Gly	Ala	Leu	Leu	Val	Ala	Gly	Thr	Thr
1			5					10					15		
Ile	Gly	Ala	Gly	Val	Leu	Ala	Val	Pro	Val	Ser	Thr	Ser	Glu	Gly	Gly
		20						25					30		

Phe	Leu	Pro	Thr	Thr	Leu	Leu	Tyr	Ile	Val	Ser	Trp	Phe	Ile	Ala	Val
		35					40					45			
Ala	Ser	Gly	Tyr	Cys	Phe	Leu	Glu	Val	Leu	Thr	Trp	Thr	His	Ser	Arg
	50					55					60				
Lys	Asn	Val	Asn	Met	Val	Ser	Leu	Ala	Glu	Tyr	Thr	Leu	Gly	His	Lys
65				70						75					80
Ser	Lys	Ile	Ile	Met	Trp	Leu	Ile	Tyr	Leu	Leu	Leu	Phe	Tyr	Ser	Leu
				85					90					95	
Leu	Val	Ala	Tyr	Phe	Cys	Asp	Gly	Gly	Asn	Ile	Leu	Met	Arg	Val	Met
			100					105					110		
Gly	Cys	Arg	Ser	Trp	Asp	Thr	Pro	Trp	Ile	Arg	His	Ala	Met	Pro	Val
	115						120					125			
Val	Phe	Phe	Ala	Leu	Phe	Ser	Pro	Leu	Leu	Met	Ala	Lys	Thr	Ser	Ile
	130					135					140				
Ile	Asp	Gln	Cys	Asn	Arg	Val	Phe	Val	Phe	Gly	Leu	Gly	Ile	Ala	Phe
145				150						155					160
Ala	Met	Phe	Cys	Tyr	Phe	Gly	Phe	Pro	Leu	Met	Lys	Thr	Asp	Leu	Leu
				165					170					175	
Val	Arg	Ser	Ala	Trp	Gly	Ala	Thr	Leu	Lys	Gly	Phe	Pro	Ile	Leu	Phe
			180					185					190		
Leu	Ala	Phe	Gly	Phe	Gln	Asn	Val	Pro	Thr	Leu	Tyr	His	Tyr	Met	
		195					200					205			
Asp	Lys	Asn	Val	Lys	Asp	Val	Lys	Lys	Ala	Ile	Val	Ile	Gly	Ser	Ser
	210					215					220				
Ile	Pro	Leu	Val	Leu	Tyr	Ile	Ile	Trp	Glu	Ala	Ile	Val	Leu	Gly	Ala
225					230					235					240
Val	Pro	Ile	Ser	Phe	Leu	Glu	Gln	Ala	Lys	Val	Glu	Gly	Trp	Thr	Ala
				245					250					255	
Ile	Gly	Ala	Leu	Gln	Thr	Ala	Leu	Lys	Cys	Ala	Ala	Phe	Tyr	Val	Ala
			260					265					270		
Gly	Glu	Phe	Phe	Gly	Phe	Phe	Ala	Leu	Ile	Ser	Ser	Phe	Ile	Gly	Val
		275					280						285		
Ser	Leu	Gly	Leu	Lys	Asp	Phe	Phe	Ile	Asp	Ala	Phe	Gln	Trp	Asp	Glu
	290					295					300				
Lys	Lys	Arg	Lys	Val	Glu	Ile	Phe	Phe	Leu	Val	Phe	Val	Phe	Pro	Leu
305					310					315					320
Val	Trp	Ala	Val	Phe	Tyr	Pro	Gly	Ile	Val	Leu	Lys	Cys	Leu	Glu	Cys
				325					330					335	
Thr	Gly	Ala	Leu	Gly	Glu	Thr	Ile	Val	Leu	Gly	Val	Cys	Pro	Val	Leu
			340					345					350		
Met	Val	Trp	Lys	Gly	Arg	Tyr	Gly	Lys	Lys	Arg	Tyr	Tyr	Gly	Lys	Arg
		355					360					365			
Ile	Leu	Pro	Gly	Gly	Lys	Gly	Thr	Leu	Leu	Val	Met	Ser	Gly	Leu	Val
	370					375					380				
Leu	Leu	Asn	Leu	Val	Leu	Ile	Ala	Gln	Lys	Phe	Leu	Gly	Tyr		
385					390					395					

(2) INFORMATIONS POUR LA SEQ ID NO: 566:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 606 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(553096..554913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 566:

Met	Cys	Gly	Ile	Phe	Gly	Tyr	Leu	Gly	Glu	Lys	Asn	Ala	Val	Pro	Leu	1	5	10	15
Val	Leu	Glu	Gly	Leu	Ser	Glu	Leu	Glu	Tyr	Arg	Gly	Tyr	Asp	Ser	Ala	20	25	30	
Gly	Ile	Ala	Thr	Leu	Ile	Glu	Gly	Arg	Leu	Phe	Val	Glu	Lys	Ala	Val	35	40	45	
Gly	Pro	Val	Ser	Gln	Leu	Cys	Ser	Ala	Val	Ser	Ser	Asp	Ile	His	Ser	50	55	60	
Gln	Ala	Ala	Ile	Gly	His	Thr	Arg	Trp	Ala	Thr	His	Gly	Glu	Pro	Ser	65	70	75	80
Arg	Phe	Asn	Ala	His	Pro	His	Ile	Asp	Met	Asp	Ala	Ser	Cys	Ala	Leu	85	90	95	
Val	His	Asn	Gly	Ile	Ile	Glu	Asn	Phe	Gln	Lys	Leu	Lys	Glu	Glu	Leu	100	105	110	
Glu	Glu	Gln	Gly	Val	Val	Phe	Ser	Ser	Asp	Thr	Asp	Thr	Glu	Val	Ile	115	120	125	
Val	Gln	Leu	Phe	Ala	Arg	Arg	Tyr	Lys	Glu	Thr	Arg	Asp	Leu	Ile	Gln	130	135	140	
Ser	Phe	Ser	Trp	Thr	Leu	Lys	Arg	Leu	Gln	Gly	Ser	Phe	Ala	Cys	Ala	145	150	155	160
Leu	Met	His	Gln	Asp	His	Pro	Glu	Val	Leu	Leu	Cys	Ala	Ala	His	Glu	165	170	175	
Ser	Pro	Leu	Ile	Leu	Gly	Leu	Gly	Glu	Asp	Glu	Val	Phe	Ile	Ser	Ser	180	185	190	
Asp	Ile	His	Ala	Phe	Leu	Lys	Tyr	Ser	Gly	Cys	Thr	Gln	Thr	Leu	Ala	195	200	205	
Ser	Gly	Glu	Leu	Val	Val	Leu	Arg	Ile	Gly	Lys	Ser	Ile	Glu	Thr	Tyr	210	215	220	
Asn	Phe	Glu	Leu	Ala	Arg	Ile	Gln	Lys	Glu	Val	Arg	Cys	Ile	Asp	His	225	230	235	240
Thr	Glu	Asp	Ser	Leu	Asp	Lys	Lys	Gly	Phe	Asp	Tyr	Tyr	Met	Leu	Lys	245	250	255	
Glu	Ile	Tyr	Glu	Gln	Pro	Glu	Val	Phe	Glu	Arg	Ile	Leu	His	Leu	Thr	260	265	270	
Cys	Glu	Glu	Asn	Ser	Phe	Thr	Glu	Ser	Phe	Leu	Lys	Gly	Phe	Ser	Leu	275	280	285	
Asp	Glu	Ile	Gln	Ser	Leu	His	Ile	Val	Ala	Cys	Gly	Ser	Ser	Tyr	His	290	295	300	
Ala	Gly	Tyr	Leu	Ala	Lys	Tyr	Val	Ile	Glu	Ser	Ile	Ala	Ser	Ile	Pro	305	310	315	320
Val	Tyr	Val	Glu	Ile	Ala	Ser	Glu	Phe	Arg	Tyr	Arg	Gln	Pro	Tyr	Ile	325	330	335	
Ala	Glu	His	Ser	Leu	Ala	Ile	Leu	Ile	Ser	Gln	Ser	Gly	Glu	Thr	Ala	340	345	350	
Asp	Thr	Leu	Ala	Ala	Leu	Asn	Glu	Phe	Arg	Lys	Leu	Ser	Lys	Ala	Arg	355	360	365	
Val	Leu	Gly	Ile	Cys	Asn	Val	Arg	Glu	Ser	Ala	Leu	Ala	Ser	Arg	Val	370	375	380	
Asp	His	Cys	Leu	Phe	Ile	Glu	Ala	Gly	Leu	Glu	Val	Gly	Val	Ala	Ser	385	390	395	400
Thr	Lys	Ala	Phe	Thr	Ala	Gln	Leu	Leu	Leu	Leu	Ile	Leu	Leu	Gly	Leu	405	410	415	
Arg	Leu	Ala	Asn	His	Arg	Gln	Val	Ile	Ala	Gln	Glu	Asp	Leu	Ala	Gln	420	425	430	
Ala	Ile	Gln	Gly	Leu	Lys	Asp	Leu	Pro	Asn	Leu	Thr	Arg	Leu	Phe	Leu	435	440	445	

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Asp Ser Ser Ile His Asp Trp Arg Cys Arg Gln Ile Glu Glu Thr Ser
  450                      455                      460
Phe Ile Phe Leu Gly Arg Arg Phe Met Tyr Pro Ile Cys Met Glu Ala
465                      470                      475                      480
Ala Leu Lys Leu Lys Glu Ile Ala Tyr Val Glu Ala Asn Ala Tyr Pro
                      485                      490                      495
Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Arg Glu Gly Thr
                    500                    505                    510
Pro Val Ile Val Tyr Cys Gly Asp Arg Ser Val Tyr Thr Lys Thr Ile
                    515                    520                    525
Gly Ala Ile Met Glu Val Lys Ala Arg Lys Ala Tyr Val Ile Ala Leu
                    530                    535                    540
Ala Pro Glu Ser Asn Arg Asp Ile Ala Ala Val Ser Asp Glu Gln Ile
545                      550                      555                      560
Tyr Ile Pro Asp Ser His Asp Leu Ala Ala Pro Ile Leu Phe Thr Ile
                      565                      570                      575
Ala Gly Gln Ile Met Ala Tyr Thr Met Ala Leu Gln Arg Gly Thr Glu
                      580                      585                      590
Val Asp Arg Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
                      595                      600                      605

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(2) INFORMATIONS POUR LA SEQ ID NO: 567:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 458 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(554927..556300)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 567:

```

Met Thr Arg Asp Val Ser Gln Leu Phe Gly Thr Asp Gly Val Arg Gly
  1                      5                      10                      15
Arg Ala Asn Phe Glu Pro Met Thr Val Glu Thr Ser Val Leu Leu Gly
                      20                      25                      30
Lys Ala Ile Ala Gly Val Leu Leu Glu Lys His Ala Gly Lys His Arg
                      35                      40                      45
Val Val Val Gly Lys Asp Thr Arg Leu Ser Gly Tyr Met Phe Glu Asn
                    50                    55                    60
Ala Leu Ile Ala Gly Leu Thr Ser Met Gly Ile Glu Thr Leu Met Leu
65                      70                      75                      80
Gly Pro Ile Pro Thr Pro Gly Val Ala Phe Ile Thr Arg Ala Tyr Arg
                      85                      90                      95
Ala Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Tyr Arg Asp
                    100                   105                   110
Asn Gly Ile Lys Ile Phe Ser Ser Asp Gly Phe Lys Ile Gly Gln Ala
                    115                   120                   125
Val Glu Glu Arg Ile Glu Ala Met Val Ala Ser Lys Asp Phe Gly Lys
                    130                   135                   140
Leu Pro Asp Asp His Ala Val Gly Lys Asn Lys Arg Val Lys Asp Ala
145                      150                      155                      160
Thr Gly Arg Tyr Ile Glu Tyr Ala Lys Ala Thr Phe Pro Lys Gly Arg
                      165                      170                      175
Thr Leu Lys Gly Leu Arg Ile Val Leu Asp Cys Ala His Gly Ala Thr

```

(2) INFORMATION POUR LA SEQ ID NO: 568:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 556524..556904

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 568:

Met	Ile	Tyr	Phe	Phe	Val	Phe	Met	Thr	Pro	Tyr	Leu	Ile	Glu	Ala	Leu
1				5					10					15	
Val	Ala	Cys	Cys	Ile	Leu	Leu	Ser	Leu	Gly	Met	Val	Leu	Ile	Phe	Ala
		20						25					30		
Phe	Thr	Ile	Cys	Leu	Leu	Leu	Lys	Leu	His	Lys	Ile	Met	Lys	Leu	Val
		35					40					45			
Ser	Arg	Ile	Ser	Ser	Leu	Phe	Asn	Phe	Glu	Ala	Arg	Trp	Leu	Ala	Pro
	50					55					60				

Leu	Leu	Ile	Gly	Lys	Lys	Phe	Ile	Leu	Asn	Trp	Leu	Arg	Lys	Lys	Tyr
65					70					75					80
Ala	Asp	Arg	Lys	Met	Ser	Gln	Leu	Ala	Asp	Glu	Leu	Glu	Asp	Asn	Glu
				85					90					95	
Asp	Ser	Glu	Asn	Ser	Cys	Ser	Ser	Arg	Leu	Leu	Cys	Gly	Ala	Lys	Leu
			100					105					110		
Ala	Ala	Ile	Ala	Leu	Cys	Ala	Trp	Leu	Leu	Ile	Arg	Lys	Lys	Asp	
		115					120					125			

(2) INFORMATIONS POUR LA SEQ ID NO: 569:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 271 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(557314..558126)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 569:

Arg	Ser	Phe	Lys	Gly	Asp	Ser	Met	Thr	Thr	Leu	Pro	Asn	Thr	Cys	Thr
1				5					10					15	
Ser	Asn	Ser	Asn	Ser	Ile	Asn	Thr	Phe	Thr	Xaa	Asp	Ile	Glu	Met	Ala
			20					25					30		
Lys	Gln	Ile	Gln	Gly	Ser	Arg	Lys	Asp	Pro	Leu	Ala	Lys	Thr	Ser	Trp
		35					40					45			
Ile	Ala	Gly	Leu	Ile	Cys	Val	Val	Ala	Gly	Val	Leu	Gly	Leu	Leu	Ala
	50					55					60				
Ile	Gly	Ile	Gly	Gly	Cys	Ser	Met	Ala	Ser	Gly	Leu	Gly	Leu	Ile	Gly
65					70					75					80
Ala	Ile	Ile	Ala	Ala	Val	Val	Val	Ala	Val	Gly	Leu	Cys	Cys	Leu	Val
				85					90					95	
Ser	Ala	Leu	Cys	Leu	Xaa	Val	Glu	Lys	Ser	Gln	Trp	Trp	Gln	Lys	Glu
			100					105					110		
Phe	Lys	Ser	Trp	Ile	Glu	Gln	Lys	Ser	Gln	Phe	Arg	Ile	Val	Met	Ala
		115					120					125			
Asp	Met	Leu	Glu	Ala	Asn	Gln	Lys	Leu	Gln	Ser	Glu	Val	Glu	Phe	Leu
	130					135					140				
Ser	Lys	Gly	Trp	Ser	Asp	Ala	Ala	Ala	Val	His	Lys	Glu	Asp	Val	Thr
145					150					155					160
Lys	Tyr	Glu	Gln	Val	Val	Glu	Lys	Tyr	Gly	Glu	Lys	Ile	Met	Lys	Leu
			165						170					175	
Tyr	Lys	Gln	Thr	Gly	Val	Leu	Thr	Ile	Glu	Lys	Val	Asn	Leu	Gln	Lys
		180						185					190		
Glu	Lys	Lys	Thr	Trp	Leu	Glu	Glu	Lys	Ala	Glu	Met	Glu	Gln	Lys	Leu
		195					200					205			
Thr	Thr	Val	Thr	Asp	Leu	Glu	Ala	Ala	Lys	Gln	Gln	Leu	Glu	Glu	Lys
	210					215						220			
Val	Thr	Asp	Leu	Glu	Ser	Glu	Lys	Gln	Glu	Leu	Arg	Glu	Glu	Leu	Asp
225					230					235					240
Lys	Ala	Thr	Glu	Asn	Leu	Asp	Glu	Met	Ala	His	Glu	Ala	Met	Glu	Phe
			245						250					255	
Glu	Lys	Glu	Lys	His	Gly	Ile	Lys	Pro	Gly	Arg	Arg	Gly	Ser	Ile	
			260					265					270		



## (2) INFORMATIONS POUR LA SEQ ID NO: 570:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 142 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 557810..558235

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 570:

Asp	Phe	Ser	Thr	Xaa	Lys	His	Lys	Ala	Asp	Thr	Lys	Gln	His	Lys	Pro
1				5					10					15	
Thr	Ala	Thr	Thr	Thr	Ala	Ala	Ile	Ile	Ala	Pro	Ile	Asn	Pro	Asn	Pro
			20					25					30		
Glu	Ala	Ile	Glu	His	Pro	Pro	Ile	Pro	Ile	Ala	Arg	Ser	Pro	Asn	Thr
		35					40					45			
Pro	Ala	Thr	Thr	Gln	Ile	Asn	Pro	Ala	Ile	His	Glu	Val	Leu	Ala	Arg
	50					55					60				
Gly	Ser	Phe	Arg	Glu	Pro	Trp	Ile	Cys	Phe	Ala	Ile	Ser	Ile	Ser	Xaa
65					70				75						80
Val	Lys	Val	Phe	Ile	Glu	Leu	Glu	Phe	Glu	Val	Gln	Val	Leu	Gly	Arg
				85					90					95	
Val	Val	Ile	Glu	Ser	Pro	Leu	Asn	Asp	Arg	His	Ala	Asp	Gly	Pro	Lys
			100					105					110		
Lys	Gln	Pro	Gln	Thr	Tyr	Phe	Cys	Thr	Asn	Phe	Cys	Phe	Leu	Ala	Lys
		115					120					125			
Lys	Lys	Glu	Arg	Phe	Tyr	Leu	Leu	Leu	Asn	Leu	Leu	Thr	Ser		
	130					135					140				

## (2) INFORMATIONS POUR LA SEQ ID NO: 571:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 302 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(558310..559215)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 571:

Lys	Met	His	Ala	Leu	Leu	Ile	Asn	Leu	Thr	Ala	Gln	Arg	Met	Glu	Phe
1				5					10					15	
Asp	Tyr	Ser	Thr	Asn	Val	Trp	Gly	Phe	Ala	Phe	Gly	Gly	Phe	Arg	Thr
			20					25					30		
Leu	Ser	Ala	Glu	Asn	Leu	Val	Ala	Ile	Asp	Gly	Tyr	Lys	Gly	Ala	Tyr
		35					40					45			
Gly	Gly	Ala	Ser	Ala	Gly	Val	Asp	Ile	Gln	Leu	Met	Glu	Asp	Phe	Val
	50					55					60				
Leu	Gly	Val	Ser	Gly	Ala	Ala	Phe	Leu	Gly	Lys	Met	Asp	Ser	Gln	Lys
65					70					75					80

Phe	Asp	Ala	Glu	Val	Ser	Arg	Lys	Gly	Val	Val	Gly	Ser	Val	Tyr	Thr
				85					90					95	
Gly	Phe	Leu	Ala	Gly	Ser	Trp	Phe	Phe	Lys	Gly	Gln	Tyr	Ser	Leu	Gly
			100					105					110		
Glu	Thr	Gln	Asn	Asp	Met	Lys	Thr	Arg	Tyr	Gly	Val	Leu	Gly	Glu	Ser
		115					120					125			
Ser	Ala	Ser	Trp	Thr	Ser	Arg	Gly	Val	Leu	Ala	Asp	Ala	Leu	Val	Glu
	130					135				140					
Tyr	Arg	Ser	Leu	Val	Gly	Pro	Val	Arg	Pro	Thr	Phe	Tyr	Ala	Leu	His
145					150				155						160
Phe	Asn	Pro	Tyr	Val	Glu	Val	Ser	Tyr	Ala	Ser	Met	Lys	Phe	Pro	Gly
			165					170						175	
Phe	Thr	Glu	Gln	Gly	Arg	Glu	Ala	Arg	Ser	Phe	Glu	Asp	Ala	Ser	Leu
		180					185						190		
Thr	Asn	Ile	Thr	Ile	Pro	Leu	Gly	Met	Lys	Phe	Glu	Leu	Ala	Phe	Ile
	195						200					205			
Lys	Gly	Gln	Phe	Ser	Glu	Val	Asn	Ser	Leu	Gly	Ile	Ser	Tyr	Ala	Trp
	210					215					220				
Glu	Ala	Tyr	Arg	Lys	Val	Glu	Gly	Gly	Ala	Val	Gln	Leu	Leu	Glu	Ala
225					230				235						240
Gly	Phe	Asp	Trp	Glu	Gly	Ala	Pro	Met	Asp	Leu	Pro	Arg	Gln	Glu	Leu
			245						250					255	
Arg	Val	Ala	Leu	Glu	Asn	Asn	Thr	Glu	Trp	Ser	Ser	Tyr	Phe	Ser	Thr
			260					265					270		
Val	Leu	Gly	Leu	Thr	Ala	Phe	Cys	Gly	Gly	Phe	Thr	Ser	Thr	Asp	Ser
		275				280					285				
Lys	Leu	Gly	Tyr	Glu	Ala	Asn	Ala	Gly	Leu	Arg	Leu	Ile	Phe		
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 572:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 718 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(559196..561349)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 572:

Leu	Leu	Val	Arg	Trp	Lys	Leu	Pro	Ile	Ile	Pro	Ser	Asn	Phe	Phe	Tyr
1				5					10					15	
Arg	Lys	Cys	Glu	Xaa	Pro	Gln	Ala	Leu	Pro	Thr	Gln	Glu	Glu	Phe	Pro
		20					25					30			
Leu	Phe	Ser	Lys	Lys	Glu	Gly	Arg	Pro	Leu	Ser	Ser	Gly	Tyr	Ser	Gly
		35				40						45			
Gly	Gly	Ala	Ile	Leu	Gly	Arg	Glu	Val	Ala	Ile	Leu	His	Asn	Ala	Ala
	50				55					60					
Val	Val	Phe	Glu	Gln	Asn	Arg	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Ala	Thr
65				70					75					80	
Leu	Leu	Gly	Cys	Cys	Gly	Gly	Gly	Ala	Val	His	Gly	Met	Asp	Ser	Thr
			85					90					95		
Ser	Ile	Val	Gly	Asn	Ser	Ser	Val	Arg	Phe	Gly	Asn	Asn	Tyr	Ala	Met
		100					105				110				
Gly	Gln	Gly	Val	Ser	Gly	Gly	Ala	Leu	Leu	Ser	Lys	Thr	Val	Gln	Leu

[illegible]

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Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly
    595                      600                      605
Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro
    610                      615                      620
Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser
    625                      630                      635                      640
Asn Leu Ser Val Ser Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile
    645                      650                      655
Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile
    660                      665                      670
Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu
    675                      680                      685
Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Glu
    690                      695                      700
Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg Phe Ala Asp
    705                      710                      715

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(2) INFORMATIONS POUR LA SEQ ID NO: 573:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 594 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(561150..562931)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 573:

```

Phe Val Lys Lys Val Leu Phe Arg Arg Phe Glu Met Ser Ser Glu Lys
1          5          10          15
Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu Ser Val Val Ala Ala
    20          25          30
Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys Val Asp Leu His Ala
    35          40          45
Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala Val
    50          55          60
Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp Ser
    65          70          75          80
Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser Phe
    85          90          95
Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser Thr
    100         105         110
Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln Gln
    115         120         125
Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser Asn
    130         135         140
Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe Val
    145         150         155         160
Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala Ser
    165         170         175
Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu Lys
    180         185         190
Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln Gly
    195         200         205
Gly Ala Cys Gly Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly Leu

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210		215		220
Gln Val Lys His Cys Thr	Thr Ala Val Asn Ala Glu Gly Ser Ser Ala			
225	230	235		240
Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe Phe Val Thr Gly Ser				
	245	250		255
Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val Val				
	260	265		270
Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn Phe				
	275	280		285
Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val Ala				
	290	295		300
Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly Gly				
305	310	315		320
Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu Leu				
	325	330		335
Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu Asp Lys Gly Ser Leu				
	340	345		350
Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly Asn				
	355	360		365
His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly Ala				
	370	375		380
Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val Val				
385	390	395		400
Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Ala Ile Ala Ala Gln				
	405	410		415
Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu Gly				
	420	425		430
Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys Gly Ser Phe Ser Ser				
	435	440		445
Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn Leu				
	450	455		460
Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu Gly				
465	470	475		480
Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe Gly Glu Asn Ile Ser				
	485	490		495
Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val Lys				
	500	505		510
Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Gly Ala Ile Leu Ala				
	515	520		525
Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Val Glu Phe Leu Leu Gln				
	530	535		540
Glu Met Arg Xaa Ser Thr Ser Ser Ser Asn Ser Arg Gly Val Ser Phe				
545	550	555		560
Ile Gln Gln Lys Arg Arg Ala Thr Thr Leu Phe Arg Ile Phe Trp Gly				
	565	570		575
Arg Ser Asp Phe Arg Lys Arg Ser Ser Tyr Ser Pro Gln Arg Cys Ser				
	580	585		590
Ser Ile				

## (2) INFORMATIONS POUR LA SEQ ID NO: 574:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 321 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(563121..564083)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 574:

Met	Lys	Val	Arg	Leu	Gly	Val	Asp	Met	Met	Gly	Gly	Asp	His	Asp	Pro
1				5				10					15		
Leu	Val	Val	Trp	Glu	Ala	Leu	Gly	Glu	Val	Leu	Leu	Ser	Ser	Thr	Gly
			20					25					30		
Glu	Gln	Pro	Val	Glu	Phe	Thr	Val	Phe	Ala	Thr	Ser	Asp	Val	His	His
		35					40					45			
Gln	Leu	Met	Asn	Ser	Pro	Leu	Ser	Arg	Ser	Val	Arg	Ile	Val	Thr	Ala
	50					55				60					
Glu	Asp	Phe	Val	Ser	Met	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Val	Arg	Lys
65					70				75						80
Lys	Arg	Ser	Ser	Met	Ala	Leu	Gly	Leu	Asp	Ala	Leu	Gln	Gln	Gly	Asp
				85				90						95	
Leu	Asp	Gly	Phe	Val	Ser	Ser	Gly	Asn	Thr	Ala	Ala	Leu	Val	Thr	Leu
			100					105					110		
Ala	Arg	Ser	Lys	Ile	Pro	Met	Ile	Pro	Ala	Val	Pro	Arg	Pro	Ala	Leu
		115					120					125			
Leu	Val	Ser	Val	Pro	Thr	Leu	Ser	Gly	Phe	Ala	Val	Ile	Leu	Asp	Val
	130					135					140				
Gly	Ala	Thr	Val	Ser	Val	Asn	Pro	Asp	Glu	Met	Val	Gly	Phe	Ala	Arg
145					150				155						160
Met	Gly	Leu	Ala	Tyr	Arg	Gln	Ser	Leu	Ser	Ser	Asn	Ser	Asn	Gln	Pro
			165					170						175	
Phe	Thr	Leu	Gly	Leu	Leu	Asn	Ile	Gly	Ser	Glu	Glu	Arg	Lys	Gly	Thr
			180					185					190		
Asp	Ser	His	Lys	Gln	Thr	Phe	Arg	Met	Leu	Arg	Asn	Ile	Phe	Gly	Ser
		195					200					205			
Ala	Phe	Leu	Gly	Asn	Ile	Glu	Ser	Gly	Asp	Val	Phe	Ser	Gly	Lys	Val
	210					215					220				
Asp	Ile	Val	Val	Thr	Asp	Gly	Phe	Thr	Gly	Asn	Val	Phe	Leu	Lys	Thr
225				230					235						240
Ala	Glu	Gly	Leu	Phe	Asp	Phe	Leu	Arg	His	Ile	Leu	Gly	Asp	Arg	Leu
			245					250					255		
Glu	Lys	Ser	Ile	Lys	Met	Gln	Phe	Asp	Tyr	Thr	Ile	Tyr	Pro	Gly	Ser
		260					265						270		
Ile	Ile	Ser	Gly	Leu	Ser	Arg	Leu	Val	Ile	Lys	Cys	His	Gly	Lys	Ser
		275					280					285			
His	Gly	Thr	Ala	Leu	Phe	Gly	Gly	Ile	Ser	Gly	Ala	Ile	Asp	Leu	Ala
	290					295					300				
Arg	Ala	Asn	Val	Cys	Ser	Arg	Ile	Ala	Asp	Arg	Phe	Gly	Asp	Asn	Val
305					310				315						320
Val															

(2) INFORMATIONS POUR LA SEQ ID NO: 575:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 117 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 563593..563943

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 575:

Ala	Lys	Pro	Ile	Arg	Ala	Lys	Pro	Thr	Ile	Ser	Ser	Gly	Phe	Thr	Asp
1				5					10					15	
Thr	Val	Ala	Pro	Thr	Ser	Lys	Ile	Thr	Ala	Asn	Pro	Glu	Arg	Val	Gly
			20					25					30		
Thr	Glu	Thr	Asn	Asn	Ala	Gly	Leu	Gly	Thr	Ala	Gly	Ile	Ile	Gly	Ile
		35				40						45			
Leu	Glu	Arg	Ala	Ser	Val	Thr	Lys	Ala	Ala	Val	Phe	Pro	Glu	Glu	Thr
	50					55					60				
Lys	Pro	Ser	Arg	Ser	Pro	Cys	Cys	Asn	Ala	Ser	Asn	Pro	Arg	Ala	Ile
65					70					75					80
Glu	Asp	Arg	Phe	Leu	Arg	Thr	Ala	Ala	Asn	Lys	Glu	Ser	Ser	Ile	Glu
			85						90					95	
Thr	Lys	Ser	Ser	Ala	Val	Thr	Ile	Arg	Thr	Glu	Arg	Asp	Ser	Gly	Glu
			100					105					110		
Phe	Ile	Asn	Trp	Trp											
			115												

(2) INFORMATIONS POUR LA SEQ ID NO: 576:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 518 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 565400..566953

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 576:

Arg	Ala	Phe	Arg	Asn	Ala	Met	Glu	Asn	Asp	Ile	Leu	Leu	Asn	Ile	Glu
1				5					10					15	
Ser	Lys	Glu	Ile	Arg	Tyr	Ala	His	Leu	Lys	Asn	Gly	Gln	Leu	Phe	Asp
			20					25					30		
Leu	Ile	Ile	Glu	Arg	Lys	Lys	Ile	Arg	Gln	Leu	Lys	Gly	Asn	Ile	Tyr
		35				40						45			
Arg	Gly	Arg	Val	Thr	Asn	Ile	Leu	Arg	Asn	Ile	Gln	Ser	Ala	Phe	Ile
	50				55						60				
Asn	Ile	Asp	Glu	Arg	Glu	Asn	Gly	Phe	Ile	His	Ile	Ser	Asp	Val	Leu
65					70					75					80
Glu	Asn	Ser	Lys	Lys	Phe	Glu	Gln	Met	Phe	Asp	Ile	Asp	Ser	Asp	Ala
			85						90					95	
Asp	His	Ala	Glu	Pro	Arg	Pro	Glu	Glu	Thr	Ser	Glu	Ala	Pro	Ile	Glu
			100					105					110		
Glu	Leu	Leu	Lys	Leu	Asp	Ser	Pro	Val	Leu	Val	Gln	Val	Val	Lys	Glu
		115					120				125				
Pro	Ile	Gly	Thr	Lys	Gly	Ala	Arg	Leu	Thr	Ser	Asn	Ile	Ser	Ile	Pro
	130					135					140				
Gly	Arg	Tyr	Leu	Val	Leu	Leu	Pro	Asn	Ser	Pro	His	Arg	Gly	Val	Ser
145					150					155					160
Arg	Lys	Ile	Glu	Asp	Pro	Leu	Met	Arg	Asp	Gln	Leu	Lys	Gln	Leu	Ile
				165					170					175	

Arg	Ser	Phe	Glu	Met	Pro	Gln	Asn	Met	Gly	Leu	Ile	Cys	Arg	Thr	Ala		
			180					185					190				
Ser	Ile	Ser	Ala	Ser	Thr	Glu	Thr	Leu	Ile	Asn	Glu	Ala	Gln	Asp	Leu		
		195					200				205						
Leu	Asn	Thr	Trp	Gln	Ser	Ile	Leu	Glu	Lys	Phe	Tyr	Ser	Pro	Asp	His		
	210					215					220						
Pro	Ser	Leu	Leu	Tyr	Glu	Glu	Thr	Asp	Ile	Leu	Lys	Lys	Ala	Val	Met		
225					230					235					240		
Thr	Cys	Val	Asp	Lys	Ser	Tyr	Lys	Arg	Leu	Leu	Ile	Asp	Asp	Tyr	Ala		
			245					250						255			
Thr	Tyr	Gln	Lys	Cys	Lys	Arg	Leu	Leu	Gly	Lys	Tyr	Ser	Pro	Asp	Thr		
		260						265					270				
Thr	Val	Lys	Ile	Glu	Tyr	Tyr	Arg	Asp	Ser	Val	Pro	Met	Phe	Glu	Arg		
		275					280					285					
Phe	Asn	Ile	Glu	Lys	Glu	Ile	Asp	Arg	Ala	Thr	Lys	Arg	Lys	Ile	Trp		
	290					295					300						
Leu	Ser	Ser	Gly	Gly	Tyr	Leu	Phe	Phe	Asp	Lys	Thr	Glu	Ala	Met	His		
305					310					315					320		
Thr	Ile	Asp	Val	Asn	Ser	Gly	Arg	Ser	Thr	Gln	Leu	Glu	Asn	Gly	Val		
			325						330					335			
Glu	Glu	Thr	Leu	Val	Gln	Ile	Asn	Leu	Glu	Ala	Ala	Glu	Glu	Ile	Ala		
			340					345					350				
Arg	Gln	Leu	Arg	Leu	Arg	Asn	Ile	Gly	Gly	Leu	Val	Ile	Ile	Asp	Phe		
		355				360						365					
Ile	Asp	Met	Lys	Ser	Arg	Lys	Asn	Gln	Arg	Arg	Val	Leu	Glu	Arg	Leu		
	370					375					380						
Lys	Glu	His	Met	Lys	Tyr	Asp	Ala	Ala	Arg	Cys	Thr	Ile	Leu	Ser	Met		
385					390					395					400		
Ser	Glu	Phe	Gly	Leu	Val	Glu	Met	Thr	Arg	Gln	Arg	Asn	Arg	Glu	Ser		
			405						410					415			
Leu	Met	Gln	Thr	Leu	Phe	Thr	Thr	Cys	Pro	Tyr	Cys	Asn	Gly	Asn	Ala		
		420						425					430				
Ile	Ile	Lys	Thr	Ser	Glu	Ser	Ile	Leu	Ile	Glu	Ile	Glu	Arg	Asp	Leu		
		435					440					445					
Lys	Lys	Ile	Ile	Lys	His	Lys	Glu	His	Thr	Asn	Leu	Cys	Leu	Val	Val		
	450					455					460						
His	Pro	Glu	Ile	Ala	His	Tyr	Met	Lys	Gln	Glu	Gln	Asp	Asp	Val	Glu		
465					470					475					480		
Leu	Ile	Arg	Leu	Ala	Lys	Gln	Leu	Lys	Ala	Lys	Leu	Gln	Ile	Asn	Thr		
			485					490						495			
Ser	Asp	Ser	Ile	His	Leu	Asn	His	Tyr	Gln	Phe	Phe	Ser	Leu	Ile	Thr		
			500					505					510				
Gly	Glu	Gly	Ile	Glu	Leu												
		515															

(2) INFORMATIONS POUR LA SEQ ID NO: 577:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 296 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 567079..567966

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 577:



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Lys Ile Ser Ala Glu Lys Ala Glu Ala Leu Cys Ser Gln Trp Leu Lys
1      5      10      15
Val Ile Ile Asp Asp Leu Lys Asn Pro Ile Ile Phe Pro Pro Tyr His
20      25      30
Lys Lys Ile Arg Ser Pro Ile Asp Leu Tyr Gln Phe Gly Ile Asp Phe
35      40      45
Phe Ser Ala Leu Ile Asp His Gln Lys Ser Gln Ile Leu His Pro Glu
50      55      60
Arg Leu Asp Gln Ile Gln Glu Tyr Ile Gln Ala Gly His Asn Val Val
65      70      75      80
Leu Leu Ala Asn His Gln Thr Glu Ser Asp Pro Gln Leu Met Tyr Cys
85      90      95
Leu Leu Gly Ala Ser His Pro Gln Leu Met Glu Ser Met Ile Phe Val
100     105     110
Ala Gly Asp Arg Ile Thr Ser Asp Pro Leu Ala Arg Pro Phe Ser Met
115     120     125
Gly Cys Asp Leu Leu Cys Ile Tyr Ser Lys Arg His Ile Asn His Pro
130     135     140
Pro Glu Leu Lys Glu Glu Lys Leu Met His Asn Gln Lys Ser Met Arg
145     150     155     160
Thr Leu Lys Met Leu Leu Ser Glu Gly Gly Lys Phe Phe Tyr Val Ala
165     170     175
Pro Ser Gly Gly Arg Asp Arg Lys Asn Leu Gln Gly Glu Leu Tyr Pro
180     185     190
Ala Glu Phe His Pro Asp Ser Val Glu Met Phe Arg Leu Leu Ala Lys
195     200     205
Ser Ser Gly Lys Thr Thr His Phe Phe Pro Leu Ala Met Lys Thr Tyr
210     215     220
Asp Ile Leu Pro Pro Pro Pro Thr Ile Glu Glu Ala Ile Gly Glu His
225     230     235     240
Arg Val Ile Ser Phe Ala Pro Val Ala Phe Asn Phe Gly Asp Glu Leu
245     250     255
Leu Leu Asp Glu Leu Cys Ser Ser Glu Glu Ala Asp Ile Tyr Asp Lys
260     265     270
His Ala Leu Arg Ala Leu Arg Ala Ser Arg Ala Phe Ser Ile Val Thr
275     280     285
Asp Leu Tyr Lys Glu Ile Leu Thr
290     295

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 578:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 769 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 568093..570399

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 578:

```

Leu Leu Leu Cys Ile Pro Ser Phe Leu Thr Ala Cys Ser Lys Ser Phe
1      5      10      15
Gln Thr Ile Arg Asp Glu Asn Pro Leu Thr Ile Leu Thr Pro Ala Leu
20      25      30

```

Ala Asp Gln Lys Ile Ala Lys Ile Leu Cys Pro Asn Gly Leu Ser Leu  
 35 40 45  
 Met Ile Val Ser Ser Pro His Ala Ala Glu Ser Gly Ala Ala Leu Val  
 50 55 60  
 Val Lys Thr Gly Asn Asn Ala Asp Pro Val Glu Phe Pro Gly Leu Ala  
 65 70 75 80  
 His Phe Thr Glu His Cys Val Phe Leu Gly Asn Glu Lys Tyr Pro Glu  
 85 90 95  
 Pro Ser Gly Phe Pro Ala Phe Leu Ser Thr His Gly Gly Ile Tyr Asn  
 100 105 110  
 Ala Phe Thr Tyr Pro Asp Lys Thr Cys Phe Leu Phe Ser Val Asn Asn  
 115 120 125  
 Ala Asp Leu Asp Asn Ala Leu Asp Gln Phe Val His Leu Phe Ile Gln  
 130 135 140  
 Pro Leu Phe Arg Gln Glu Asp Leu Asn Lys Glu Val His Ala Val Glu  
 145 150 155 160  
 Gln Glu Phe Ala Met His Pro Thr Lys Asp Ser Arg Arg Met His Arg  
 165 170 175  
 Ile Gln Gln Leu Ile Ala Pro Lys Asn His Pro Leu Lys Arg Phe Gly  
 180 185 190  
 Cys Gly Asn Leu Ser Thr Leu Asn Ser Val Thr Thr Gln Asp Met Gln  
 195 200 205  
 Thr Trp Phe Ala Thr His Tyr Ser Pro Glu Asn Met Ala Ala Ile Val  
 210 215 220  
 Tyr Thr Thr Ala Pro Leu Asp Thr Ala Val Pro Tyr Ile Ala Ser Leu  
 225 230 235 240  
 Phe Ser Glu Ile Pro Ile Ser Ala Gln Tyr Thr Pro Gln Lys Pro Phe  
 245 250 255  
 Pro Lys Thr Gln Asp Thr Thr Ala Leu Asn Lys Leu Phe Ile Asn Lys  
 260 265 270  
 Ala Val Glu Pro Ser Pro Gln Leu Ala Ile Tyr Trp His Phe Tyr Asp  
 275 280 285  
 Ala Pro Gln Ser Leu Gln Gly Trp Ala Gln Ser Leu Ile Ser Ile Leu  
 290 295 300  
 Ser Ser Glu Lys Glu Asn Ser Leu Val Ala Leu Leu Lys Lys Glu Gln  
 305 310 315 320  
 Leu Ile Thr Glu Met Glu Ala Glu Leu Tyr Ser Thr Ser His Asn Thr  
 325 330 335  
 Gln Asp Phe Glu Ile Leu Tyr Lys Leu Thr Asn Lys Gly Glu Arg Glu  
 340 345 350  
 Tyr Gln Arg Val Leu Gln Leu Thr Phe Ala Phe Leu Asp Tyr Val Arg  
 355 360 365  
 His Glu Arg Leu Pro Ala Tyr Ser Leu Pro Glu Ile Gln Lys Ile Asn  
 370 375 380  
 Ser Leu Glu Tyr Thr Tyr Ser Thr Gln Thr Glu Leu Phe Ser Thr Leu  
 385 390 395 400  
 Ser Arg Met Val Pro Asn Phe Thr Ser Glu Pro Leu Ala Thr Tyr Pro  
 405 410 415  
 Tyr Arg Ser Leu Val Tyr Pro Glu Tyr Ser Gln Glu Asp Glu Gln Thr  
 420 425 430  
 Phe Ala Thr Phe Leu Ala Asp Pro Gln Gln Ala Arg Tyr Ile Leu Ser  
 435 440 445  
 Ala Thr Leu Pro Ser Ser Trp Glu Asn Ala Asp Glu Phe Tyr Asp Pro  
 450 455 460  
 Ile Phe Asp Asp Thr Phe Tyr Glu Lys Pro Leu Asp Phe Thr Pro Ile  
 465 470 475 480  
 Gln Asp Ser Ser Ser Leu Gly Phe Ala Phe Pro Asn Pro Asn Lys Phe  
 485 490 495  
 Ile Pro Gln Thr Val Gln Leu Leu Ser Gln Lys Lys Gln His Glu Gly

```
(2)  INFORMATIONNELLES POUR LA SEQ ID NO: 579:

(i)  CARACTERISTIQUES DE LA SEQUENCE:
(A)  LONGUEUR: 251 acides aminés
(B)  TYPE: acide aminé
(D)  CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 571269..572021

(xi)  DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 579:

Thr Gly Leu Arg Ser Leu Gly Asp Ser Ala Ile Leu Ser Ile Phe Ile
1      5      10      15
Tyr Arg Ser Tyr Arg Ile Thr Met Ala Tyr Phe Asp Ser Arg Asn Tyr
20      25      30
Val Phe Ser Leu Phe Ile Ile Ala Met Leu Ile Leu Leu Glu Ser Arg
35      40      45
Pro Ile Glu Tyr Phe Ser Gln Arg Val Phe Ala Thr Ile Ala Lys Ile
50      55      60
```

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 251 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 571269..572021

Thr 1	Gly	Leu	Arg	Ser 5	Leu	Gly	Asp	Ser	Ala 10	Ile	Leu	Ser	Ile	Phe	Ile
Tyr	Arg	Ser	Tyr 20	Arg	Ile	Thr	Met	Ala 25	Tyr	Phe	Asp	Ser	Arg 30	Asn	Tyr
Val	Phe	Ser 35	Leu	Phe	Ile	Ile	Ala 40	Met	Leu	Ile	Leu	Leu 45	Glu	Ser	Arg
Pro	Ile 50	Glu	Tyr	Phe	Ser	Gln 55	Arg	Val	Phe	Ala	Thr 60	Ile	Ala	Lys	Ile

Gly	Lys	Gln	Ser	Pro	Ile	Cys	Trp	Trp	Trp	Thr	Ile	Met	Ile	Ala	Ala	
65					70					75					80	
Pro	Leu	Ser	Ala	Phe	Phe	Leu	Lys	Glu	Ser	Gly	Ala	Met	Ile	Ile	Ala	
				85					90					95		
Ala	Thr	Leu	Leu	Ser	Lys	Gln	Phe	Tyr	Lys	Phe	Ser	Pro	Ser	Pro	Lys	
			100					105					110			
Phe	Cys	Tyr	Ala	Thr	Met	Gly	Leu	Leu	Phe	Ser	Asn	Ile	Ser	Ile	Ser	
		115					120					125				
Gly	Leu	Thr	Ser	Ser	Phe	Ser	Ser	Arg	Ala	Leu	Leu	Thr	Ile	Leu	Pro	
	130					135						140				
Glu	Ile	Lys	Trp	Thr	Asn	Ser	Phe	Ile	Ile	Ser	His	Phe	Cys	Trp	Lys	
145					150					155					160	
Val	Ile	Leu	Ala	Ile	Leu	Val	Ser	Thr	Thr	Ile	Leu	Phe	Cys	Leu	Phe	
				165					170					175		
Arg	Lys	Glu	Phe	Lys	Lys	Phe	Pro	Lys	Thr	Ile	Pro	Ser	Thr	Thr	Met	
			180					185					190			
Met	Asn	Asp	Arg	Leu	Pro	Ser	Trp	Ile	Ile	Phe	Ile	His	Val	Val	Leu	
		195					200					205				
Val	Gly	Cys	Val	Ile	Leu	Ser	Arg	Ala	Ile	Pro	Leu	Phe	Leu	Gly	Phe	
	210					215				220						
Leu	Phe	Ile	Phe	Tyr	Leu	Gly	Phe	Gln	Arg	Phe	Thr	Ile	Phe	Tyr	Gln	
225					230					235					240	
His	Pro	Ile	Gln	Asn	Ser	Lys	Ser	Ser	Val	Ser						
				245					250							

(2) INFORMATIONS POUR LA SEQ ID NO: 580:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 79 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 572519..572755

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 580:

Gly	Tyr	Asn	Ser	Ala	Gly	Phe	Ile	Arg	Ser	Trp	Asn	Met	Gln	His	Thr	
1				5					10				15			
Ile	Met	Leu	Ser	Leu	Glu	Asn	Asp	Asn	Asp	Lys	Leu	Ala	Ser	Met	Met	
			20				25						30			
Asp	Arg	Val	Val	Ala	Ala	Ser	Ser	Ser	Ile	Leu	Ser	Ala	Ser	Lys	Asp	
		35				40						45				
Ser	Glu	Ser	Asn	Arg	Gln	Phe	Thr	Ile	Ser	Lys	Ala	Pro	Asp	Lys	Glu	
	50				55					60						
Ala	Pro	Cys	Arg	Val	Ser	Tyr	Val	Ala	Ala	Ser	Ala	Leu	Ser	Glu		
65					70					75						

(2) INFORMATIONS POUR LA SEQ ID NO: 581:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 263 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 581:

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 582:

Arg Thr Asn Lys Val Ala Pro Asp Pro Val Ser Pro Ile Cys Thr Gly  
1 5 10 15

```

Ser Ser Ala His Arg Leu Ser Ser Gln Cys Phe Phe Ser Phe Lys Ser
      20                      25                      30
Lys Arg Asn Arg Lys Thr Gly Phe Ser Lys Ser Phe Cys Val Tyr Ser
      35                      40                      45
Lys Phe Phe Leu Glu Glu Gln Ser Glu Gly Cys Thr Thr Ala Lys Ala
      50                      55                      60
Arg Leu Val Arg Thr Pro Ser Leu Glu Lys Tyr Lys Thr Tyr Leu Ser
65      70                      75                      80
Glu Thr Leu Ser Ser Arg Ala Ile Ile Phe Ser Pro Arg Ala Thr Pro
      85                      90                      95
Lys Ala Ala Pro Val Glu Lys Lys Lys Gly Val Ser Met Pro Ile Cys
      100                     105                     110
Ser Ala Lys Glu Arg Ile Ser Ser Ser Asp Ser Pro Val Leu Lys Ile
      115                     120                     125
Trp Phe Lys Ala Asn Asn Ala Val Ala Ala Leu Leu Leu Pro Pro Ala
      130                     135                     140
Arg Pro Ala Pro Thr Gly Ile Cys Leu Thr Thr Arg Gln Leu Thr Gly
145      150                     155                     160
Val Val Met Pro Val Tyr Arg Arg Lys Ser Ala Thr Leu Phe His Ile
      165                     170                     175
Glu Leu Leu Gly Val Ser Arg
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 583:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 77 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(573660..573890)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 583:

```

Met Tyr Gly Ser Val Thr Val Asn Asp Met Ile Ser Ala Ala Glu Gln
1      5                      10                      15
Gln Gly Val Val Leu Thr Arg Lys Asn Phe Pro Arg Ser His Ser Gly
      20                      25                      30
Ile Lys Asn Leu Gly Arg His Val Val Gly Leu Lys Leu Lys Glu Gly
      35                      40                      45
Val Thr Ala Asp Leu His Leu Glu Val Arg Ala Asp His Glu Ile Ile
      50                      55                      60
Glu Gln Lys Glu Leu Gln Ser Ala Glu Glu Gln Glu Gly
65      70                      75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 584:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 81 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(574184..574426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 584:

Met	Asn	Arg	Pro	Val	His	Asn	Glu	His	Arg	Arg	Lys	Arg	Phe	Ala	Lys
1				5				10					15		
Lys	Cys	Pro	Phe	Val	Ser	Ala	Gly	Trp	Lys	Thr	Ile	Asp	Tyr	Lys	Asp
			20				25					30			
Val	Thr	Thr	Leu	Lys	Arg	Phe	Ile	Thr	Glu	Arg	Gly	Lys	Ile	Leu	Pro
		35				40					45				
Arg	Arg	Ile	Thr	Gly	Val	Ser	Ser	Arg	Phe	Gln	Ala	Leu	Leu	Ala	Gln
	50				55					60					
Ala	Val	Lys	Arg	Ala	Arg	His	Val	Gly	Leu	Leu	Pro	Phe	Val	Gly	Glu
65					70				75						80
Asp															

(2) INFORMATIONS POUR LA SEQ ID NO: 585:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 112 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(574446..574781)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 585:

Met	Gln	Lys	Lys	Thr	Gly	Gln	Leu	Tyr	Glu	Gly	Ala	Tyr	Val	Phe	Ser
1				5				10					15		
Val	Thr	Leu	Ser	Glu	Asp	Ala	Arg	Arg	Lys	Ala	Leu	Glu	Lys	Val	Thr
			20				25					30			
Ser	Gly	Ile	Thr	Asn	Tyr	Gly	Gly	Glu	Val	Leu	Lys	Ile	His	Asp	Gln
		35				40					45				
Gly	Arg	Lys	Lys	Leu	Ala	Tyr	Thr	Ile	Arg	Gly	Ala	Arg	Glu	Gly	Tyr
	50				55					60					
Tyr	Tyr	Phe	Ile	Tyr	Phe	Thr	Val	Ala	Pro	Glu	Ala	Ile	Ala	Glu	Leu
65					70				75						80
Trp	Arg	Glu	Tyr	His	Leu	Asn	Glu	Asp	Leu	Leu	Arg	Phe	Met	Thr	Leu
			85				90						95		
Lys	Ala	Ser	Ala	Val	Lys	Glu	Val	Leu	Glu	Phe	Ala	Thr	Leu	Pro	Glu
			100				105						110		

(2) INFORMATIONS POUR LA SEQ ID NO: 586:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(574923..575243)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 586:

```

Ser Cys Leu Ser Cys Gln Glu Val Phe Arg Cys Phe His Gly Arg Tyr
1          5          10          15
Ser Cys Cys Ser Arg Arg His His Arg Glu Phe Gly Phe Val Arg Phe
20          25          30
Arg Gln Asp Cys Gly Ser Gly Gly His Asn Gly Ile Lys Asn Thr Thr
35          40          45
Gln Ile Leu Gln Ser Asn His Tyr Trp Gln Leu Arg Leu Gly Val Gly
50          55          60
Arg Pro Ser Tyr Pro Gly Ala Glu Gly Val Ala Asp Tyr Val Leu Ser
65          70          75          80
Ser Phe Ser Leu Asn Glu Lys Glu Lys Leu Asn Asp Phe Leu Glu Lys
85          90          95
Gly Ile Glu Glu Ile Leu Pro Trp Leu Gly Cys
100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 587:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(575057..575458)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 587:

```

Met Val Lys Leu Val Val Gly Ile Gly Asn Pro Gly Arg Gln Tyr Val
1          5          10          15
Trp Thr Arg His Asn Ile Gly Phe Leu Leu Leu Asp Ser Leu Ala Ser
20          25          30
Arg Phe Leu Gly Ala Phe Arg Glu Ala Pro Arg Leu Tyr Ala Ser Phe
35          40          45
Ala Lys Val Glu Ile Ser Ser Glu Ala Val Val Leu Met Lys Pro Thr
50          55          60
Thr Tyr Val Asn Leu Thr Gly Lys Ala Val Leu Ala Ala Lys Lys Phe
65          70          75          80
Phe Asp Val Ser Met Glu Asp Ile Leu Val Val Ala Asp Asp Ile Ile
85          90          95
Gly Asn Ser Val Leu Cys Val Phe Gly Lys Ile Val Ala Leu Val Gly
100          105          110
Thr Met Glu Leu Arg Ile Pro Arg Arg Phe Cys Asn Pro Ile Ile Ile
115          120          125
Gly Asn Tyr Val Leu Gly
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 588:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé



(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(575469..575849)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 588:

```

Leu Leu Leu Cys Ser Arg Phe Leu Asn Glu Gly Arg Glu Ile Lys Ala
1          5          10          15
Leu Val Lys Asp Ile Gln Tyr His Val Thr Thr Tyr Asp Val Ile His
          20          25          30
Leu Asp Phe Glu Glu Leu Val Asp Gly Arg Asp Val Arg Leu Asn Val
          35          40          45
Pro Ile Arg Cys Ile Asn Thr Val Asp Cys Val Gly Val Lys Leu Gly
          50          55          60
Gly Ser Leu Arg Gln Val Ile Arg Cys Ile Arg Val Val Cys Lys Pro
65          70          75          80
Lys Asp Ile Val Pro Phe Leu Glu Leu Asp Val Gln Ser Leu Gly Leu
          85          90          95
Ser Gln Thr Leu Lys Leu Ser Asp Ile Cys Ile Pro Glu Gly Ile Arg
          100          105          110
Pro Val Thr Ser Leu Lys Glu Val Ala Val Thr Val Ala Arg Arg
          115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 589:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 474 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 576602..578023

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 589:

```

Met Lys Ile Ile His Thr Ala Ile Glu Phe Ala Pro Val Ile Lys Ala
1          5          10          15
Gly Gly Leu Gly Asp Ala Leu Tyr Gly Leu Ala Lys Ala Leu Ala Ala
          20          25          30
Asn His Thr Thr Glu Val Val Ile Pro Leu Tyr Pro Lys Leu Phe Thr
          35          40          45
Leu Pro Lys Glu Gln Asp Leu Cys Ser Ile Gln Lys Leu Ser Tyr Phe
          50          55          60
Phe Ala Gly Glu Gln Glu Ala Thr Ala Phe Ser Tyr Phe Tyr Glu Gly
65          70          75          80
Ile Lys Val Thr Leu Phe Lys Leu Asp Thr Gln Pro Glu Leu Phe Glu
          85          90          95
Asn Ala Glu Thr Ile Tyr Thr Ser Asp Asp Ala Phe Arg Phe Cys Ala
          100          105          110
Phe Ser Ala Ala Ala Ala Ser Tyr Ile Gln Lys Glu Gly Ala Asn Ile
          115          120          125
Val His Leu His Asp Trp His Thr Gly Leu Val Ala Gly Leu Leu Lys
          130          135          140

```

Gln Gln Pro Cys Ser Gln Leu Gln Lys Ile Val Leu Thr Leu His Asn  
 145 150 155 160  
 Phe Gly Tyr Arg Gly Tyr Thr Thr Arg Glu Ile Leu Glu Ala Ser Ser  
 165 170 175  
 Leu Asn Glu Phe Tyr Ile Ser Gln Tyr Gln Leu Phe Arg Asp Pro Gln  
 180 185 190  
 Thr Cys Val Leu Leu Lys Gly Ala Leu Tyr Cys Ser Asp Phe Val Thr  
 195 200 205  
 Thr Val Ser Pro Thr Tyr Ala Lys Glu Ile Leu Glu Asp Tyr Ser Asp  
 210 215 220  
 Tyr Glu Ile His Asp Ala Ile Thr Ala Arg Gln His His Leu Arg Gly  
 225 230 235 240  
 Ile Leu Asn Gly Ile Asp Thr Thr Ile Trp Gly Pro Glu Thr Asp Pro  
 245 250 255  
 Asn Leu Ala Lys Asn Tyr Thr Lys Glu Leu Phe Glu Thr Pro Ser Ile  
 260 265 270  
 Phe Phe Glu Ala Lys Ala Glu Asn Lys Lys Ala Leu Tyr Glu Arg Leu  
 275 280 285  
 Gly Leu Ser Leu Glu His Ser Pro Cys Val Cys Ile Ile Ser Arg Ile  
 290 295 300  
 Ala Glu Gln Lys Gly Pro His Phe Met Lys Gln Ala Ile Leu His Ala  
 305 310 315 320  
 Leu Glu Asn Ala Tyr Thr Leu Ile Ile Ile Gly Thr Cys Tyr Gly Asn  
 325 330 335  
 Gln Leu His Glu Glu Phe Ala Asn Leu Gln Glu Ser Leu Ala Asn Ser  
 340 345 350  
 Pro Asn Val Arg Ile Leu Leu Thr Tyr Ser Asp Val Leu Ala Arg Gln  
 355 360 365  
 Ile Phe Ala Ala Ala Asp Met Ile Cys Ile Pro Ser Met Phe Glu Pro  
 370 375 380  
 Cys Gly Leu Thr Gln Met Ile Gly Met Arg Tyr Gly Thr Val Pro Leu  
 385 390 395 400  
 Val Arg Ala Thr Gly Gly Leu Ala Asp Thr Val Ala Asn Gly Ile Asn  
 405 410 415  
 Gly Phe Ser Phe Phe Asn Pro His Asp Phe Tyr Glu Phe Arg Asn Met  
 420 425 430  
 Leu Leu Glu Ala Val Thr Thr Tyr Arg Thr Asn His Asp Lys Trp Gln  
 435 440 445  
 His Ile Val Arg Ala Cys Leu Asn Phe Ser Ser Asp Leu Glu Thr Ala  
 450 455 460  
 Ala Asn Lys Tyr Leu Glu Ile Tyr Lys Gln  
 465 470

(2) INFORMATIONS POUR LA SEQ ID NO: 590:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 208 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(578017..578640)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 590:

Met Arg Val Ser Leu Pro Asn Phe Leu Thr Val Phe Arg Leu Phe Ile

1				5				10					15				
Thr	Pro	Ile	Phe	Met	Ile	Leu	Tyr	Leu	Lys	Gly	Arg	Trp	Phe	Gly	Leu		
			20					25					30				
Ser	Ala	Ala	Phe	Leu	Pro	Tyr	Val	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Thr		
		35					40					45					
Glu	Ile	Thr	Asp	Ala	Val	Asp	Gly	Tyr	Ile	Ala	Arg	Lys	Phe	Ser	Gln		
	50					55					60						
Val	Thr	Asp	Leu	Gly	Lys	Leu	Leu	Asp	Pro	Met	Ala	Asp	Ser	Val	Tyr		
65					70					75					80		
Arg	Ile	Ser	Leu	Tyr	Leu	Thr	Phe	Thr	Gln	Pro	Pro	Val	Asn	Leu	Pro		
				85					90					95			
Leu	Ile	Leu	Val	Phe	Ile	Phe	Leu	Ala	Arg	Asp	Ser	Val	Ile	Ser	Thr		
			100					105					110				
Leu	Arg	Thr	Leu	Cys	Ala	Ser	Arg	Gly	Gln	Val	Leu	Ala	Ala	Arg	Met		
		115					120					125					
Ser	Gly	Lys	Leu	Lys	Ala	Ile	Leu	Gln	Ala	Ile	Ser	Phe	Phe	Phe	Ile		
	130					135					140						
Ile	Phe	Ser	Met	Phe	Leu	Cys	Ala	Lys	Gly	Ile	Ile	Ser	Thr	Asp	Asp		
145				150						155					160		
Leu	Glu	Phe	Phe	Ser	Thr	Val	Ile	Val	Ser	Leu	Val	Ala	Phe	Tyr	Ser		
				165					170					175			
Ile	Cys	Ser	Gly	Val	Glu	Tyr	Ile	Trp	Val	Asn	Lys	Ser	His	Leu	Leu		
			180					185					190				
Gln	Lys	Asn	Asp	Ser	Arg	Met	Ala	Ser	His	Arg	Glu	Val	Tyr	Cys	Leu		
		195					200					205					

(2) INFORMATIONS POUR LA SEQ ID NO: 591:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1003 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 579096..582104

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 591:

Met	Ser	Ser	Gln	Pro	Leu	Thr	Leu	Gln	Ala	Met	Met	Ala	Ala	Ile	Leu		
1				5				10						15			
Asn	Phe	Trp	Ser	Glu	Gln	Gly	Cys	Ile	Ile	His	Gln	Gly	Tyr	Asp	Leu		
			20					25					30				
Glu	Val	Gly	Ala	Gly	Thr	Phe	Asn	Pro	Ala	Thr	Phe	Leu	Gln	Ser	Leu		
		35					40					45					
Gly	Pro	Glu	Pro	Phe	Arg	Thr	Ala	Tyr	Ile	Glu	Pro	Ser	Arg	Arg	Pro		
	50					55					60						
Gln	Asp	Gly	Arg	Tyr	Gly	Gln	His	Pro	Asn	Arg	Leu	Gln	Lys	Tyr	His		
65				70						75					80		
Gln	Leu	Gln	Val	Ile	Leu	Lys	Pro	Val	Pro	Glu	Asn	Phe	Leu	Ser	Leu		
				85				90						95			
Tyr	Leu	Glu	Ser	Leu	Lys	Val	Ile	Gly	Leu	Asn	Leu	Val	Asp	His	Asp		
			100					105					110				
Ile	Arg	Phe	Val	His	Asp	Asp	Trp	Glu	Asn	Pro	Thr	Ile	Gly	Ala	Trp		
		115					120						125				
Gly	Leu	Gly	Trp	Glu	Val	Trp	Leu	Asn	Gly	Met	Glu	Ile	Thr	Gln	Leu		
	130						135					140					

Thr	Tyr	Phe	Gln	Ala	Val	Gly	Ser	Lys	Pro	Leu	Asp	Ala	Ile	Ser	Gly
145					150					155					160
Glu	Ile	Thr	Tyr	Gly	Val	Glu	Arg	Ile	Ala	Met	Tyr	Leu	Gln	Lys	Lys
				165					170					175	
Asn	Ser	Val	Tyr	Asp	Val	Met	Trp	Asn	Gly	Ser	Leu	Thr	Tyr	Gly	Asp
			180					185					190		
Ile	Thr	Gln	Tyr	Ala	Glu	Gln	Ala	Trp	Ser	Gln	Tyr	Asn	Phe	Glu	Thr
		195					200					205			
Ala	Asn	Thr	Thr	Met	Trp	Leu	Lys	His	Phe	Asp	Asp	Phe	Ser	Ala	Glu
	210					215					220				
Ala	Leu	Ala	Thr	Leu	Asp	Gln	Gly	Leu	Pro	Leu	Pro	Ala	Tyr	Asp	Phe
225					230					235					240
Val	Ile	Lys	Ala	Ser	His	Ala	Phe	Asn	Met	Leu	Asp	Ser	Arg	Gly	Val
				245					250					255	
Ile	Ser	Val	Thr	Glu	Arg	Thr	Arg	Tyr	Ile	Ala	Lys	Ile	Arg	Gln	Leu
			260					265						270	
Ala	Arg	Ala	Ala	Ala	Asp	Lys	Tyr	Val	Ala	Trp	Arg	Glu	Ser	Leu	Gly
		275					280					285			
Phe	Pro	Leu	Leu	Lys	Thr	Pro	Pro	Ser	Thr	Pro	Thr	Val	Thr	Pro	Lys
	290					295					300				
Lys	Ile	Pro	Thr	Ile	Cys	Gln	Pro	Glu	Asp	Phe	Leu	Leu	Glu	Ile	Gly
305					310					315					320
Ser	Glu	Glu	Leu	Pro	Ala	Thr	Phe	Val	Pro	Thr	Gly	Ile	Gln	Gln	Leu
				325					330					335	
Glu	Ser	Leu	Ala	Lys	Lys	Leu	Leu	Ala	Asp	His	Gly	Ile	Ala	Tyr	Lys
			340					345					350		
His	Leu	Glu	Val	Leu	Gly	Thr	Pro	Arg	Arg	Leu	Ala	Leu	Cys	Ile	Glu
		355					360					365			
Gly	Leu	Ser	His	Val	Thr	Ile	Arg	Pro	Glu	Ser	Glu	Lys	Lys	Gly	Pro
	370					375					380				
Pro	Leu	Ser	Leu	Leu	Phe	Met	Thr	Asp	Gly	Ser	Val	Ser	Pro	Gln	Gly
385					390					395					400
Glu	Gln	Phe	Phe	Pro	Ser	His	Gly	Leu	Ser	Ile	Ser	His	Arg	Ser	Ala
				405					410					415	
Leu	Asp	Gln	Pro	Ser	Ala	Ile	Cys	Arg	Val	Arg	Ser	Ile	Asn	Gly	Thr
			420					425					430		
Asp	Tyr	Leu	Phe	Leu	Val	Ile	Pro	Glu	Glu	Arg	Lys	Glu	Thr	Ala	Ala
		435					440					445			
Ile	Leu	Val	Asn	Glu	Leu	Pro	Gln	Leu	Ile	Arg	Ser	Ile	Arg	Phe	Pro
	450					455					460				
Gln	Lys	Met	Thr	Trp	Asp	Asn	Gly	Gly	Val	Glu	Tyr	Ala	Arg	Pro	Ile
465					470					475					480
Arg	Trp	Leu	Val	Ala	Leu	Tyr	Gly	Asp	Gln	Ile	Leu	Pro	Ile	Ser	Leu
				485		-			490					495	
Gly	Phe	Val	Ser	Ser	Gly	Asn	Thr	Ser	Trp	Gly	His	Arg	Gln	Leu	Asp
			500					505					510		
Asn	Arg	Gln	Leu	Thr	Ile	Pro	Ser	Ser	Asn	Met	Tyr	Val	Asp	Thr	Leu
		515					520					525			
Arg	Ser	Ala	Cys	Val	Ile	Val	Ser	Gln	Lys	Glu	Arg	Arg	Ala	Ile	Ile
	530					535					540				
Lys	Gln	Gly	Leu	Gln	Asn	Leu	Thr	Gly	Asp	Gln	Ile	Val	Ala	Ile	Ala
545					550					555					560
Pro	Glu	His	Leu	Val	Asp	Glu	Thr	Val	Phe	Leu	Thr	Glu	His	Pro	Phe
				565					570					575	
Val	Ile	Ser	Ala	Gln	Phe	Asp	Pro	Ala	Phe	Cys	Ser	Leu	Pro	Lys	Glu
			580					585					590		
Leu	Leu	Ile	Ala	Glu	Met	Ile	Gln	His	Gln	Arg	Tyr	Phe	Pro	Thr	Gln
		595					600					605			
Asn	Met	Gln	Gly	Glu	Ile	Thr	Asn	Arg	Phe	Leu	Ile	Val	Cys	Asp	Asn

610	615	620
Ser Pro Thr Asp Ser Ile Val Glu Gly Asn Glu Lys Ala Leu Ala Pro		
625	630	635
Arg Leu Thr Asp Gly Asn Phe Leu Phe Lys Gln Asp Leu Leu Thr Pro		640
	645	650
Leu Ser Ser Phe Val Glu Lys Leu Lys Ser Val Thr Tyr Phe Glu Ser		655
	660	665
Leu Gly Ser Leu Ala Asp Lys Thr Ser Arg Leu Lys Leu His Leu Glu		670
	675	680
Glu Ala Tyr Ala Leu Leu Pro Leu Cys Ala Lys Glu Asp Ile Asp Thr		685
	690	695
Ala Ile His Tyr Cys Lys Ala Asp Leu Val Ser Ser Val Val Asn Glu		700
705	710	715
Phe Pro Glu Leu Gln Gly Ile Met Gly Arg Tyr Tyr Leu Gln Asn Ala		720
	725	730
Ser Leu Ser Arg Ala Ala Ala Leu Ala Ile Gly Glu His Leu Gln His		735
	740	745
Ile Thr Leu Gly Ser Asn Ile Ser Thr Thr Gly Ala Leu Leu Ser Ile		750
	755	760
Leu Asp Arg Ile Asp Asn Leu Leu Ser Cys Phe Ile Leu Gly Leu Leu		765
	770	775
Pro Thr Ser Ser His Asp Pro Tyr Ala Leu Arg Arg Gln Ser Leu Glu		780
785	790	795
Ile Leu Thr Leu Leu Tyr Thr Thr Gln Ser Ser Val Asp Ile Glu Asp		800
	805	810
Leu Phe Ala Arg Leu Ile Arg His Phe Pro Ser Ser Ile Pro Asn Thr		815
	820	825
Val Trp Ser Pro Glu Glu Val Leu Ser Lys Leu Asn Thr Phe Val Trp		830
	835	840
Gly Arg Leu Arg Thr Ile Leu Ser Ser Leu Gly Phe Asp Lys Glu Ile		845
	850	855
Ile Ala Thr Val Leu Thr Asp Asn Cys Pro Lys Asn Pro Leu Thr Ile		860
865	870	875
Ile Gln Ser Ala Gln Ser Ile Gln Glu Leu Lys Asn Thr Gln Ile Leu		880
	885	890
Lys Thr Ile Ala Ala Thr His Asn Arg Leu Lys Lys Ile Leu Ala Ser		895
	900	905
Leu Ser Phe Ser Val Thr Glu Gln Met Phe Ser Leu Gln Ser Ala Glu		910
	915	920
Asp Leu Leu Phe Lys Gln Ala Leu Asp Arg Phe Val Glu Glu Thr Thr		925
	930	935
Ala Leu Pro Ile Ser Ser Lys Asp Tyr Leu His Leu Leu Lys Glu Leu		940
945	950	955
Ala Gln Ser Thr Glu Leu Phe Leu Asp Ser Val Arg Val Ala Ser Asp		960
	965	970
Asp Glu Ser Thr Arg Asn Gln Arg Ile Ala Leu Leu Ile Ala Ala Gln		975
	980	985
Lys Cys Phe Gly Phe Tyr Ala Trp Asp Val Leu		990
	995	1000

(2) INFORMATIONS POUR LA SEQ ID NO: 592:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 164 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 592:

(2) INFORMATION POUR LA SEQ ID NO: 593:

(A) LONGUEUR: 104 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(582811..583122)

[illegible]

Xaa	His	Ser	Tyr	Glu	Gln	Phe	Thr	Pro	Arg	Glu	Lys	Ala	Arg	Val	Ile
1				5					10					15	
Glu	Glu	Val	Ile	Gln	Gln	Val	Arg	Cys	Trp	Gly	Ser	Pro	Ile	Thr	Ile
			20					25					30		
His	Glu	Tyr	Leu	Arg	Gln	Leu	Ala	Ser	Leu	Val	Lys	Val	Pro	Glu	Pro
		35				40						45			
Ala	Val	Leu	Ser	Tyr	Leu	Ser	Ser	Ile	Thr	Ser	Ala	Ala	Glu	Asp	Lys
	50					55					60				
Gly	Lys	Lys	Val	Ser	Ala	Lys	Glu	Pro	Ser	Ser	Glu	Ser	Glu	Gln	Thr
65				70						75				80	
Ser	Thr	Glu	Gly	Lys	Ile	Ser	Lys	Lys	Ile	Ser	Pro	Arg	Met	Ile	Leu
			85						90					95	
Glu	Ala	Asp	Val	Ile	Arg	Cys	Leu	Leu	Phe	Xaa	Lys	Pro	Glu	Asp	Glu
			100					105					110		

Phe	Val	Pro	Ala	Thr	Val	Lys	Gln	Tyr	Leu	Ser	Pro	Glu	Glu	Phe	His
		115					120					125			
Cys	Gly	Arg	Ile	Ser	Ser	Tyr	Ile	Cys	Tyr	Gly	Tyr	Glu	Ser	Leu	Gln
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 596:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(583827..584435)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 596:

Ser	Gly	Leu	Gly	Ile	Ser	Leu	Lys	Thr	Gly	Phe	Cys	Leu	Leu	Arg	Ser
1				5					10					15	
Ile	Met	Phe	Pro	Ile	Gln	Asp	Ala	Leu	Gly	Tyr	Thr	Ile	Gly	Phe	Ser
			20					25					30		
Ser	Arg	Arg	Phe	Lys	Glu	Gly	Gly	Arg	Gly	Gly	Lys	Tyr	Ile	Asn	Ser
		35				40						45			
Pro	Glu	Thr	Ile	Leu	Phe	Lys	Lys	Ser	Arg	Val	Leu	Tyr	Gly	Leu	Gln
	50					55					60				
Phe	Ser	Arg	Lys	Arg	Ile	Ala	Lys	Glu	Arg	Arg	Val	Ile	Leu	Val	Glu
65				70					75						80
Gly	Gln	Ala	Asp	Cys	Leu	Gln	Met	Ile	Asp	Phe	Gly	Phe	Asn	Cys	Thr
			85						90					95	
Leu	Ala	Ala	Gln	Gly	Thr	Ser	Phe	Thr	Glu	Thr	His	Val	His	Glu	Leu
			100					105					110		
Val	Lys	Leu	Gly	Val	Ser	Lys	Ala	Tyr	Leu	Leu	Phe	Asp	Gly	Asp	Ala
		115					120					125			
Ala	Gly	Glu	Lys	Ala	Ser	Leu	Arg	Val	Gly	Asp	Leu	Cys	Gln	Ala	Ala
	130					135					140				
Gly	Ile	Thr	Ala	Ile	Val	Cys	Arg	Leu	Pro	Ser	Gly	Gln	Asp	Pro	Asp
145				150					155						160
Ser	Phe	Leu	Met	Gln	Arg	Gly	Pro	Glu	Glu	Leu	Arg	Glu	Leu	Leu	Asp
			165						170					175	
Arg	Gly	Glu	Asp	Tyr	Leu	Ser	Phe	Leu	Val	Trp	His	Lys	Xaa	Ile	Leu
		180						185					190		
Met	Asn	Ser	Leu	Leu	Gln	Glu	Lys	Lys	Leu	Glu					
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 597:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 223 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(584299..584967)



## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 597:

Met	Tyr	Tyr	Thr	Glu	Glu	Ser	Leu	Glu	Thr	Leu	Lys	His	Ser	Ile	Asp	1	5	10	15
Ile	Val	Ser	Val	Leu	Gly	Glu	Tyr	Val	His	Leu	Lys	Arg	Ser	Gly	Ala	20	25	30	
Asp	Tyr	Lys	Ala	Cys	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe	35	40	45	
Ile	Val	Tyr	Pro	Thr	Arg	Gly	His	Tyr	His	Cys	Tyr	Gly	Cys	Gly	Glu	50	55	60	
His	Gly	Asp	Ala	Ile	Asn	Phe	Leu	Met	Lys	Gln	Gln	Gly	Tyr	Ser	Phe	65	70	75	80
Ser	Glu	Ala	Val	Leu	Phe	Leu	Ala	Lys	Lys	Phe	His	Val	Asp	Leu	Val	85	90	95	
Val	Arg	Thr	Arg	Glu	Thr	Ser	Gly	Gln	Asp	Ser	Lys	Asp	Ser	Phe	Arg	100	105	110	
Arg	Ile	Asn	Arg	Glu	Ala	Glu	Arg	Phe	Phe	Gln	Tyr	Cys	Leu	Leu	His	115	120	125	
Leu	Pro	Glu	Gly	Glu	Glu	Ala	Leu	Ala	Tyr	Leu	Tyr	Lys	Arg	Gly	Phe	130	135	140	
Ser	Pro	Asp	Thr	Ile	Asp	Arg	Phe	Gln	Ile	Gly	Tyr	Ala	Pro	Glu	Gln	145	150	155	160
Arg	Leu	Phe	Ile	Gln	Ala	Met	Glu	Glu	Arg	Asn	Ile	Cys	Val	Lys	Gln	165	170	175	
Leu	Glu	Trp	Ala	Gly	Tyr	Leu	Ala	Lys	Asp	Trp	Phe	Leu	Phe	Ala	Gln	180	185	190	
Glu	His	His	Val	Pro	Asp	Ser	Arg	Cys	Phe	Arg	Leu	Tyr	His	Trp	Ile	195	200	205	
Phe	Phe	Ser	Glu	Val	Gln	Arg	Arg	Trp	Ala	Trp	Trp	Lys	Ile	Tyr		210	215	220	

## (2) INFORMATIONS POUR LA SEQ ID NO: 598:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 94 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(585016..585297)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 598:

Leu	Tyr	Leu	Val	Leu	Arg	Asp	Arg	Lys	Asn	Phe	Leu	Phe	Val	Val	Gly	1	5	10	15
Glu	Gln	Ala	Leu	Met	Tyr	Gln	Arg	Thr	Phe	Glu	Thr	Arg	Val	Tyr	Asn	20	25	30	
Gly	Val	Glu	Phe	Leu	Gly	Asn	Thr	Arg	Leu	Trp	Glu	Ala	Lys	Phe	Leu	35	40	45	
Arg	Glu	Lys	Gly	Ile	His	Gln	Gly	Glu	Arg	Ser	Thr	His	Ser	Gln	Glu	50	55	60	
Asn	Tyr	Ser	Ala	Leu	Pro	Trp	Arg	Ile	Leu	Tyr	Arg	Arg	Arg	Ala	Gly	65	70	75	80
Ile	Ala	Cys	Lys	Lys	Ile	Leu	Tyr	Asp	Ala	Tyr	Ile	His	Glu			85	90		

(2) INFORMATIONS POUR LA SEQ ID NO: 599:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 457 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 585240..586610

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 599:

Glu	Pro	Val	Pro	Leu	Leu	Arg	Ile	Lys	Asn	Phe	Phe	Asp	His	Ala	Ile
1				5					10					15	
Leu	Asp	Lys	Ala	Met	Thr	His	Lys	Leu	Thr	Pro	Met	Met	Gln	Gln	Trp
			20					25					30		
His	Gln	Cys	Lys	Glu	Gln	Ala	Gly	Asp	Cys	Leu	Leu	Leu	Phe	Arg	Leu
		35					40					45			
Gly	Glu	Phe	Tyr	Glu	Ala	Phe	Phe	Asp	Asp	Ala	Leu	Ile	Leu	Ala	Gln
	50					55					60				
Asn	Leu	Asp	Ile	Thr	Leu	Thr	Gln	Arg	Gln	Asn	Val	Pro	Met	Ser	Gly
65					70					75					80
Ile	Pro	Ala	Thr	Cys	Leu	Asp	Gly	Tyr	Val	Asp	Arg	Leu	Val	Ser	Arg
				85					90					95	
Gly	Phe	Lys	Val	Ala	Ile	Ala	Glu	Gln	Ala	Asp	Asn	Thr	Glu	Gly	Ser
			100					105					110		
Lys	Gly	Leu	Val	Pro	Arg	Thr	Ile	Asn	Arg	Leu	Ile	Thr	Pro	Gly	Ala
		115					120					125			
Leu	Leu	Ser	Ser	Ser	Leu	Leu	Pro	Glu	Lys	Ala	Asn	Asn	Tyr	Val	Leu
	130					135					140				
Ala	Ile	Asn	Gln	Val	Gly	Ser	Leu	Tyr	Gly	Leu	Ser	Cys	Leu	Asp	Leu
145					150					155					160
Ser	Ile	Gly	Thr	Phe	Leu	Val	Ala	Glu	Tyr	Asp	Asn	Thr	Lys	Asp	Leu
				165					170					175	
Ile	Glu	Ala	Ile	Cys	Arg	Leu	Ala	Pro	Thr	Glu	Leu	Leu	Ser	His	Ala
			180					185					190		
Lys	Phe	Tyr	Gln	Lys	Asn	Ala	Ala	Val	Ile	Lys	Gln	Leu	Gln	Gln	His
		195					200					205			
Leu	Arg	Ile	Thr	Leu	Ser	Glu	Tyr	Val	Ser	Trp	Ala	Phe	Glu	Tyr	Gln
	210					215					220				
Ser	Ala	Thr	Lys	Lys	Leu	Tyr	Thr	Cys	Phe	Gln	Val	Ser	Ser	Leu	Asp
225					230					235					240
Gly	Phe	Gly	Leu	Gln	Gly	Leu	Val	Pro	Ala	Ile	Asn	Ala	Ala	Gly	Ala
				245					250					255	
Leu	Leu	Ser	Tyr	Ile	Gln	Asp	Lys	Leu	Leu	Leu	Pro	Ile	Ser	His	Leu
			260					265					270		
Ser	Ile	Pro	Lys	Ile	Tyr	Gly	Gln	Lys	His	Leu	Leu	Ile	Asp	Lys	
		275					280					285			
Ala	Ser	Gln	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Pro	Ile	His	Gly	Glu	His
	290					295					300				
Gly	Lys	Gly	Ser	Leu	Leu	Gln	Val	Met	Glu	Arg	Thr	Ser	Thr	Pro	Met
305					310					315					320
Gly	Gly	Arg	Leu	Leu	Arg	Asn	Thr	Leu	Ile	Asn	Pro	Phe	Tyr	Asp	Leu
				325					330					335	
Lys	Glu	Ile	Thr	Leu	Arg	Gln	Asp	Ser	Val	Glu	Phe	Phe	Leu	Gln	Gln

(2) INFORMATION POUR LA SEQ ID NO: 600:

(A) LONGUEUR: 425 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 586484..587758

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 600:

Val 1	Phe	Asp	Cys	Ser 5	Pro	Ser	Met	Leu	Ser 10	His	Lys	Asn	Val	Ile 15	Asp
Arg	Ala	Tyr	Pro 20	Arg	Thr	Ser	Phe	Lys 25	Ser	Val	Arg	Arg	Asn 30	Ile	Phe
Ala	Asn	His 35	Tyr	His	Pro	Asp	Leu 40	Leu	Arg	Leu	Arg	Asn 45	Ile	Lys	Glu
Asn	Ser 50	Lys	Ser	Trp	Ile	Leu 55	Glu	Tyr	Gln	Glu	Arg 60	Ile	Arg	Asn	Glu
Thr 65	Gly	Ile	Lys	Lys	Leu 70	Lys	Val	Cys	Tyr	Ala 75	Gln	Ala	Leu	Gly 80	Tyr
Tyr	Ile	Glu	Val 85	Ala	Ser	Asn	Leu	Ala 90	Pro	Gln	Leu	Pro	Lys	Glu 95	Phe
Ile	Arg	Arg	Gln 100	Ser	Arg	Leu	His	Ala 105	Glu	Arg	Phe	Thr	Thr	Gln	Glu
Leu	Gln	Gln 115	Phe	Gln	Asp	Glu	Val 120	Phe	Ser	Val	Glu	Asp 125	Lys	Leu	Gln
Thr 130	Leu	Glu	Thr	Lys	Leu	Phe 135	Lys	Glu	Leu	Cys	Phe 140	Tyr	Ile	Val	Glu
His 145	Arg	Asp	Leu	Ile 150	Leu	Lys	Leu	Ser	Thr	Ala 155	Val	Ala	Asp	Leu 160	Asp
Tyr	Val	Val	Ser 165	Leu	Ala	Glu	Leu	Ala 170	Ala	Glu	Tyr	Asp	Tyr	Arg 175	Arg
Pro	Leu	Val	Asp 180	His	Ser	Asp	Ala 185	Leu	Ser	Ile	Thr	Lys	Gly 190	Met	His
Pro	Val	Ala 195	Leu	Thr	Leu	Leu 200	Asp	Lys	Gly	Thr	Phe 205	Ile	Pro	Asn 210	Asp
Thr	Val	Met	His 210	Ser	Ala	Gln 215	Thr	Arg	Met	Ile 220	Leu	Leu	Thr	Gly	Pro

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Asn Met Ala Gly Lys Ser Thr Tyr Ile Arg Gln Ile Ala Leu Leu Val
225                230                235                240
Ile Met Ala Gln Met Gly Ser Phe Ile Pro Ala Arg Ser Ala His Ile
                245                250                255
Gly Ile Val Asp Lys Ile Phe Thr Arg Ile Gly Ala Gly Asp Asn Leu
                260                265                270
Ser Lys Gly Met Ser Thr Phe Met Val Glu Met Ala Glu Thr Ala Asn
                275                280                285
Ile Leu His Asn Ala Thr Asp Arg Ser Leu Val Ile Leu Asp Glu Ile
                290                295                300
Gly Arg Gly Thr Ser Thr Tyr Asp Gly Leu Ala Ile Ala Gln Ala Val
305                310                315                320
Val Glu Phe Leu Leu Phe Thr Asp Gly Lys Lys Ala Lys Thr Leu Phe
                325                330                335
Ala Thr His Tyr Lys Glu Leu Thr Glu Leu Glu Met His Cys Gln His
                340                345                350
Val Glu Asn Phe His Ala Met Val Lys Glu Asn Ser Gly Gln Pro Ile
                355                360                365
Phe Met Tyr Glu Ile Val Lys Gly His Ser Lys Lys Ser Phe Gly Ile
                370                375                380
His Val Ala Lys Leu Ala Gly Phe Pro Leu Ser Val Val Ser Arg Ala
385                390                395                400
Gln Gln Ile Leu His Gln Phe Glu Gly Pro Asp Leu Arg Pro Glu Pro
                405                410                415
Glu Lys Ala Gln Gln Leu Val Met Phe
                420                425

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(2) INFORMATIONS POUR LA SEQ ID NO: 601:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 541 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 587786..589408

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 601:

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Val Arg Ile Glu Asp Phe Ser Leu Lys Asp Val Ser Ser Ser Pro Gly
1                5                10                15
Val Tyr Leu Met Lys Asp Ser Gln Gly Thr Val Leu Tyr Val Gly Lys
                20                25                30
Ala Lys Asn Leu Arg Asn Arg Leu Ser Ser Tyr Leu Gln Lys Lys Gly
                35                40                45
Asp Ser Arg Glu Arg Ile Pro Phe Leu Met Lys Lys Thr Thr Asp Ile
                50                55                60
Asp Thr Ile Val Val Ser Asn Glu Thr Glu Ala Ile Leu Leu Glu Asn
65                70                75                80
Asn Leu Ile Lys Lys Tyr Gln Pro Arg Tyr Asn Val Leu Leu Lys Asp
                85                90                95
Asp Lys Thr Phe Phe Cys Leu Ser Val Ser Leu Glu His Pro Trp Pro
                100                105                110
Arg Ile Glu Ala Ile Arg Thr Arg Ala Leu Ser Pro Gly Lys Lys Lys
                115                120                125
Gln Trp Leu Phe Gly Pro Tyr Val Ser Ala Glu Ala Cys Tyr Ala Leu

```

130		135		140
Leu Glu Val Ile Ser	Leu Trp Phe Pro Leu Arg Thr Cys Ser Asp Arg			
145	150	155	160	
Glu Phe Ser Thr Arg Gln Arg Pro Cys Val Leu Tyr Glu Met Lys Arg				
	165	170	175	
Cys Leu Ala Pro Cys Val Gly Leu Cys Ser Gln Thr Glu Tyr Gln Glu				
	180	185	190	
Thr Leu Asp Lys Ala Ile Leu Phe Leu Lys Gly Asp Val Arg Ser Thr				
	195	200	205	
Ile Ser Asn Leu Glu Lys Ala Ile Glu Lys Ala Ser Gln Glu Gln Lys				
	210	215	220	
Phe Glu His Ala Ala Ala Leu Tyr Arg Thr Leu Thr Leu Ile Arg Gln				
225	230	235	240	
Thr Met Ala Lys Gln His Val Glu Lys Phe Gln Ala Tyr Asp Ile Asp				
	245	250	255	
Val Leu Gly Leu Tyr Arg Lys Gly Ser Leu Ala Ile Val Ser Val Leu				
	260	265	270	
Ser Val Tyr Ser Gly Lys Leu Leu Gly Ala Arg Tyr Phe Ile Phe Pro				
	275	280	285	
Glu Asn Ala Gln Glu Asp Ser Ala Leu Phe Pro Ser Phe Ile Leu Gln				
	290	295	300	
Tyr Tyr Ala Glu Asn Pro Arg Ile Pro Lys Glu Ile Phe Val Pro Val				
305	310	315	320	
Ser Leu Asp Ser Pro Glu Leu Pro Tyr Leu Leu Asn Thr Ala Glu Pro				
	325	330	335	
Pro Lys Ile Arg Cys Pro Lys Thr Glu Tyr Gly Lys Glu Leu Leu Ala				
	340	345	350	
Leu Ala His Lys Asn Ala Ala Glu Gln Ala Lys Pro Phe Asn Ser Ile				
	355	360	365	
Thr Pro Pro Tyr Glu Glu Leu Gln His Phe Phe Asn Leu Ser Gln Tyr				
	370	375	380	
Pro Tyr Arg Ile Glu Cys Tyr Asp Asn Ala His Leu Gln Gly Glu His				
385	390	395	400	
Asn Val Gly Val Cys Ile Val Phe Glu Asn Asp Leu Phe Ser Pro Lys				
	405	410	415	
Gln Tyr Arg Thr Phe Ser Ile Thr Ser His Gly Asp Asp Leu Ala Ala				
	420	425	430	
Phe Glu Glu Val Leu Thr Arg Arg Phe Arg Ser Leu Thr Thr Glu Leu				
	435	440	445	
Pro Asn Leu Ile Val Ile Asp Gly Gly Arg Asn Gln Phe Lys Arg Ala				
	450	455	460	
Gln Arg Ile Leu Glu Glu Leu Asn Leu Thr Gly Ile Thr Val Val Thr				
465	470	475	480	
Ile Ala Lys Glu Ser Gly Asn His Ser Lys Ser Cys Ala Lys Lys Ser				
	485	490	495	
Tyr Phe Val Lys Leu Ser Pro Lys Glu Ser Phe Phe Ile Pro His Pro				
	500	505	510	
Gln Phe Phe Ser Ser Phe Ser Tyr Tyr Glu Met Lys Pro Thr Val Ser				
	515	520	525	
Arg Phe Asn Thr Ile Val Lys Asn Met Gln Lys Gln Cys				
530	535	540		

## (2) INFORMATIONS POUR LA SEQ ID NO: 602:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 589198..589578

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 602:

Glu	Phe	Asn	Arg	Asp	Tyr	Arg	Ser	Asn	His	Arg	Gln	Gly	Ile	Trp	Gln
1				5					10					15	
Ser	Gln	Gln	Lys	Leu	Arg	Gln	Glu	Lys	Leu	Phe	Cys	Glu	Thr	Phe	Pro
			20					25					30		
Gln	Gly	Ile	Leu	Leu	His	Pro	Thr	Ser	Ala	Ile	Leu	Gln	Phe	Phe	Gln
		35					40					45			
Leu	Leu	Arg	Asp	Glu	Ala	His	Arg	Phe	Ala	Ile	Gln	His	Tyr	Arg	Lys
	50					55					60				
Lys	His	Ala	Lys	Ala	Val	Leu	Thr	Thr	Lys	Lys	Ile	Pro	Gly	Ile	Gly
65					70					75					80
Glu	Val	Lys	Thr	Lys	Arg	Leu	Leu	Gln	Lys	Phe	Lys	Ser	Trp	Lys	Arg
				85					90					95	
Val	Phe	Ile	Ala	Ser	Glu	Glu	Glu	Leu	Lys	Thr	Val	Gln	Gly	Ile	Thr
			100					105					110		
Ala	Lys	Asp	Ile	Gln	Arg	Ile	Gln	Glu	Glu	Gly	Ala	Lys	Pro	Glu	
		115					120					125			

(2) INFORMATIONS POUR LA SEQ ID NO: 603:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(589630..590061)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 603:

Ser	Arg	Tyr	Arg	Asp	Pro	Cys	Asp	Ser	Ser	Asp	His	Cys	Ser	Leu	Leu
1				5					10					15	
Ser	Lys	Asn	Arg	Trp	Gly	Phe	Ile	Ile	Arg	Xaa	Arg	Ile	Ser	Leu	Thr
			20			-		25					30		
Arg	Phe	Leu	Asp	Ala	Ile	Ser	Lys	Xaa	Xaa	Lys	Gly	Ile	Tyr	Val	Glu
		35					40					45			
Gln	Asp	Ser	Lys	Asn	Ser	Leu	Val	Lys	Val	Arg	Val	Glu	Val	Asn	Val
	50				55						60				
Asp	Tyr	Gly	Val	Ser	Ile	Pro	Glu	Lys	Thr	Glu	Glu	Ile	Gln	Gly	Cys
65					70					75					80
Ile	Val	Ser	Glu	Ile	Ser	Glu	Tyr	Thr	Gly	Leu	His	Val	Ala	Ala	Val
				85					90					95	
His	Val	Val	Val	Lys	Gly	Leu	Thr	His	Pro	Lys	Ala	Lys	Asp	Glu	Glu
			100					105					110		
Val	Pro	Ala	Ile	Glu	Val	Ile	Glu	Glu	Pro	Cys	Leu	Glu	Glu	Phe	Ser
		115					120					125			
Ser	Ala	Glu	Glu	Tyr	Leu	Glu	Glu	Val	Ser	Val	Ile	Gln	Thr	Glu	Glu
		130					135					140			

(2) INFORMATIONS POUR LA SEQ ID NO: 604:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 178 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 590739..591272

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 604:

Leu	Phe	Thr	Thr	Asn	Leu	Lys	Leu	Gly	Ser	Pro	Pro	Met	Asn	Ser	Gly
1				5					10					15	
Met	Phe	Pro	Phe	Thr	Phe	Phe	Leu	Leu	Tyr	Ile	Cys	Leu	Gly	Met	Leu
			20					25					30		
Thr	Ala	Tyr	Leu	Ala	Asn	Lys	Lys	Asn	Arg	Asn	Leu	Ile	Gly	Trp	Phe
		35					40					45			
Leu	Ala	Gly	Met	Phe	Phe	Gly	Ile	Phe	Ala	Ile	Ile	Phe	Leu	Leu	Ile
	50					55					60				
Leu	Pro	Pro	Leu	Pro	Ser	Ser	Thr	Gln	Asp	Asn	Arg	Ser	Met	Asp	Gln
65					70					75					80
Gln	Asp	Ser	Glu	Glu	Phe	Leu	Leu	Gln	Asn	Thr	Leu	Glu	Asp	Ser	Glu
				85					90					95	
Ile	Ile	Ser	Ile	Pro	Asp	Thr	Met	Asn	Gln	Ile	Ala	Ile	Asp	Thr	Glu
			100					105					110		
Lys	Trp	Phe	Tyr	Leu	Asn	Lys	Asp	Cys	Thr	Asn	Val	Gly	Pro	Ile	Ser
		115					120					125			
Ile	Val	Gln	Leu	Thr	Ala	Phe	Leu	Lys	Glu	Cys	Lys	His	Ser	Pro	Glu
	130					135					140				
Lys	Gly	Ile	Asp	Pro	Gln	Glu	Leu	Trp	Val	Trp	Lys	Lys	Gly	Met	Pro
145					150					155					160
Asn	Trp	Glu	Lys	Val	Lys	Asn	Ile	Pro	Glu	Leu	Ser	Gly	Thr	Val	Lys
				165					170					175	
Asp	Glu														

(2) INFORMATIONS POUR LA SEQ ID NO: 605:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 592412..592765

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 605:

Arg	Leu	Thr	Leu	Pro	Lys	Asn	Ala	Arg	Leu	Leu	Lys	Arg	Lys	Gln	Phe
1				5					10					15	
Val	Tyr	Val	Gln	Arg	Asn	Gly	Arg	Cys	Cys	Arg	Ala	Asp	Gln	Val	Thr
			20					25					30		

```

Leu Arg Val Val Pro Ser Arg His Ser Asn Thr Ser Lys Val Gly Ile
      35              40              45
Thr Val Ser Lys Lys Phe Gly Lys Ala His Gln Arg Asn Arg Phe Lys
      50              55              60
Arg Ile Val Arg Glu Ala Phe Arg His Val Arg Pro Asn Leu Pro Gly
65      70              75              80
Cys Gln Val Val Ile Ser Pro Arg Gly Asn Ser Gln Pro Asp Phe Leu
      85              90              95
Lys Leu Ser Glu Glu Leu Leu Gln Arg Ile Pro Glu Ala Leu Pro Leu
      100             105             110
Ala Ser Ser Ser Arg Cys
      115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 606:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(592849..593145)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 606:

```

Ala Val Thr His Phe Thr Val Ala Leu Ile Glu Phe Gln Glu Leu Ala
1      5              10              15
Lys Arg Ser Gln Gly Gln Ser His Val Asn Val Ala Glu Val Ile Ala
      20              25              30
Pro Leu Ala Glu Tyr Leu Thr Gln Phe Gly Glu Gln Asp Lys Glu Asn
      35              40              45
Gln Trp Arg Leu Glu Met Ile Ile Ser Gln Tyr Tyr Leu Asp Ala Gly
50      55              60
Leu Pro Asn Ser Ala Leu Glu His Ala Lys Ile Ala Phe Glu Ser Ala
65      70              75              80
Pro Gln Asp Ile Gln Ser Ser Ile Ser Arg Ser Leu Val His Ile Glu
      85              90              95
His Gln Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 607:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(593121..593900)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 607:

```

Glu Phe Met Ser Ser Leu Arg Ile Ala Arg Ser Cys Ser Phe Lys Gln

```



```

1           5           10           15
Lys Thr Leu Leu Ala Ala Leu Val Phe Phe Gly Leu Gly Ala Ser Gln
20           25           30
Val Cys Ala Thr Pro Ser Asn Ser Arg Glu Ile Ala Trp Tyr Val Asp
35           40           45
Tyr Gln Glu Ala Arg Asp Glu Ser Arg Glu Lys Asp Leu Pro Met Leu
50           55           60
Leu Phe Phe Ser Gly Ser Asp Trp Asn Gly Ser Cys Met Lys Ile Arg
65           70           75           80
Asp Glu Val Leu Ser Ser Ser Asp Phe Ile Ser Ala Val Ala Asp Gln
85           90           95
Phe Val Cys Val Val Val Asp Phe Pro Arg His Thr Glu Leu Arg Asp
100          105          110
Pro Leu Ile Asn Glu Gln Asn Glu Asp Leu Lys Asn Arg Leu Tyr Val
115          120          125
Asn Thr Phe Pro Ser Leu Val Leu Leu Ser Pro Glu Glu Arg Ala Ile
130          135          140
Tyr Lys Ile Glu Ser Phe Gly Asn Glu Asn Gly Ser Asn Leu Gly Glu
145          150          155          160
Ser Leu Cys Arg Val Ile Ala Asn Asp Gln Glu Leu Glu Gln Val Phe
165          170          175
Pro Leu Ile Pro Thr Leu Ser Ser Val Ala Leu Arg Lys Tyr Tyr Gln
180          185          190
Leu Ala Glu Glu Leu Ser Arg Lys Asp Phe Met Ala Thr Ala Leu Glu
195          200          205
Gln Gly Val Leu Cys Asp Asp Ser Phe Phe Leu Ser Glu Lys Phe Arg
210          215          220
Gln Leu Val Glu Ala Gly Arg Met Asp Ser Glu Glu Cys Arg Ala Val
225          230          235          240
Lys Asn Arg Leu Leu Glu Leu Asp Pro Glu Asn Glu Gln Ser Arg Ile
245          250          255
Ser Gln Trp Leu
260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 608:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 481 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 594195..595637

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 608:

```

Met Asn Thr Ala Ile Asp Leu Phe Leu Tyr Asn Thr Leu Ser Arg Glu
1           5           10           15
Lys Glu Arg Phe Leu Pro Val Asn Asp Pro Val Lys Leu Tyr Thr Cys
20           25           30
Gly Pro Thr Val Tyr Asp Tyr Ala His Ile Gly Asn Phe Arg Thr Tyr
35           40           45
Ile Phe Glu Asp Leu Leu Lys Arg Val Leu Leu Phe Leu Gly Tyr Ser
50           55           60
Val Tyr His Val Met Asn Ile Thr Asp Val Asp Asp Lys Thr Leu Ala
65           70           75           80

```

1				5					10					15			
Lys	Thr	Leu	Leu	Ala	Ala	Leu	Val	Phe	Phe	Gly	Leu	Gly	Ala	Ser	Gln		
			20					25					30				
Val	Cys	Ala	Thr	Pro	Ser	Asn	Ser	Arg	Glu	Ile	Ala	Trp	Tyr	Val	Asp		
		35					40					45					
Tyr	Gln	Glu	Ala	Arg	Asp	Glu	Ser	Arg	Glu	Lys	Asp	Leu	Pro	Met	Leu		
	50					55					60						
Leu	Phe	Phe	Ser	Gly	Ser	Asp	Trp	Asn	Gly	Ser	Cys	Met	Lys	Ile	Arg		
65					70				75						80		
Asp	Glu	Val	Leu	Ser	Ser	Asp	Phe	Ile	Ser	Ala	Val	Ala	Asp	Gln			
				85				90						95			
Phe	Val	Cys	Val	Val	Val	Asp	Phe	Pro	Arg	His	Thr	Glu	Leu	Arg	Asp		
			100					105						110			
Pro	Leu	Ile	Asn	Glu	Gln	Asn	Glu	Asp	Leu	Lys	Asn	Arg	Leu	Tyr	Val		
		115					120					125					
Asn	Thr	Phe	Pro	Ser	Leu	Val	Leu	Leu	Ser	Pro	Glu	Glu	Arg	Ala	Ile		
	130					135					140						
Tyr	Lys	Ile	Glu	Ser	Phe	Gly	Asn	Glu	Asn	Gly	Ser	Asn	Leu	Gly	Glu		
145					150					155					160		
Ser	Leu	Cys	Arg	Val	Ile	Ala	Asn	Asp	Gln	Glu	Leu	Glu	Gln	Val	Phe		
			165					170						175			
Pro	Leu	Ile	Pro	Thr	Leu	Ser	Ser	Val	Ala	Leu	Arg	Lys	Tyr	Tyr	Gln		
			180					185						190			
Leu	Ala	Glu	Glu	Leu	Ser	Arg	Lys	Asp	Phe	Met	Ala	Thr	Ala	Leu	Glu		
		195					200				205						
Gln	Gly	Val	Leu	Cys	Asp	Asp	Ser	Phe	Phe	Leu	Ser	Glu	Lys	Phe	Arg		
	210					215					220						
Gln	Leu	Val	Glu	Ala	Gly	Arg	Met	Asp	Ser	Glu	Glu	Cys	Arg	Ala	Val		
225					230					235					240		
Lys	Asn	Arg	Leu	Leu	Glu	Leu	Asp	Pro	Glu	Asn	Glu	Gln	Ser	Arg	Ile		
				245					250					255			
Ser	Gln	Trp	Leu														
			260														

(2) INFORMATIONS POUR LA SEQ ID NO: 608:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 481 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 594195..595637

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 608:

Met	Asn	Thr	Ala	Ile	Asp	Leu	Phe	Leu	Tyr	Asn	Thr	Leu	Ser	Arg	Glu		
1				5					10					15			
Lys	Glu	Arg	Phe	Leu	Pro	Val	Asn	Asp	Pro	Val	Lys	Leu	Tyr	Thr	Cys		
			20					25					30				
Gly	Pro	Thr	Val	Tyr	Asp	Tyr	Ala	His	Ile	Gly	Asn	Phe	Arg	Thr	Tyr		
		35					40					45					
Ile	Phe	Glu	Asp	Leu	Leu	Lys	Arg	Val	Leu	Leu	Phe	Leu	Gly	Tyr	Ser		
	50					55					60						
Val	Tyr	His	Val	Met	Asn	Ile	Thr	Asp	Val	Asp	Asp	Lys	Thr	Leu	Ala		
65					70				75						80		

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(595640..596122)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 609:

Asn	Phe	Arg	Asn	Thr	Asn	Ile	Ser	Pro	Glu	Lys	Thr	Tyr	Val	His	Ala
1				5					10					15	
Ser	Arg	Gly	Glu	Leu	Ile	Ala	Leu	Leu	Phe	Asp	Glu	Leu	Val	Cys	Asp
		20						25					30		
Lys	Leu	Ile	Ala	Pro	His	His	Ile	Thr	Asp	His	Pro	Leu	Glu	Thr	Thr
		35					40					45			
Pro	Leu	Cys	Lys	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Thr	Leu	Val	Glu	Arg
	50					55				60					
Phe	Glu	Ser	Phe	Cys	Leu	Gly	Lys	Glu	Leu	Cys	Asn	Ala	Tyr	Ser	Glu
65				70					75						80
Leu	Asn	Asp	Pro	Leu	Gln	Gln	Arg	Lys	Leu	Glu	Glu	Gln	Met	Arg	
			85					90					95		
Lys	Lys	Ala	Leu	Asn	Pro	Asp	Ser	Glu	Tyr	His	Pro	Ile	Asp	Glu	Glu
		100						105					110		
Phe	Leu	Glu	Ala	Leu	Cys	Gln	Gly	Met	Pro	Pro	Ala	Gly	Gly	Phe	Gly
		115					120					125			
Ile	Gly	Ile	Asp	Arg	Leu	Val	Met	Met	Leu	Thr	Asp	Ala	Ala	Ser	Ile
	130					135					140				
Arg	Asp	Val	Leu	Phe	Phe	Pro	Val	Met	Arg	Arg	Ile	Glu	Ala	Lys	Lys
145					150					155					160
Asp															

(2) INFORMATIONS POUR LA SEQ ID NO: 610:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 237 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(596154..596864)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 610:

Glu	Ile	Ala	Lys	Pro	Phe	Arg	Lys	Glu	Thr	Pro	Lys	Val	Arg	Phe	Ala
1				5					10					15	
Gly	Arg	Leu	Val	Leu	Phe	Arg	Ser	Met	Gly	Lys	Asn	Ala	Phe	Gly	Gln
		20						25					30		
Ile	Leu	Asp	Asn	Asp	Ala	Lys	Ile	Gln	Val	Met	Phe	Asn	Arg	Asp	Phe
		35					40					45			
Ser	Ala	Val	Ala	Gly	Leu	Ala	Ala	Asp	Ala	Gly	Ile	Ser	Pro	Ile	Lys
	50					55				60					
Phe	Ile	Glu	Lys	Lys	Leu	Asp	Leu	Gly	Asp	Ile	Leu	Gly	Leu	Glu	Gly
65				70					75						80
Tyr	Leu	Phe	Phe	Thr	His	Ser	Gly	Glu	Leu	Thr	Val	Leu	Val	Glu	Thr
			85						90					95	

```

Val Thr Leu Leu Cys Lys Ser Leu Ile Ser Leu Pro Asp Lys His Ala
      100      105      110
Gly Leu Ala Asp Lys Glu Ile Arg Tyr Arg Lys Arg Trp Ala Asp Leu
      115      120      125
Ile Ser Ser Glu Asp Val Arg Lys Thr Phe Leu Thr Arg Ser Arg Ile
      130      135      140
Leu Lys Leu Ile Arg Glu Tyr Met Asp Gln Gln Ser Phe Leu Glu Val
      145      150      155      160
Glu Thr Pro Ile Leu Gln Thr Val Tyr Gly Gly Ala Glu Ala Thr Pro
      165      170      175
Phe Val Thr Thr Leu Gln Gly Leu His Ala Glu Met Phe Leu Arg Ile
      180      185      190
Ser Leu Glu Ile Ala Leu Lys Lys Leu Leu Val Gly Gly Met Ser Arg
      195      200      205
Val Tyr Glu Ile Gly Lys Val Phe Arg Asn Glu Gly Ile Asp Arg Thr
      210      215      220
His Asn Pro Glu Phe Thr Met Ile Glu Ala Ala Ser Met
      225      230      235

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 611:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(597282..597731)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 611:

```

Gly Ala Cys Ser Ser His Val Trp Arg Ser Gln Leu Leu Val Leu Leu
1      5      10      15
Gln Asn Val Val Leu Arg Val Arg Arg Arg Ser Asn Arg Val Ala Glu
      20      25      30
Thr Gly Ile His Trp Met Ser Tyr Gln Asp Ala Leu Asn Lys Ala Lys
      35      40      45
Gln Glu Gly Lys His Val Ala Val Phe Phe Thr Gly Ser Asp Trp Cys
      50      55      60
Ile Trp Cys Met Arg Met Gln Asp Gln Ile Leu Gln Thr Ala Ala Phe
      65      70      75      80
Ser Glu Phe Asp Lys Gln Tyr Leu Cys Met Val Glu Ile Asp Phe Pro
      85      90      95
His Asn Lys Glu Gln Thr Ala Glu Gln Lys Glu Gln Asn Arg His Leu
      100      105      110
Lys Ser Leu Tyr Ser Val Asp Gly Phe Pro Thr Leu Val Phe Leu Asp
      115      120      125
Ser Glu Gly Xaa Glu Val Ala Lys Met Gly Phe Glu Pro Gly Gly Gly
      130      135      140
Gly His Met Phe Ile Asp
      145      150

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 612:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 762 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 598524..600809

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 612:

Lys	Arg	Phe	Ser	Ile	Lys	Lys	Arg	Phe	Met	Asp	Pro	Thr	His	Gln	Pro	1	5	10	15
Phe	Arg	Leu	Tyr	Ala	Glu	Val	Ile	Val	Asn	Ala	Asn	Ile	Asn	Lys	Ile	20	25	30	
Leu	Asp	Tyr	Gly	Ile	Pro	Ala	Glu	Leu	Glu	Asn	Leu	Val	Thr	Val	Gly	35	40	45	
Ser	Val	Val	Lys	Val	Pro	Leu	Gln	Arg	Lys	Leu	Thr	Asn	Asp	Lys	Tyr	50	55	60	
Lys	Ile	Ala	Ile	Val	Leu	Lys	Ile	Lys	Ser	Ser	Ser	Asp	Phe	Val	His	65	70	75	80
Val	Ile	Gln	Pro	Ile	Leu	Asp	Ile	Ser	Tyr	Glu	Gly	Ile	Thr	Leu	Pro	85	90	95	
Gln	Asp	Leu	Ile	Asp	Leu	Ile	Phe	Trp	Ile	Ser	Gln	Tyr	Tyr	Phe	Cys	100	105	110	
Pro	Leu	Gly	Ser	Ala	Val	Ser	Leu	Phe	Leu	Pro	Thr	Val	Tyr	Ala	Gln	115	120	125	
Thr	His	Ser	Thr	Lys	His	Gln	Asn	Asn	Val	Phe	Leu	Gly	Gln	Asn	Ala	130	135	140	
Glu	Arg	Thr	Gln	Glu	Ile	Leu	Lys	Thr	Leu	Asp	Asn	Pro	Gln	Gln	Ile	145	150	155	160
Ala	Val	Leu	Arg	Lys	Leu	Leu	Lys	Thr	Thr	Lys	Pro	Leu	Thr	Pro	Pro	165	170	175	
Glu	Leu	Met	Arg	Lys	Thr	Glu	Val	Ser	Ala	Lys	Thr	Leu	Asp	Ala	Leu	180	185	190	
Val	Lys	Gln	Lys	Phe	Ile	Arg	Ile	Val	Asp	Ser	Ala	Asp	Leu	Glu	Ile	195	200	205	
Gln	Asp	Glu	Gln	Leu	His	Tyr	Phe	Leu	Pro	Glu	Thr	Pro	Thr	Leu	Asn	210	215	220	
Gln	Glu	Gln	Leu	Asp	Ala	Ile	Asn	Thr	Ile	Ser	Gln	Ser	Leu	Val	Ala	225	230	235	240
Glu	Gln	Phe	Gln	Thr	Cys	Leu	Leu	Phe	Gly	Val	Thr	Gly	Ser	Gly	Lys	245	250	255	
Thr	Glu	Val	Tyr	Leu	Gln	Val	Ile	Arg	Lys	Ala	Arg	Ala	Leu	Gly	Lys	260	265	270	
Ser	Val	Ile	Leu	Leu	Val	Pro	Glu	Val	Ala	Leu	Thr	Ile	Gln	Thr	Leu	275	280	285	
Ser	Phe	Phe	Lys	Met	His	Phe	Gly	Ser	Glu	Val	Gly	Val	Leu	His	Tyr	290	295	300	
Lys	Leu	Ser	Asp	Ser	Glu	Arg	Thr	Gln	Thr	Trp	His	Lys	Ala	Ser	Arg	305	310	315	320
Gly	Leu	Ile	Asn	Ile	Ile	Ile	Gly	Pro	Arg	Ser	Ala	Ile	Phe	Cys	Pro	325	330	335	
Ile	Gln	Asn	Leu	Gly	Leu	Ile	Ile	Val	Asp	Glu	Glu	His	Asp	Ser	Ala	340	345	350	
Tyr	Lys	Gln	Ser	Asp	Leu	Pro	Pro	Phe	Tyr	Gln	Ala	Arg	Asp	Val	Ala	355	360	365	
Val	Met	Arg	Gly	Lys	Met	Thr	Asn	Ala	Thr	Val	Ile	Leu	Gly	Ser	Ala	370	375	380	

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(600734..601876)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 613:

Gly	Lys	Trp	Val	Leu	Lys	Glu	Ala	Leu	Ser	Ile	Asp	Phe	Ile	Thr	Asn
1				5					10					15	
Asp	Phe	Leu	Gly	Phe	Ser	Arg	Leu	Asp	Ser	Leu	Val	His	Ala	Val	Glu
		20						25					30		
Ala	Arg	Tyr	Arg	Leu	Tyr	Cys	Arg	Asp	Lys	Pro	His	Ala	Gln	Leu	Gly
		35					40					45			
Tyr	Gly	Gly	Ser	Arg	Ala	Ile	Leu	Gly	Ser	Ser	Ser	Leu	Leu	Asp	Gly
	50					55					60				
Val	Glu	His	Gln	Ile	Ala	His	Phe	His	Gly	Ala	Pro	Glu	Ala	Leu	Ile
65				70					75						80
Leu	Pro	Ser	Gly	Phe	Val	Ala	Asn	Thr	Ala	Ile	Cys	Ala	His	Leu	Ser
			85						90					95	
Ser	Val	Ala	Asp	Tyr	Val	Leu	Trp	Asp	Glu	Gln	Val	His	Ile	Ser	Val
			100					105					110		
Ser	Tyr	Asn	Leu	Ser	Val	Phe	Leu	Ser	Gly	Trp	His	Gln	Ser	Phe	Arg
		115					120					125			
His	Asn	Asp	Leu	Asp	His	Leu	Glu	Ser	Leu	Leu	Glu	Ser	Cys	Gln	Gln
	130					135					140				
Arg	Gly	Phe	Gln	Arg	Val	Phe	Ile	Leu	Val	Cys	Ser	Val	Tyr	Ser	Phe
145				150						155					160
Lys	Gly	Ser	Phe	Ala	Pro	Leu	Glu	Gln	Ile	Val	Ala	Leu	Ser	His	Gln
			165						170					175	
Tyr	His	Ala	Gln	Leu	Ile	Val	Asp	Glu	Ala	His	Ala	Val	Gly	Leu	Phe
			180					185					190		
Gly	Asp	Ala	Gly	Lys	Gly	Phe	Cys	Ala	Ser	Leu	Gly	Tyr	Glu	Asn	Phe
		195					200					205			
Tyr	Ser	Val	Leu	Val	Thr	Phe	Ser	Lys	Ala	Leu	Gly	Ser	Ala	Gly	Ala
	210					215					220				
Ala	Trp	Leu	Ser	Ser	Cys	Asp	Arg	Lys	Gln	Asp	Leu	Ile	Lys	Glu	Pro
225				230						235					240
Met	Val	Ser	Leu	Ser	Thr	Gly	Ile	Pro	Pro	Tyr	Leu	Leu	Val	Ser	Ile
			245						250					255	
Gln	Val	Ala	Tyr	Glu	Phe	Leu	Ser	Gln	Glu	Gly	Glu	Leu	Ala	Arg	Thr
		260						265					270		
Arg	Leu	Arg	Arg	Ile	Arg	Asp	Tyr	Phe	Ala	Gln	Lys	Ile	Ser	Trp	Ala
		275				280						285			
Ala	Ala	Gly	Phe	Val	Gln	Pro	Leu	Ser	Leu	Pro	Gly	Ile	Ser	Glu	Gln
	290					295					300				
Glu	Leu	Tyr	Gln	Lys	Leu	Val	Ala	Thr	Gly	Ile	Arg	Val	Gly	Val	Ala
305				310						315					320
Cys	Pro	Pro	Thr	Gly	Lys	Val	Leu	Arg	Ala	Asn	Leu	His	Ala	Phe	Asn
			325						330					335	
Thr	Glu	Gln	Glu	Val	Asp	Ile	Leu	Val	Ser	Leu	Leu	Ala	Thr	Glu	Gln
			340					345					350		
Val	Thr	Tyr	Gln	Lys	Asn	Val	Val	Thr	Gly	Ser	Thr	Ser	Thr	Met	Gln
		355				360						365			
Arg	Thr	Leu	Glu	Asp	Asn	Phe	Ala	Ala	Ala	Asn	Ala	Ser			
	370					375					380				

(2) INFORMATIONS POUR LA SEQ ID NO: 614:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 538 acides aminés



(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(601910..603523)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 614:

Glu	Met	Arg	Asp	Asn	Arg	Asn	Thr	Ala	Arg	Ser	Lys	Arg	Gly	Lys	Leu	1	5	10	15
Arg	Ser	Glu	Lys	Thr	Val	Leu	Arg	Ser	Phe	Leu	Lys	Leu	Cys	Ala	Glu	20	25	30	
Met	Thr	Thr	Ala	Thr	Val	Phe	Trp	Asp	Glu	Gln	Leu	Gly	Lys	Leu	Ser	35	40	45	
Tyr	Asn	Gln	Val	Tyr	Lys	Ala	Val	Cys	Ala	Leu	Ala	Thr	Arg	Leu	Ala	50	55	60	
Asn	Tyr	Pro	Asp	Gln	His	Ile	Gly	Ile	Met	Met	Pro	Ala	Ser	Ala	Gly	65	70	75	80
Ala	Tyr	Ile	Ala	Tyr	Phe	Ala	Thr	Leu	Leu	Ser	Gly	Lys	Ile	Pro	Val	85	90	95	
Met	Ile	Asn	Trp	Ser	Gln	Gly	Leu	Arg	Glu	Val	Thr	Ala	Cys	Ala	Asn	100	105	110	
Leu	Val	Gly	Val	Thr	His	Val	Ile	Thr	Ala	Lys	Pro	Leu	Met	Gln	Lys	115	120	125	
Leu	Ala	Gln	Thr	His	Gly	Glu	Asp	Ala	Glu	Tyr	Pro	Phe	Ser	Leu	Xaa	130	135	140	
Phe	Leu	Asp	Glu	Val	Arg	Lys	Glu	Leu	Ser	Phe	Leu	Glu	Lys	Cys	Arg	145	150	155	160
Val	Gly	Ile	Cys	Met	Ser	Ile	Pro	Phe	Glu	Trp	Met	Met	Arg	Trp	Phe	165	170	175	
Gly	Val	Phe	Asp	Lys	Asp	Pro	Glu	Asp	Val	Ala	Val	Ile	Leu	Phe	Thr	180	185	190	
Ser	Gly	Thr	Glu	Lys	Leu	Pro	Lys	Gly	Val	Pro	Leu	Thr	Asn	Ala	Ser	195	200	205	
Leu	Leu	Ala	Asn	Gln	Arg	Ala	Cys	Phe	Asp	Cys	Phe	Ser	Pro	Lys	Glu	210	215	220	
Asp	Asp	Ala	Met	Ile	Ser	Phe	Leu	Pro	Pro	Phe	His	Ala	Tyr	Gly	Phe	225	230	235	240
Asn	Ser	Cys	Thr	Leu	Phe	Pro	Leu	Leu	Ser	Gly	Ile	Pro	Val	Val	Phe	245	250	255	
Ala	Tyr	Asn	Pro	Leu	Tyr	Ala	Lys	Lys	Ile	Val	Glu	Met	Ile	Asp	Glu	260	265	270	
Ala	Lys	Val	Thr	Leu	Leu	Gly	Ser	Thr	Pro	Val	Phe	Leu	Ser	Tyr	Ile	275	280	285	
Ile	Asn	Ala	Ala	Lys	Lys	Ser	Glu	Thr	Thr	Leu	Pro	Ser	Leu	Arg	Phe	290	295	300	
Val	Val	Val	Gly	Gly	Asp	Val	Phe	Lys	His	Ser	Leu	Tyr	Gln	Glu	Ala	305	310	315	320
Leu	Lys	Thr	Phe	Pro	His	Val	Gln	Leu	Arg	Gln	Gly	Tyr	Gly	Thr	Thr	325	330	335	
Glu	Cys	Ser	Pro	Val	Ile	Thr	Ile	Asn	Thr	Val	Asn	Ser	Pro	Lys	His	340	345	350	
Glu	Ser	Cys	Val	Gly	Met	Pro	Val	Arg	Gly	Met	Glu	Val	Leu	Ile	Val	355	360	365	
Ser	Glu	Glu	Thr	Lys	Val	Pro	Val	Ser	Thr	Gly	Val	Thr	Gly	Leu	Val	370	375	380	
Leu	Thr	Arg	Gly	Thr	Ser	Leu	Phe	Lys	Gly	Tyr	Leu	Gly	Glu	Asp	Phe				

```

385          390          395          400
Gly His Gly Phe Ile Glu Leu Ala Gly Glu Thr Trp Tyr Val Thr Gly
          405          410          415
Asp Leu Gly Tyr Val Asp Arg His Gly Glu Leu Phe Leu Lys Gly Arg
          420          425          430
Leu Ser Arg Phe Val Lys Ile Gly Ala Glu Met Val Ser Leu Glu Ala
          435          440          445
Met Glu Ser Ile Ile Met Glu Gly Cys Gly Gln Asn Ala Ala Asp His
          450          455          460
Pro Leu Val Val Cys Gly Leu Pro Gly Glu Lys Glu Arg Leu Cys Leu
465          470          475          480
Phe Thr Ile Phe Pro Thr Ser Val Ser Glu Val Asn Asp Ile Leu Lys
          485          490          495
Asn Ser Lys Thr Ser Asn Leu Leu Lys Ile Ser Tyr His His Gln Val
          500          505          510
Glu Ala Ile Pro Met Leu Gly Thr Gly Lys Pro Asp Tyr Cys Ser Leu
          515          520          525
Asn Ala Leu Ala Lys Arg Leu Phe Ser Glu
          530          535

```

(2) INFORMATIONS POUR LA SEQ ID NO: 615:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(603531..603794)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 615:

```

Leu Arg His Arg Ile Trp Gly Ser Ser Phe Ser Arg Tyr Arg Thr Gly
1          5          10          15
Ser Thr Pro Lys Leu Gly Lys Val Phe Lys Glu Ala Val Lys Ala Leu
          20          25          30
Leu Arg Cys Gly Ile Phe Phe Met Pro Lys Arg Glu Val Arg Val Ser
          35          40          45
Val Cys Pro Ala Asp Tyr Ser Val Leu Lys Gln Phe Pro Thr Lys Gln
          50          55          60
Glu Phe Asn Thr Phe Leu Ser Asp Trp Phe Asn Gln Glu Gly Gly Glu
65          70          75          80
Thr Pro Leu Glu Val Pro Tyr Ala
          85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 616:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 219 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(603757..604413)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 616:

Ser	His	Asp	Ile	Phe	Leu	Ile	Ile	Asn	Glu	Lys	Asn	Ser	Ser	Phe	Gln
1				5					10					15	
Asn	Ala	Asn	Leu	Leu	Ile	Trp	Ile	Trp	Lys	Tyr	Cys	Thr	Leu	Trp	Cys
		20						25					30		
Lys	Asn	Asn	Phe	Asn	Lys	Pro	Arg	Gly	Ser	Met	Lys	Ile	Gly	Phe	Trp
		35					40					45			
Arg	Arg	Leu	Tyr	Glu	Val	Cys	Tyr	Thr	Ser	Leu	Ile	Gly	Cys	Ala	Leu
	50					55					60				
Lys	Leu	Arg	Tyr	Arg	Val	Leu	Val	Glu	Gly	Ile	Glu	Ser	Ile	Asn	Gln
65					70					75					80
Asn	Ser	Gln	Lys	Gly	Ala	Leu	Phe	Leu	Ser	Asn	His	Val	Ala	Glu	Ile
				85					90					95	
Asp	Pro	Val	Ile	Leu	Glu	His	Val	Phe	Trp	Leu	Lys	Phe	His	Val	Arg
			100					105					110		
Pro	Ile	Ala	Val	Asp	Tyr	Leu	Phe	Asn	Asn	Pro	Val	Val	Lys	Trp	Phe
		115					120						125		
Leu	Asp	Ser	Val	Arg	Ala	Ile	Pro	Val	Pro	Ser	Val	Val	Pro	Gly	Arg
	130					135					140				
Asp	Asp	Lys	Arg	Leu	Leu	Glu	Arg	Ile	Glu	Arg	Phe	Tyr	Val	Cys	Val
145					150					155					160
Thr	Gln	Ala	Leu	Asp	Arg	Lys	Glu	Ser	Leu	Leu	Leu	Tyr	Pro	Ser	Gly
				165					170					175	
Arg	Leu	Ser	Arg	Asn	Gly	Lys	Glu	Glu	Ile	Val	Asn	Gln	Gln	Ala	Ala
			180					185					190		
Tyr	Thr	Ile	Leu	His	Arg	Ala	Lys	Glu	Cys	Asp	Val	Phe	Leu	Val	Lys
		195					200					205			
Thr	Gln	Asp	Leu	Gly	Lys	Phe	Phe	Phe	Thr	Leu					
	210					215									

(2) INFORMATIONS POUR LA SEQ ID NO: 617:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 354 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 604549..605610

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 617:

Val	Ile	Val	Thr	Ser	Leu	Gln	Pro	Ala	Glu	Lys	Leu	Met	Phe	Ser	Leu
1				5					10					15	
Leu	Asn	Asp	Cys	Gln	Lys	Ala	Ala	Glu	Thr	Val	Val	Met	Gln	Ala	Met
		20						25					30		
Leu	Ser	Leu	Met	Arg	Tyr	Arg	Lys	Ala	His	Lys	Phe	Ile	Pro	Phe	Trp
		35					40					45			
Lys	Lys	Pro	Asp	Gln	Thr	Tyr	Val	Thr	Pro	Ala	Asp	Tyr	Ala	Ile	Gln
	50					55					60				
Tyr	Tyr	Phe	Tyr	Gln	Lys	Leu	Thr	Ser	Leu	Phe	Pro	His	Ile	Pro	Leu
65					70					75					80
Val	Gly	Glu	Glu	Thr	Leu	Asn	Pro	Ala	Thr	Asp	His	Pro	Arg	Ile	Pro

(2) INFORMATIONS POUR LA SEQ ID NO: 618:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(605582..606619)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 618:

Met	Lys	Tyr	Ser	Leu	Gln	Ile	Glu	Asp	Leu	His	Ile	Glu	Gly	Tyr	Glu
1				5					10					15	
Gln	Val	Leu	Lys	Val	Thr	Cys	Glu	Ser	Val	Gln	Leu	Val	Ala	Val	Ile
			20					25					30		
Ala	Ile	His	Gln	Thr	Lys	Val	Gly	Pro	Ala	Leu	Gly	Gly	Ile	Arg	Ala
		35					40					45			
Phe	Pro	Tyr	Leu	Gln	Phe	Glu	Asp	Gly	Leu	Gln	Asp	Ala	Leu	Arg	Leu
	50					55					60				

Met	Lys	Tyr	Ser	Leu	Gln	Ile	Glu	Asp	Leu	His	Ile	Glu	Gly	Tyr	Glu
1				5					10					15	
Gln	Val	Leu	Lys	Val	Thr	Cys	Glu	Ser	Val	Gln	Leu	Val	Ala	Val	Ile
			20					25					30		
Ala	Ile	His	Gln	Thr	Lys	Val	Gly	Pro	Ala	Leu	Gly	Gly	Ile	Arg	Ala
		35					40					45			
Phe	Pro	Tyr	Leu	Gln	Phe	Glu	Asp	Gly	Leu	Gln	Asp	Ala	Leu	Arg	Leu
	50					55					60				

```

Ser Lys Ala Met Thr Tyr Lys Ala Leu Leu Ser Ser Thr Glu Thr Gly
65      70      75      80
Gly Gly Lys Ser Val Ile Phe Leu Pro Lys Gly Met Thr Ser Pro Thr
      85      90      95
Glu Gly Met Leu Arg Ala Phe Gly Gln Ala Val Asn Ser Leu Gln Gly
      100      105      110
Lys Tyr Ile Ala Ala Glu Asp Val Gly Val Ser Val Gln Asp Val Met
      115      120      125
Ile Ile Arg Glu Glu Thr Pro Tyr Val Cys Gly Leu Val Thr Val Ser
      130      135      140
Gly Asp Pro Ser Ile Tyr Thr Ala His Gly Val Phe Leu Cys Ile Gln
145      150      155      160
Glu Thr Ala Asp Tyr Leu Trp Lys Thr Asp Ile Arg Gly Lys Arg Val
      165      170      175
Ala Val Gln Gly Leu Gly Ala Val Gly Arg Lys Leu Val His Glu Leu
      180      185      190
Phe Phe Ala Gly Ala Glu Leu Ile Val Tyr Asp Thr Arg Lys Asp Leu
      195      200      205
Leu Asp Glu Val Val Thr Leu Tyr Gly Ala Gln Val Asp Glu Asn Ile
      210      215      220
Ile Ser Ser Asp Cys Asp Ile Leu Cys Pro Cys Ala Leu Gly Gly Ile
225      230      235      240
Ile Asn Ser Met Ser Ile Asp Gln Leu Arg Cys Arg Ala Ile Val Gly
      245      250      255
Ala Thr Asn Asn Gln Leu Glu Asn Pro Ala Ile Gly Arg Glu Leu Val
      260      265      270
Ala Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Leu Ala Asn Ala Gly Gly
      275      280      285
Leu Leu Asn Val Ala Gly Ser Val Gly Arg Ala Tyr Ser Pro Lys Glu
      290      295      300
Val Leu Ser Lys Val Glu Gly Leu Pro Lys Ile Leu Arg Lys Leu Tyr
305      310      315      320
Glu Gln Gly Ala Lys Glu Asn Arg Asp Thr Gly Thr Leu Ala Asp Ala
      325      330      335
Ile Val Glu Glu Arg Leu Ala Val Tyr Ala
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 619:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 217 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 606843..607493

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 619:

```

Asn Thr Leu Ile Glu Ser Asp Leu Met Ser Lys Thr Pro Leu Ser Ile
1      5      10      15
Ala His Pro Trp His Gly Pro Val Leu Thr Arg Asp Asp Tyr Glu Ser
      20      25      30
Leu Cys Cys Tyr Ile Glu Ile Thr Pro Ala Asp Ser Val Lys Phe Glu
      35      40      45
Leu Asp Lys Glu Thr Gly Ile Leu Lys Val Asp Arg Pro Gln Lys Phe

```

50		55		60
Ser Asn Phe Cys Pro Cys Leu Tyr Gly Leu Leu Pro Lys Thr Tyr Cys				
65		70		75
Gly Asp Leu Ser Gly Glu Tyr Ser Gly Gln Gln Ser Asn Arg Glu Asn				80
	85		90	
Ile Lys Gly Asp Gly Asp Pro Leu Asp Ile Cys Val Leu Thr Glu Lys				95
	100		105	
Asn Ile Thr Gln Gly Asn Ile Leu Leu Gln Ala Arg Pro Ile Gly Gly				110
	115		120	
Ile Arg Ile Leu Asp Ser Glu Glu Ala Asp Asp Lys Ile Ile Ala Val				125
	130		135	
Leu Glu Asp Asp Leu Val Tyr Gly Asn Ile Glu Asp Ile Ser Glu Cys				140
145		150		155
Pro Gly Thr Val Leu Asp Met Ile Gln His Tyr Phe Leu Thr Tyr Lys				160
	165		170	
Ala Thr Pro Glu Ser Leu Ile Gln Ala Lys Pro Ala Lys Ile Glu Ile				175
	180		185	
Val Gly Leu Tyr Gly Lys Lys Glu Ala Gln Lys Val Ile Arg Leu Ala				190
	195		200	
His Glu Asp Tyr Cys Asn Leu Phe Met				205
210		215		

(2) INFORMATIONS POUR LA SEQ ID NO: 620:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(608031..609068)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 620:

Ser Phe Tyr Tyr Leu Cys Ser Cys Ser Arg Lys Glu Gly Asn Ser Tyr				
1	5		10	15
Val Arg Trp Asp Gln Asp Thr Leu Pro Ala Asp Ser His Arg Cys Gly				
	20		25	30
Val Ile Ile Gly Ser Gly Met Gly Gly Leu Arg Thr Leu Asp Glu Gly				
	35		40	45
Ile Glu Lys Leu Ser Ala Gly Asn Arg Lys Leu Ser Pro Phe Phe Ile				
	50		55	60
Pro Tyr Ile Ile Thr Asn Met Ala Pro Ala Leu Ile Ala Met Asp Tyr				
65		70		75
Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ala				
	85		90	95
Asn Tyr Cys Ile Asp Ala Ala Tyr Gln His Leu Ile Glu Gly Arg Ala				
	100		105	110
Asp Val Ile Val Cys Gly Gly Thr Glu Ala Ala Ile Asn Arg Val Gly				
	115		120	125
Leu Ala Gly Phe Ile Ala Asn Arg Ala Leu Ser Glu Arg Asn Asp Ala				
	130		135	140
Pro Glu Gln Ala Ser Arg Pro Trp Asp Arg Asp Arg Asp Gly Phe Val				
145		150		155
Leu Gly Glu Gly Ala Gly Ile Leu Val Leu Glu Thr Leu Asp Asn Ala				
	165		170	175

```

Leu Lys Arg Gly Ala Pro Ile Phe Ala Glu Val Leu Gly Thr Tyr Lys
      180      185      190
Thr Cys Asp Ala Phe His Ile Thr Ala Pro Arg Asp Asp Gly Glu Gly
      195      200      205
Ile Thr Ala Cys Ile Leu Gly Ala Leu Asn Lys Ala Gly Ile Pro Lys
      210      215      220
Glu Arg Val Asn Tyr Ile Asn Ala His Gly Thr Ser Thr Pro Leu Gly
      225      230      235      240
Asp Leu Ser Glu Val Leu Ala Leu Lys Lys Ala Phe Gly Ser His Val
      245      250      255
Lys Asn Leu Arg Leu Asn Ser Thr Lys Ser Leu Ile Gly His Cys Leu
      260      265      270
Gly Ala Ala Gly Gly Val Glu Ala Val Ala Thr Ile Gln Ala Ile Gln
      275      280      285
Thr Gly Lys Leu His Pro Thr Ile Asn Val Glu Asn Pro Ile Ala Glu
      290      295      300
Ile Glu Glu Phe Asp Val Val Ala Asn Lys Ala Gln Asp Trp Asp Val
      305      310      315      320
Asp Val Ala Met Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Thr
      325      330      335
Ile Leu Phe Ser Arg Tyr Glu Pro Ser Leu
      340      345

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 621:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(609296..609652)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 621:

```

Met Asp Ser Phe Cys Leu Asn Leu Leu Lys Val Ile Val Lys Ala Ile
1      5      10      15
Asp Asn Lys Lys Gly Arg Asn Pro Val Val Leu Asp Val Gln Asn Ile
      20      25      30
Ser Gln Leu Thr Asp Tyr Phe Val Phe Val Glu Gly Asn Val Gly Val
      35      40      45
His Ile Lys Ala Ile Ala Asp Thr Ile Ile Glu Glu Leu Lys Lys Leu
      50      55      60
Lys Val Tyr Pro Leu Asn Val Glu Gly Leu Ser His Ser Asp Trp Val
      65      70      75      80
Val Ile Asp Tyr Gly Phe Ile Val Ile His Leu Phe Val Ser Xaa Xaa
      85      90      95
Arg Glu Gln Tyr Cys Leu Glu Glu Leu Trp Lys Asp Gly Ala Ile Ile
      100      105      110
Thr Ser Asp Cys Leu Ala Ser
      115

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 622:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 584 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(610109..611860)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 622:

Cys	Ile	Ala	Arg	Ala	Asn	Phe	Asp	Tyr	Gln	Leu	Phe	Phe	Leu	Ser	Arg	1	5	10	15
Leu	Thr	Leu	Thr	Asn	Ser	Tyr	His	Met	Asp	Ile	Pro	Glu	Gln	Gly	Ser	20	25	30	
Asn	Thr	Pro	Glu	Val	Glu	Gln	Ala	Ala	Cys	Cys	Asn	Gln	Glu	Ala	Ala	35	40	45	
Glu	Asn	Asp	Arg	Ala	Lys	Asp	Lys	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Ala	50	55	60	
Glu	Ala	Val	Gln	Ser	Cys	Glu	Ser	Met	Glu	Ala	Phe	Glu	Gln	Val	Val	65	70	75	80
Ala	Glu	Arg	Ser	Ser	Ile	Glu	Glu	Lys	Ile	Leu	Phe	Ala	Leu	Glu	Gln	85	90	95	
Met	Gly	Ala	Leu	Leu	Lys	Gly	Ala	Asp	Gln	Asn	Ser	Asp	Leu	Lys	Leu	100	105	110	
Phe	Trp	Asn	Val	Arg	Lys	Phe	Cys	Leu	Pro	Leu	Phe	Gln	Gln	Leu	Glu	115	120	125	
Asp	Pro	Val	Gln	Arg	Ala	Asn	Leu	Trp	Gly	Arg	Tyr	Thr	Glu	Leu	Thr	130	135	140	
Arg	Glu	Gly	Arg	Tyr	Ile	Lys	Thr	Leu	Gln	Asp	Glu	Glu	Gly	Ala	Phe	145	150	155	160
Leu	Val	Gly	Gln	Ile	Glu	Leu	Ala	Ile	Ser	Cys	Leu	Glu	Ser	Gly	Val	165	170	175	
Gln	Gly	Phe	Phe	Ser	Lys	Thr	Glu	Lys	Glu	Glu	Ile	Ser	Glu	Glu	Asp	180	185	190	
Arg	Ala	Ala	Leu	Glu	Ile	Pro	Ser	Leu	Ser	Ala	His	Lys	Asp	Phe	Tyr	195	200	205	
Leu	Ser	Thr	His	Ala	Asp	Leu	Arg	Trp	Leu	Gly	Ser	Phe	Ser	Ser	Gln	210	215	220	
Ile	Ile	Asn	Leu	Arg	Lys	Glu	Leu	Met	Asn	Ile	Ser	Met	Arg	Met	Arg	225	230	235	240
Leu	Lys	Ser	Gln	Phe	Gln	Lys	Leu	Ser	Val	Leu	Gly	Asn	Lys	Val		245	250	255	
Phe	Pro	Arg	Arg	Lys	Glu	Leu	Thr	Glu	Lys	Val	Ser	Glu	Leu	Phe	Ala	260	265	270	
Gln	Asp	Val	Glu	Ala	Phe	Val	Glu	Arg	Tyr	Phe	Ser	Arg	Ala	Ser	Arg	275	280	285	
Glu	Ser	Leu	Lys	Lys	Ser	Val	Phe	Phe	Leu	Arg	Lys	Glu	Ile	Lys	Arg	290	295	300	
Leu	Gln	Gln	Ala	Ala	Lys	Tyr	Leu	Ser	Ile	Ser	Ser	Gly	Val	Phe	Ser	305	310	315	320
Ser	Thr	Arg	Leu	Gly	Leu	Ser	Gln	Cys	Trp	Asp	Gln	Leu	Lys	Gly	Leu	325	330	335	
Glu	Lys	Glu	Ile	Arg	Gln	Glu	Gln	Ser	Arg	Leu	Ala	Ala	Thr	Ser	Ala	340	345	350	
Glu	Asn	Met	Lys	Glu	Val	Gln	Gly	Arg	Leu	Asp	Gln	Val	Glu	Val	Leu	355	360	365	
Leu	Gln	Glu	Asn	Glu	Glu	Val	His	Lys	Ile	Arg	Lys	Glu	Ile	Glu	Ala	370	375	380	



```

Ile Ser Lys His Ile Arg Gly Ile Ser Leu Val His Asp Asp Val Val
385          390          395          400
Leu Leu Lys Gly Arg Ile Gln Thr Leu Leu Gly Glu Val Arg Glu Arg
          405          410          415
Glu Ala Val Ile Glu Lys Glu Met Lys Glu Leu Gln Ala Lys Ala Glu
          420          425          430
Gln Ala Arg Ala Glu Ala Ile Gln Ala Leu Glu Asn Glu Val Gln Ser
          435          440          445
Phe Cys Asp Gln Cys Asn Glu Gly Asp Leu Pro Glu Gly Ala Lys Glu
          450          455          460
Arg Cys Gln Glu Leu Lys Glu Ala Val Lys Lys Met Ala Tyr Leu Pro
465          470          475          480
Tyr Ala Lys Lys Val Ala Leu Asp Asn Gln Ile Asn Ala Ala Gln Arg
          485          490          495
Ser Val Leu Ala Arg Leu Glu Glu Gln Met Leu Ala Cys Pro Asp Glu
          500          505          510
Lys Val Leu Asn Met Arg Gln Val Leu Glu Gln Arg Met Leu Arg Arg
          515          520          525
Lys Glu Leu Lys Ala Lys Phe Glu Cys Asp Lys Lys Leu Leu Gly Gly
          530          535          540
Ser Gly Leu Asp Phe Asp Arg Ala Leu Gln Tyr Ser Ala Met Val Glu
545          550          555          560
Glu Asp Arg Lys Ala Leu Glu Glu Leu Asp Ala Ala Ile Ile Glu Leu
          565          570          575
Lys Arg Gln Ile Gln Gln Phe Val
          580

```

(2) INFORMATIONS POUR LA SEQ ID NO: 623:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 372 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 611812..612927

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 623:

```

Val Leu Thr Lys Lys Thr Ile Gly Ser Gln Ser Leu Leu Trp Gln Cys
1          5          10          15
Ile Ile Val Asn Gly Phe Met Gly Ser Pro Ala Arg Thr Ser Phe Gln
          20          25          30
Glu Gly Leu Arg Leu Phe Leu Tyr Ser Pro Leu Glu Glu Leu Arg Ile
          35          40          45
His Ala Asp Ser Leu Arg Lys Gln Arg Tyr Pro Gln Asn Thr Ile Thr
          50          55          60
Tyr Val Leu Asp Ala Asn Pro Asn Tyr Thr Asn Ile Cys Lys Ile Asp
65          70          75          80
Cys Ala Phe Cys Ala Phe Tyr Arg Lys Pro Arg Ser Ser Asp Ala Tyr
          85          90          95
Leu Leu Ser Phe Asp Glu Phe Arg Gln Leu Met Gln Arg Tyr Val Gln
          100          105          110
Ala Gly Ile Lys Thr Val Leu Leu Gln Gly Gly Val His Pro Gln Ile
          115          120          125
Gly Ile Asp Tyr Leu Glu Thr Leu Val Ser Ile Thr Lys Lys Glu Phe

```

130		135		140
Pro Ser Leu His Pro His Phe Phe Ser Ala Val Glu Ile Ala His Ala				
145		150		155
Ala Gln Ile Ser Gly Ile Ser Thr Glu Gln Ala Leu Glu Arg Leu Trp				160
	165		170	175
Glu Ala Gly Gln Arg Thr Ile Pro Gly Gly Gly Ala Glu Ile Leu Ser				
	180		185	190
Glu Arg Ile Arg Lys Gln Ile Ser Pro Lys Lys Met Gly Pro Asp Gly				
	195		200	205
Trp Ile Gln Phe His Lys Leu Ala His Arg Leu Gly Phe Arg Ser Thr				
	210		215	220
Ala Thr Met Met Phe Gly His Val Glu Ser Pro Glu Asp Ile Leu Leu				
	225		230	235
His Leu Gln Thr Leu Arg Asp Ala Gln Asp Glu Asn Pro Gly Phe Phe				240
	245		250	255
Ser Phe Ile Pro Trp Ser Tyr Lys Pro Asn Asn Thr Ala Leu Gly Arg				
	260		265	270
Arg Val Pro His Gln Ala Ser Pro Glu Leu Tyr Tyr Arg Ile Leu Ala				
	275		280	285
Val Ala Arg Ile Phe Leu Asp Asn Phe Asp His Ile Ala Ala Ser Trp				
	290		295	300
Phe Gly Glu Gly Lys Glu Gly Val Lys Gly Leu Phe Tyr Gly Ala				
	305		310	315
Asp Asp Phe Gly Gly Thr Ile Leu Asp Glu Ser Val His Lys Cys Thr				
	325		330	335
Gly Trp Asp Leu Gln Ser Ser Glu Lys Glu Ile Cys Ala Met Leu Leu				
	340		345	350
Gln Ala Gly Phe Thr Pro Val Glu Arg Asp Thr Phe Tyr Arg Pro Leu				
	355		360	365
Ser Leu Ala Arg				
370				

(2) INFORMATIONS POUR LA SEQ ID NO: 624:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 220 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE-GENOME: complement(612938..613597)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 624:

Ser Pro His Ser Arg Arg Arg Asp Arg Phe Leu Phe Pro Tyr Phe Ser				
1	5	10	15	
Ile Arg Ser Ala Ile Trp Ala Phe Ser Arg Phe Cys Ile Ala Gly Xaa				
	20	25	30	
Leu Thr Leu Glu Ala Gln Glu Arg Gly Ile Ser Ala Leu Tyr Gln Glu				
	35	40	45	
Leu Glu Leu Leu Asp Pro Val Tyr Ala Ala Thr Ile Thr Lys His Asp				
	50	55	60	
Lys Asn Lys Ile Ile Arg Ala Leu Glu Ile Ile Arg Lys Thr Gly Ser				
	65	70	75	80
Lys Val Ser Ser Tyr Ala Trp Gln Ser Thr Val Asn Glu Ser Lys Glu				
	85	90	95	

Tyr	His	Cys	Arg	Gly	Trp	Leu	Leu	Ser	Pro	Asp	Pro	Glu	Leu	Leu	Arg
			100					105					110		
His	Asn	Ile	Leu	Glu	Arg	Cys	Asp	Gln	Met	Leu	Glu	Glu	Gly	Leu	Leu
		115					120					125			
Asp	Glu	Val	Gln	Ala	Leu	Leu	Ala	Ala	Gly	Ile	Lys	Gly	Asn	Ser	Ser
		130				135					140				
Ala	Ser	Arg	Ala	Ile	Gly	Tyr	Arg	Glu	Trp	Ile	Glu	Phe	Leu	Asp	Leu
145					150					155					160
Gly	Ser	Pro	Pro	Asp	Leu	Phe	Glu	Ile	Thr	Lys	Gln	Lys	Phe	Ile	Thr
				165					170					175	
Asn	Thr	Trp	Arg	Tyr	Thr	Lys	Lys	Gln	Arg	Thr	Trp	Phe	Lys	Arg	Tyr
			180					185					190		
Ser	Leu	Phe	Arg	Glu	Leu	Arg	Pro	Met	Gly	Met	Thr	Leu	Asp	Asp	Met
		195					200					205			
Ala	Lys	Lys	Ile	Ala	Gln	Asp	Tyr	Phe	Leu	Cys	Gly				
	210					215					220				

(2) INFORMATIONS POUR LA SEQ ID NO: 625:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 68 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(613692..613895)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 625:

Gln	Lys	Ser	Phe	Ser	Lys	Met	Phe	Lys	Arg	Thr	Val	Ile	Leu	Leu	Ala
1				5				10						15	
Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Ala	Val	Ser	Leu	Lys	Leu	Ala	Pro
			20					25					30		
Leu	Val	Asp	Gly	Glu	Ile	Ile	Ser	Val	Asp	Ser	Met	Gln	Val	Tyr	Gln
		35					40					45			
Gly	Met	Asp	Ile	Gly	Thr	Ala	Lys	Val	Ser	Leu	Ala	Asp	Arg	Lys	Arg
	50					55					60				
Phe	Arg	Ile	Thr												
65															

(2) INFORMATIONS POUR LA SEQ ID NO: 626:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 310 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 614315..615244

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 626:

Ser Asn Asp Glu Ile Leu Asp Gly Arg Ser Leu Tyr Leu Leu Ser Ser

```

1           5           10           15
Asn Lys Gly Phe Ser Leu Phe Phe Tyr Leu Lys Lys Gln Phe Phe Leu
20           25           30
Asp Ser Ser Arg Cys Thr Leu Glu Val Ile Leu Pro Pro Arg Ser Pro
35           40           45
Ser Phe Leu Val His Ile Trp Arg Leu Phe Phe Ala Lys Gly Pro Asn
50           55           60
Tyr Ser Leu Pro Tyr Ala Phe Leu Cys Ile Phe Val Ser Val Leu Val
65           70           75           80
Phe Leu Pro Ile Gly Leu Trp Leu Thr Leu Pro Ser Phe Leu Asn Phe
85           90           95
Lys His Ser Leu Thr Pro Ile Lys Thr Leu Phe Leu Thr Cys Thr Glu
100          105          110
Pro Pro Cys Leu Pro Glu Pro Phe Phe Ser Asp Ile Leu His Leu Ser
115          120          125
Ala Asp Ser Pro Pro Ala Leu Gln Thr Phe Ser Thr Lys Ser Ala Glu
130          135          140
His Phe Leu Asn Glu Leu Gly Val Phe Ser Phe Ile Ser Ile Glu Lys
145          150          155          160
Val Pro Asp His Lys Gly Leu Asp Ile Ser Tyr Ala Leu His Thr Pro
165          170          175
Leu Ala Phe Leu Gly Asn Gln Thr His Thr Phe Ile Gly Tyr Glu Gly
180          185          190
Gln Thr Phe Pro Ala Leu Pro Phe Phe Gln Ser Leu Glu Leu Pro Thr
195          200          205
Val Phe Phe Ser Gln Gln Ala Leu Ser Gln Thr Arg Ile Pro His Gln
210          215          220
Thr Leu Ser Ile Val Thr Ser Leu Ile Asp Gln Leu Gln Met Asp Pro
225          230          235          240
Pro Ser Ile Ile Asp Leu Ser Gln Ile Asp His Tyr Pro Gly Glu Phe
245          250          255
Val Val Ser Leu Ser Ser Gly Thr Leu Leu Arg Phe Arg Lys Asp Ser
260          265          270
Phe Leu Pro Gly Ile Gln His Tyr Gln Gln Ala Leu Ser Leu Gly Ala
275          280          285
Phe Ser Pro Gln Gln Ala Val Ile Cys Asp Leu Arg Cys Glu Asp Tyr
290          295          300
Leu Leu Leu Lys Arg Lys
305          310

```

(2) INFORMATIONS POUR LA SEQ ID NO: 627:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 93 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 615405..615683

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 627:

```

Met Glu Asp Phe Ala Ala Tyr Ile Val Lys Asn Leu Val Thr Asp Pro
1           5           10           15
Asn Ala Val Glu Ile Arg Ser Ser Glu Asp Lys Ala Ser Ala Thr Leu
20           25           30

```

```

Lys Leu Glu Ile His Ala Ala Ser Glu Asp Ile Gly Lys Ile Ile Gly
      35              40              45
Arg Lys Gly Gln Thr Ile Gln Ala Leu Arg Thr Ile Leu Lys Arg Val
      50              55              60
Gly Ala Arg Leu Gln Lys Lys Ile Leu Val Glu Leu Ala Gln Pro Glu
      65              70              75              80
Asn Gly Ser Leu Thr Asp Glu Glu Val Leu Ser Leu Asp
      85              90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 628:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 616 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(615864..617711)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 628:

```

Arg Arg Ser Arg Ala Ser Ser Gly Phe Phe Glu Arg Phe Ala Leu Lys
1      5      10      15
Thr Gln Gln Ile Cys Trp Tyr Asn Gly Tyr Cys Pro Arg Leu Arg Ser
      20      25      30
Cys Leu Gln Gly His Thr Phe Gly Leu Asp Ser Ser Cys Asp Leu His
      35      40      45
Ile Leu Ser Tyr Tyr Gln Glu Gly Trp Arg Leu Tyr Phe Thr Ala Lys
      50      55      60
Tyr Gln Asp Val Val Tyr Ala Asp Ile Glu Val Gln Leu Val Gly Met
      65      70      75      80
His Asn Val Leu Asn Ala Ala Ala Ala Met Gly Ile Ala Leu Ser Leu
      85      90      95
Gly Ile Asp Glu Gly Ala Ile Arg Asn Ala Phe Arg Gly Phe Ser Gly
      100      105      110
Val Gln Arg Arg Leu Gln Arg Lys Asn Ser Ser Glu Thr Phe Leu Phe
      115      120      125
Leu Glu Asp Tyr Ala His His Pro Ser Glu Ile Ser Cys Thr Leu Arg
      130      135      140
Ala Val Arg Thr Ala Val Gly Gln Arg Arg Ile Leu Ala Ile Cys Gln
      145      150      155      160
Pro His Arg Phe Ser Arg Leu Arg Glu Cys Ile Asp Ser Phe Pro Ser
      165      170      175
Ala Phe Lys Asp Ala Asp Glu Val Leu Leu Thr Glu Val Tyr Ser Ala
      180      185      190
Gly Glu Glu Ala Glu Asp Ile Ser Tyr Gln Glu Leu Ala Glu Ala Ile
      195      200      205
Ser Gln Glu Ser Ile Val Lys Cys Thr His Ile Pro Phe His Glu Leu
      210      215      220
Gln Arg His Leu Glu Gln Ser Ile Arg Val His Asp Val Cys Val Ser
      225      230      235      240
Leu Gly Ala Gly Asn Ile Val Asn Leu Gly Glu Lys Leu Arg Asp Phe
      245      250      255
Glu Pro Gln Lys Leu His Leu Gly Ile Ile Cys Gly Gly Lys Ser Cys
      260      265      270
Glu His Glu Ile Ser Val Leu Ser Ala Lys Asn Ile Ala Lys His Leu

```

	275		280		285										
Ser	Lys	Ser	Phe	Tyr	Asp	Val	Ser	Tyr	Phe	Leu	Ile	Thr	Arg	Glu	Gly
	290					295					300				
Leu	Trp	Glu	Ser	Val	Ser	Ser	Leu	Glu	Thr	Ala	Glu	Asp	Ser	Gly	Lys
305					310					315					320
Ser	Val	Phe	Asp	Pro	Glu	Ile	Ala	Gln	Arg	Leu	Glu	Lys	Val	Asp	Val
			325						330					335	
Val	Leu	Pro	Ile	Leu	His	Gly	Pro	Tyr	Gly	Glu	Asp	Gly	Ala	Met	Gln
			340					345					350		
Gly	Phe	Leu	Glu	Thr	Ile	Gly	Lys	Pro	Tyr	Thr	Gly	Pro	Ala	Ile	Ala
		355					360					365			
Phe	Ser	Ala	Ile	Ala	Met	Asn	Lys	Val	Phe	Thr	Lys	Arg	Phe	Met	Ser
	370					375					380				
Asp	Leu	Gly	Ile	Pro	Val	Val	Pro	Tyr	Leu	Pro	Leu	Thr	Leu	Ala	Gly
385				390						395					400
Trp	Asn	Gln	Glu	Gln	Xaa	Lys	Trp	Leu	Ala	His	Ile	Val	Glu	Ala	Phe
				405					410					415	
Ser	Phe	Pro	Met	Phe	Val	Lys	Ser	Ser	His	Leu	Gly	Ser	Ser	Ile	Gly
			420					425					430		
Val	Phe	Glu	Val	His	Asn	Val	Ile	Glu	Leu	Arg	Asp	Ala	Ile	Asn	Glu
		435					440					445			
Ala	Phe	Met	Arg	Asp	Asn	Asp	Val	Phe	Val	Glu	Glu	Asn	Arg	Leu	Gly
	450					455					460				
Cys	Lys	Glu	Ile	Glu	Val	Ser	Val	Leu	Gly	Asp	Gly	Ser	Gly	Ala	Phe
465				470						475					480
Val	Ile	Ala	Gly	Leu	His	Glu	Arg	Arg	Gly	Ser	Gly	Gly	Phe	Ile	Asp
				485					490					495	
Tyr	Gln	Glu	Lys	Tyr	Gly	Leu	Ser	Gly	Lys	Ser	Ser	Ala	Gln	Ile	Val
			500					505					510		
Phe	Asp	Thr	Asp	Leu	Ser	Lys	Glu	Ile	Gln	Glu	Gln	Ile	Leu	Glu	Ala
	515						520					525			
Ala	Asp	Lys	Ile	Tyr	Arg	Leu	Leu	Gly	Lys	Gly	Ser	Cys	Arg	Ile	
	530					535				540					
Asp	Phe	Phe	Val	Asp	Glu	Glu	Gly	Asn	Phe	Trp	Leu	Ser	Glu	Met	Asn
545				550						555					560
Pro	Ile	Pro	Gly	Met	Thr	Glu	Thr	Ser	Pro	Phe	Leu	Thr	Ser	Phe	Ile
				565					570					575	
Arg	Lys	Gly	Trp	Ser	Tyr	Glu	Gln	Ile	Val	His	Gln	Leu	Val	Ile	Asp
			580					585					590		
Gly	Leu	Gln	Arg	Phe	Asn	Gln	Arg	Gln	Arg	Leu	Ile	Ser	Thr	Ser	Phe
		595					600					605			
Val	Asp	Gln	Ala	Phe	Ala	Ile	Gln								
	610					615									

(2) INFORMATIONS POUR LA SEQ ID NO: 629:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 268 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(617510..618313)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 629:

```

Ser Asn His Cys Ile Ser Leu Phe Val Asn Leu Tyr Arg Leu Met Met
1      5      10      15
Lys Ser Leu Phe Tyr His Phe Ile Gly Ile Gly Gly Ile Gly Met Ser
20      25      30
Ala Leu Ala His Val Leu Leu Asp Arg Gly Tyr Ser Val Ser Gly Ser
35      40      45
Asp Leu Ser Glu Gly Lys Val Val Glu Lys Leu Lys Asn Lys Gly Ala
50      55      60
Glu Phe Phe Leu Gly Asn Gln Glu Glu His Ile Pro Glu Gly Ala Val
65      70      75      80
Val Val Tyr Ser Ser Ser Ile Ser Lys Glu Asn Pro Glu Phe Leu Ser
85      90      95
Ala Lys Ser Arg Gly Asn Arg Val Val His Arg Ala Glu Leu Leu Ala
100     105     110
Glu Leu Ala Gln Asp Gln Ile Ser Ile Phe Val Thr Gly Ser His Gly
115     120     125
Lys Thr Thr Val Ser Ser Leu Ile Thr Ala Ile Leu Gln Glu Ala Lys
130     135     140
Lys Asn Pro Ser Phe Val Ile Gly Gly Leu Asn Gln Glu Gly Ile Asn
145     150     155     160
Gly Gly Ser Gly Ser Glu Tyr Phe Val Ala Glu Ala Asp Glu Ser Asp
165     170     175
Gly Ser Ile Arg Cys Tyr Thr Pro Glu Phe Ser Val Ile Thr Asn Ile
180     185     190
Asp Asp Glu His Leu Ser Asn Phe Glu Gly Asp Arg Glu Leu Leu Leu
195     200     205
Ala Ser Leu Lys Asp Leu His Ser Arg Leu Ser Arg Ser Val Gly Ile
210     215     220
Met Asp Ile Val Leu Ala Cys Val His Ala Cys Lys Gly Ile Leu Leu
225     230     235     240
Asp Trp Thr Leu Leu Val Ile Tyr Ile Phe Tyr Leu Ile Ile Lys Lys
245     250     255
Asp Gly Asp Cys Thr Leu Gln Gln Ser Ile Lys Met
260     265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 630:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 325 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(618361..619335)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 630:

```

Met Lys Lys Ile Asn Lys Ile Val Leu Ala Val Gly Gly Thr Gly Gly
1      5      10      15
His Ile Ile Pro Ala Leu Ala Ala Arg Glu Thr Phe Ile His Glu Asp
20      25      30
Ile Glu Val Leu Leu Leu Gly Lys Gly Leu Ala His Phe Leu Gly Asp
35      40      45
Asp Ser Glu Ile Ala Tyr Cys Asp Ile Pro Ser Gly Ser Pro Phe Ser
50      55      60
Leu Arg Val Asn Arg Met Phe Ser Gly Ala Lys Gln Leu Tyr Lys Gly

```

65					70					75					80
Tyr	Val	Ala	Ala	Leu	Gln	Lys	Ile	Arg	Asp	Phe	Thr	Pro	Asp	Leu	Ala
				85					90					95	
Ile	Gly	Phe	Gly	Ser	Tyr	His	Ser	Leu	Pro	Ala	Met	Leu	Ala	Ser	Ile
			100					105					110		
Arg	Ser	Arg	Ile	Pro	Leu	Phe	Leu	His	Glu	Gln	Asn	Ile	Val	Pro	Gly
			115				120					125			
Lys	Val	Asn	Lys	Leu	Phe	Ser	Arg	Phe	Ala	Lys	Gly	Val	Gly	Met	Ser
			130			135					140				
Phe	Ala	Ala	Ala	Gly	Glu	His	Phe	His	Cys	Arg	Ala	Glu	Glu	Val	Phe
145					150				155						160
Leu	Pro	Ile	Arg	Lys	Leu	Ser	Glu	Gln	Ile	Val	Phe	Pro	Gly	Ala	Ser
				165					170					175	
Pro	Val	Ile	Cys	Val	Val	Gly	Gly	Ser	Gln	Gly	Ala	Lys	Ile	Leu	Asn
			180					185					190		
Asp	Val	Val	Pro	Lys	Ala	Leu	Ala	Arg	Ile	Arg	Glu	Ser	Tyr	Ser	Asn
			195				200					205			
Leu	Tyr	Val	His	His	Ile	Val	Gly	Pro	Lys	Gly	Asp	Leu	Gln	Ala	Val
	210				215						220				
Ser	Gln	Val	Tyr	Gln	Asp	Ala	Gly	Ile	Asn	His	Thr	Val	Thr	Ala	Phe
225					230					235					240
Asp	His	Asn	Met	Leu	Gly	Val	Leu	Gln	Ala	Ser	Asp	Leu	Val	Ile	Ser
				245					250					255	
Arg	Ser	Gly	Ala	Thr	Met	Leu	Asn	Glu	Leu	Leu	Trp	Val	Gln	Val	Pro
			260					265					270		
Ala	Ile	Leu	Ile	Pro	Tyr	Pro	Gly	Ala	Tyr	Gly	His	Gln	Glu	Val	Asn
		275					280					285			
Ala	Lys	Phe	Phe	Thr	His	Thr	Val	Gly	Gly	Gly	Thr	Met	Ile	Leu	Gln
	290					295					300				
Lys	Tyr	Leu	Thr	Glu	Glu	Ser	Leu	Ser	Lys	Gln	Val	Leu	Leu	Cys	Phe
305					310					315					320
Arg	Ser	Cys	Asn	Gln											
				325											

(2) INFORMATIONS POUR LA SEQ ID NO: 631:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 390 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(619247..620416)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 631:

Ile	Ser	Gly	Ile	Ile	Met	Lys	Trp	Phe	Leu	Ile	Ser	Cys	Leu	Leu	Gly
1				5				10					15		
Ile	Phe	Ser	Leu	Gly	Leu	Ile	Met	Val	Phe	Asp	Thr	Ser	Ser	Ala	Glu
			20				25					30			
Val	Leu	Asp	Arg	Ala	Leu	Ser	Cys	Ser	Thr	His	Lys	Ala	Leu	Ile	Arg
		35				40					45				
Gln	Ile	Thr	Tyr	Leu	Gly	Leu	Gly	Leu	Gly	Ile	Ala	Ser	Phe	Val	Tyr
	50				55					60					
Ile	Leu	Gly	Trp	Lys	Asp	Phe	Leu	Lys	Met	Ser	Pro	Met	Leu	Leu	Ile
65				70				75						80	



Phe Val Gly Ile Thr Leu Val Leu Val Leu Ile Pro Gly Ile Gly Val  
                                     85                                    90                                    95  
 Cys Arg Asn Gly Ala Lys Arg Trp Leu Gly Val Gly Gln Leu Thr Leu  
                                     100                                    105                                    110  
 Gln Pro Ser Glu Phe Val Lys Tyr Leu Val Pro Cys Val Ala Ile Glu  
                                     115                                    120                                    125  
 Cys Leu Thr Thr Lys Pro Ser Ile Arg Ser Ser Phe Lys Arg Phe Val  
                                     130                                    135                                    140  
 Ala Phe Val Ala Leu Leu Phe Ile Pro Ile Met Leu Ile Ala Ile Glu  
                                     145                                    150                                    155                                    160  
 Pro Asp Asn Gly Ser Ala Ala Val Ile Ser Phe Ser Leu Ile Pro Val  
                                     165                                    170                                    175  
 Phe Ile Val Thr Ala Val Arg Leu Arg Tyr Trp Leu Val Pro Leu Leu  
                                     180                                    185                                    190  
 Cys Val Leu Cys Ile Gly Gly Thr Phe Ala Tyr Arg Leu Pro Tyr Val  
                                     195                                    200                                    205  
 Arg Asn Arg Leu Gln Val Tyr Leu His Pro Glu Leu Asp Ile Lys Gly  
                                     210                                    215                                    220  
 Arg Gly His Gln Pro Tyr Gln Ala Lys Ile Ala Ala Gly Ser Gly Gly  
                                     225                                    230                                    235                                    240  
 Val Phe Gly Lys Gly Pro Gly Lys Gly Leu Gln Lys Leu Thr Tyr Leu  
                                     245                                    250                                    255  
 Pro Glu Ala Gln Asn Asp Tyr Ile Ala Ala Ile Tyr Ala Glu Glu Phe  
                                     260                                    265                                    270  
 Gly Phe Ile Gly Met Leu Leu Leu Ile Leu Leu Tyr Met Gly Phe Ile  
                                     275                                    280                                    285  
 Tyr Ser Gly Tyr Val Ile Ala Met Arg Ala Ser Leu Leu Ser Gly Ala  
                                     290                                    295                                    300  
 Ala Leu Ala Ile Ser Ile Thr Val Ile Ile Gly Met Gln Ala Phe Ile  
                                     305                                    310                                    315                                    320  
 Asn Leu Gly Val Val Ser Gly Leu Leu Pro Ser Lys Gly Val Asn Leu  
                                     325                                    330                                    335  
 Pro Phe Phe Ser Gln Gly Gly Ser Ser Leu Ile Ala Asn Met Cys Gly  
                                     340                                    345                                    350  
 Met Gly Leu Leu Leu Arg Ile Cys Asp Glu Glu Asn Gln Gln Asn Arg  
                                     355                                    360                                    365  
 Ile Gly Ser Gly Gly Asn Arg Arg Ala His Tyr Pro Cys Ser Ser Ser  
                                     370                                    375                                    380  
 Lys Arg Asp Phe Tyr Ser  
                                     385                                    390

(2) INFORMATIONS POUR LA SEQ ID NO: 632:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 619863..620261

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 632:

Arg Asn Arg Thr Ala Val Thr Ile Lys Thr Gly Ile Lys Glu Asn Glu  
 1                                    5                                    10                                    15  
 Ile Thr Ala Ala Asp Pro Leu Ser Gly Ser Ile Ala Ile Asn Ile Met

(2) INFORMATIONS POUR LA SEQ ID NO: 633:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 255 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(620420..621184)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 633:

Ala	Phe	Gly	Trp	Asp	Gly	Arg	Gly	Ser	Phe	Met	Asn	Arg	Arg	Asn	Thr
1				5					10					15	
Met	Ile	Val	Ala	Thr	Thr	Val	Asn	Ala	Val	Leu	Leu	Ala	Val	Leu	Phe
			20					25					30		
Met	Thr	Ala	Arg	His	Ser	Glu	Gln	Glu	Ile	Glu	Tyr	Pro	Gln	Lys	Ile
		35					40					45			
Ala	Pro	Ile	Lys	Ile	Leu	Glu	Pro	Val	Pro	Val	Val	Asp	Lys	Ala	Pro
	50					55					60				
Glu	Lys	Leu	Glu	Lys	Lys	Pro	Glu	Val	Ile	Ala	Lys	Pro	Ser	Gln	Val
65					70					75					80
Val	Arg	Asn	Pro	Val	Val	Ser	Lys	Ala	Glu	Leu	Ala	Ala	Gln	Phe	Ala
				85					90					95	
Asp	Lys	Asn	Pro	Lys	Thr	Glu	Lys	Glu	Ser	Ser	Gly	Gly	Ser	Lys	Lys
			100					105					110		
Ile	Ser	Ser	Thr	Pro	Val	Glu	Ser	Thr	Thr	Pro	Val	Ala	Pro	Glu	Ile
		115						120					125		
Ser	Val	Val	Asn	Ala	Lys	Val	Val	Glu	Lys	Thr	Pro	Glu	Lys	Glu	Glu
	130					135					140				
Phe	Ser	Thr	Val	Ile	Val	Lys	Lys	Gly	Asp	Phe	Leu	Glu	Arg	Ile	Ala
145					150					155					160
Arg	Ser	Asn	His	Thr	Thr	Val	Ser	Ala	Leu	Met	Gln	Leu	Asn	Asp	Leu
				165					170					175	
Ser	Ser	Thr	Gln	Leu	Gln	Ile	Gly	Gln	Val	Leu	Arg	Val	Pro	Lys	Thr
			180					185					190		
Asn	Lys	Thr	Glu	Lys	Asp	Leu	Gln	Val	Lys	Thr	Pro	Asn	Pro	Glu	Asp
		195					200					205			
Tyr	Tyr	Val	Val	Lys	Glu	Gly	Asp	Ser	Pro	Trp	Ala	Ile	Ala	Leu	Ser
	210					215					220				

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 255 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(620420..621184)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 633:

Ala 1	Phe	Gly	Trp	Asp 5	Gly	Arg	Gly	Ser	Phe 10	Met	Asn	Arg	Arg	Asn 15	Thr
Met	Ile	Val	Ala 20	Thr	Thr	Val	Asn 25	Ala	Val	Leu	Leu	Ala 30	Val	Leu	Phe
Met	Thr	Ala 35	Arg	His	Ser	Glu	Gln 40	Glu	Ile	Glu	Tyr	Pro 45	Gln	Lys	Ile
Ala	Pro 50	Ile	Lys	Ile	Leu	Glu 55	Pro	Val	Pro	Val	Val 60	Asp	Lys	Ala	Pro
Glu 65	Lys	Leu	Glu	Lys	Lys	Pro 70	Glu	Val	Ile	Ala 75	Lys	Pro	Ser	Gln	Val 80
Val	Arg	Asn	Pro	Val 85	Val	Ser	Lys	Ala	Glu 90	Leu	Ala	Ala	Gln	Phe 95	Ala
Asp	Lys	Asn	Pro 100	Lys	Thr	Glu	Lys	Glu 105	Ser	Ser	Gly	Gly	Ser 110	Lys	Lys
Ile	Ser	Ser 115	Thr	Pro	Val	Glu	Ser	Thr 120	Thr	Pro	Val	Ala 125	Pro	Glu	Ile
Ser	Val	Val 130	Asn	Ala	Lys	Val	Val	Glu 135	Lys	Thr	Pro	Glu 140	Lys	Glu	Glu
Phe 145	Ser	Thr	Val	Ile	Val 150	Lys	Lys	Gly	Asp	Phe 155	Leu	Glu	Arg	Ile	Ala 160
Arg	Ser	Asn	His	Thr 165	Thr	Val	Ser	Ala	Leu 170	Met	Gln	Leu	Asn	Asp 175	Leu
Ser	Ser	Thr	Gln	Leu 180	Gln	Ile	Gly	Gln 185	Val	Leu	Arg	Val	Pro	Lys	Thr
Asn	Lys	Thr 195	Glu	Lys	Asp	Leu	Gln	Val 200	Lys	Thr	Pro	Asn 205	Pro	Glu	Asp
Tyr	Tyr 210	Val	Val	Lys	Glu	Gly	Asp 215	Ser	Pro	Trp	Ala 220	Ile	Ala	Leu	Ser

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 635:

```

Met Gly Leu Glu Arg Val Val Val Ile Gly Leu Gly Val Ser Gly Arg
1      5      10      15
Ser Ile Xaa Xaa Phe Leu Ala Gln Lys Gly Val Cys Val Leu Gly Val
      20      25      30
Asp Lys Ser Leu His Ala Leu Gln Asn Cys Pro Tyr Ile Xaa Lys Asn
      35      40      45
Ile Trp Arg Thr Lys Ser Ser Leu His Arg Trp Ile Met Leu Ser Ser
      50      55      60
Pro Gly Val Ser Lys Glu His Pro Trp Val Gln Ala Ala Ile Ala Ser
65      70      75      80
His Ile Pro Val Met Thr Asp Ile Gln Leu Ala Phe Gln Thr Glu Lys
      85      90      95
Phe Thr Glu Arg Glu Ser Leu Ala Ile Thr Gly Thr Thr Gly Lys Thr
      100      105      110
Thr Thr Ile Leu Phe Leu Glu Tyr Leu Phe Lys Arg Ser Gly Ile Pro
      115      120      125
Ala Phe Ala Met Gly Asn Val Gly Ile Pro Ile Leu Asp Gly Met Gln
130      135      140
Asn Pro Gly Val Arg Ile Val Glu Ile Ser Ser Phe Gln Leu Ala Asp
145      150      155      160
Gln Glu Lys Ser Tyr Pro Val Leu Ser Gly Gly Met Ile Leu Asn Ile
      165      170      175
Ser Asp Asn His Leu Asp Tyr His Gly Asn Phe Ser Glu Tyr Phe Gln
      180      185      190
Ala Lys Gln Asn Leu Ala Leu Cys Met Arg Asn Pro Asp Asp Leu Trp
      195      200      205
Val Gly Asp Glu Arg Phe Tyr Gly His Leu Tyr Leu Glu Glu Val Gln
210      215      220
Lys Tyr Met Arg Leu Leu Asp Lys Glu Ser Ala Leu Lys Pro Leu Val
225      230      235      240
Leu Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 636:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 351 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(622414..623466)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 636:

```

Arg Glu Phe Leu Ile Arg Ala Ser His Asn Lys Thr Arg Lys Gln Met
1      5      10      15
Leu Pro Leu Thr Tyr Val Val Lys Ala Phe Ser Ile Gly Leu Phe Phe
      20      25      30
Ser Leu Phe Leu Met Lys Pro Leu Ile Ser Trp Leu Lys Lys Gln Gly
      35      40      45
Phe Gln Asp His Ile His Lys Asp His Cys Glu Lys Leu Glu Glu Leu
50      55      60
His Lys Asp Lys Ala Tyr Ile Pro Thr Ala Gly Gly Ile Val Phe Val
65      70      75      80

```

```

Phe Ala Ser Val Leu Ala Val Leu Leu Leu Phe Pro Ile Gln Leu Trp
      85                      90                      95
Ser Thr Trp Phe Cys Ile Gly Thr Ile Leu Leu Trp Gly Ala Leu Gly
      100                    105                    110
Trp Cys Asp Asp Gln Ile Lys Asn Arg Arg Arg Val Gly His Gly Leu
      115                    120                    125
Ser Ala Lys His Lys Phe Leu Ile Gln Asn Cys Leu Ala Ala Gly Val
      130                    135                    140
Val Leu Pro Ile Met Phe Ala Tyr Lys Glu Ser Phe Leu Ser Phe His
      145                    150                    155                    160
Leu Pro Phe Leu Gly Ile Val Ser Leu Pro His His Trp Trp Ser Tyr
      165                    170                    175
Leu Leu Ser Phe Ala Ile Ala Thr Leu Ala Ile Val Gly Thr Ser Asn
      180                    185                    190
Ser Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ala Gly Ala Met
      195                    200                    205
Val Ile Ala Cys Leu Gly Met Leu Val Val Ala Cys Thr Asn Gly Ala
      210                    215                    220
Pro Trp Ala Phe Ile Cys Cys Val Leu Leu Ala Thr Leu Ala Gly Ser
      225                    230                    235                    240
Cys Leu Gly Phe Leu Arg Tyr Asn Lys Ser Pro Ala Arg Val Phe Met
      245                    250                    255
Gly Asp Thr Gly Ser Leu Phe Leu Gly Ala Met Leu Gly Met Cys Ala
      260                    265                    270
Val Leu Leu Arg Ala Glu Phe Leu Leu Leu Phe Met Gly Gly Ile Phe
      275                    280                    285
Val Leu Glu Ser Leu Ser Val Ile Val Gln Val Gly Ser Tyr Lys Leu
      290                    295                    300
Arg Lys Lys Arg Val Phe Leu Cys Ala Pro Leu His His His Tyr Glu
      305                    310                    315                    320
Tyr Lys Gly Leu Ser Glu Lys Ala Val Val Arg Asn Phe Leu Ile Val
      325                    330                    335
Glu Leu Ile Cys Val Val Val Gly Ile Ile Ala Val Phe Val Asp
      340                    345                    350

```

(2) INFORMATIONS POUR LA SEQ ID NO: 637:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(623570..624178)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 637:

```

Asn Gly Arg Phe Leu Leu Ser Ser Asp Ser Phe Arg Arg Val Leu Ile
1      5                      10                      15
Ser Ala Pro Asp Gly Asp Ile Glu Leu Pro Ala Val Phe Pro Tyr Ser
      20                    25                    30
Pro Ala Tyr Met Asn Phe Ile Ile Ala Val Ala Leu Ala Trp Ile Thr
      35                    40                    45
Asn Val Pro Met Asp Arg Leu Glu Gln Val Ser Gln Ser Leu Phe Leu
      50                    55                    60
Pro Ala Met Arg Phe Glu Gln Gln Glu His Asn Gly Ile Arg Val Ile

```

```

65          70          75          80
Asn Asp Ala Tyr Asn Ala Ser Pro Asp Ala Met Leu Ala Ala Leu Asp
85          90          95
Ala Val Pro Val Pro Pro Glu Gly Gly Lys Ile Ile Phe Ile Leu Gly
100         105         110
His Met Ala Glu Leu Gly Arg Tyr Ser Asp Glu Cys His Ile Ala Val
115         120         125
Ala Arg Lys Ala Val Thr Lys Ala His Ile Ile Phe Phe Val Gly Glu
130         135         140
Lys Trp Phe Pro Val Arg Asp Ile Val Arg Asp Ala Asp Cys Gln Ile
145         150         155
Gly Phe Tyr Ser Ala Val Ser Glu Ile Met Asp Thr Val Lys Ala Leu
165         170         175
Val Gln Gln Gly Asp Val Val Leu Leu Lys Gly Ser Arg Ser Leu Glu
180         185         190
Leu Glu Thr Leu Leu Pro Cys Phe Ser Ile Ser
195         200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 638:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(624073..624918)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 638:

```

Met Arg Pro Ile Leu Leu Glu Glu Trp Ser Ser Leu Leu Leu Gly Met
1          5          10          15
Glu Ile Pro Arg Ser Gly Lys Lys Val Thr Gly Val Ala Ile Asp Ser
20         25         30
Arg Leu Val Leu Pro Gly Asp Val Phe Phe Ala Leu Pro Gly Asn Arg
35         40         45
Thr Ser Gly His Leu Phe Leu Lys Gln Ala Ala Gln Ser Gly Ala Val
50         55         60
Ala Ala Val Val Ala Ser Asp Tyr His Gly Pro Ser Tyr Gly Leu Gln
65         70         75         80
Leu Leu Arg Val Ala Asp Pro Arg Glu Ala Leu Arg Ala Ala Gly Arg
85         90         95
Thr Gln Gly Ala Leu Phe His Gly Glu Val Ile Gly Ile Thr Gly Ser
100        105        110
Val Gly Lys Thr Thr Thr Lys Asn Phe Ala Asn Gln Leu Leu Ser Ser
115        120        125
Val Tyr Lys Val Phe Met Ser Pro Lys Ser Tyr Asn Ser Gln Leu Thr
130        135        140
Leu Pro Leu Ser Val Leu Met Ala Asp Gly Asp Glu Asp Phe Leu Leu
145        150        155        160
Leu Glu Met Gly Val Ser Glu Pro Asn Asn Met Lys Asn Leu Leu Glu
165        170        175
Ile Ile Glu Pro Thr Ile Gly Val Ile Thr His Ile Asp Val Gln His
180        185        190
Ala Met His Phe Leu Asp Lys Gly Ala Gln Gly Ile Val Glu Glu Lys
195        200        205

```

```

Ser Leu Leu Leu Glu Arg Cys Gly Leu Gln Leu Ile Pro Lys Asp Ser
  210                      215                      220
Ser Trp Phe Gln Phe Phe Ala Lys Lys Asn Ser Ala Ala Glu Arg Phe
225                      230                      235                      240
Ser Phe Ser Met Ser Asn Glu Thr Ala Asp Phe Tyr Tyr Arg Ala Ile
                      245                      250                      255
His Ser Glu Glu Ser Leu Leu Val Leu Leu Met Gly Thr Leu Ser Cys
                      260                      265                      270
Leu Pro Tyr Phe Arg Ile Leu Gln Arg Ile
      275                      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 639:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 440 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 625346..626665

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 639:

```

Pro Leu Gln Glu Tyr Pro Ala Met Pro His Asp Asn Asn Glu Met His
1      5      10      15
Arg Asn Thr Ile His Gln Leu Phe Thr Gly Leu Asp Lys Ala Tyr Gln
      20      25      30
Ile Val Lys Gly Phe Tyr Gly Pro Ala Tyr Ser Ser Ser Lys Asp
      35      40      45
Phe Phe Lys Gly Arg Gly Tyr His Ile Leu Ser Arg Ile Glu Leu Ser
      50      55      60
Asp Pro Phe Glu Arg Ile Gly Val Tyr Phe Ala Arg Ser Leu Ala Lys
      65      70      75      80
Arg Ile His Lys Arg His Ala Asp Gly Val Ile Ser Ser Val Ile Leu
      85      90      95
Leu Arg Ala Phe Leu Lys Ala Ser Ile Pro Phe Ile Asp Gln Gly Leu
      100     105     110
Ser Pro Arg Leu Leu Ala Ser Ala Leu Ala Ser Gln Lys Glu Ala Val
      115     120     125
Cys Ala Tyr Leu His Ser His Ser Phe Leu Leu Lys Asp Ala Ser Lys
      130     135     140
Val Leu Gly Leu Ile Arg Ser His Leu Pro Asp Pro Leu Ile Gly Glu
      145     150     155     160
Ala Phe Ala Glu Ala Val Ala Tyr Thr Gly His Glu Gly Ala Val Ala
      165     170     175
Leu Ser Gln Arg Ser Gly Ser Thr Leu His Leu Val Lys Gly Ile Gln
      180     185     190
Thr Gln Lys Gly Tyr Arg Met Pro Ser Phe Phe Pro His Asp Ser Phe
      195     200     205
His Glu Asn Pro Ile Val Ala Pro Lys Ile Phe Val Thr Asp Gln Lys
      210     215     220
Ile His Cys Leu Phe Pro Phe Leu Pro Leu Leu Lys Lys Phe Ser Glu
      225     230     235     240
Glu Gln Thr Pro Leu Ile Ile Phe Cys Lys Glu Ile Ala Pro Asp Pro
      245     250     255
Leu Ala Thr Cys Ile Ala Asn Arg Ile Ala Gly Leu Leu Asp Val Leu

```

[illegible]



## (2) INFORMATIONS POUR LA SEQ ID NO: 641:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 300 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 626954..627853

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 641:

Ile	Gly	Phe	Ser	Ile	Asn	His	Arg	Phe	Ser	Met	Pro	Asn	Lys	Pro	Ser	1	5	10	15
His	Ala	Phe	Arg	Leu	Ile	His	Cys	Ser	Asp	Ile	His	Phe	Cys	Val	Leu	20	25	30	
Pro	Lys	Asn	Pro	Phe	Gln	Cys	Phe	Asn	Lys	Arg	Phe	Lys	Gly	Leu	Leu	35	40	45	
Arg	Gln	Leu	Ile	Gly	Gly	Val	Ser	Phe	Gln	Ala	Phe	Ala	Ile	Ser	Gln	50	55	60	
Arg	Phe	Pro	Gln	Leu	Val	Lys	Gln	Leu	Glu	Ala	Asp	Ser	Val	Cys	Val	65	70	75	80
Thr	Gly	Asp	Met	Thr	Ile	Thr	Ala	Leu	Asp	Thr	Glu	Phe	Arg	Phe	Ala	85	90	95	
Lys	Glu	Phe	Leu	Ser	Arg	Val	Glu	Ser	Val	Ala	Pro	Val	Tyr	Ile	Val	100	105	110	
Pro	Gly	Asn	His	Asp	Val	Xaa	Thr	His	Arg	Ala	Leu	Lys	Lys	Gln	Thr	115	120	125	
Phe	Tyr	Ser	Tyr	Phe	Pro	Asn	Lys	Glu	Leu	Gln	Thr	His	Arg	Ile	Ala	130	135	140	
Phe	Lys	Lys	Leu	Thr	Pro	Thr	Trp	Trp	Leu	Val	Leu	Leu	Asp	Cys	Ser	145	150	155	160
Cys	Phe	Asn	Gly	Trp	Tyr	Thr	Ala	Asn	Gly	Glu	Val	Thr	Asp	Ser	Gln	165	170	175	
Leu	Leu	Ala	Leu	Glu	Gln	Phe	Leu	Ser	Ser	Leu	Pro	Ala	Ser	Glu	His	180	185	190	
Val	Ile	Val	Ala	Asn	His	Tyr	Pro	Leu	Ser	Pro	Thr	Thr	Arg	Pro	Ala	195	200	205	
His	Asp	Leu	Leu	Asn	Tyr	Ala	Pro	Leu	Lys	Ser	Leu	Leu	Met	Asn	Ser	210	215	220	
Pro	Ser	Val	Arg	Leu	Tyr	Leu	His	Gly	His	Asp	His	Tyr	Val	Glu	Leu	225	230	235	240
Asp	His	Leu	Pro	Pro	Leu	Val	Val	Asn	Ser	Gly	Ser	Leu	Thr	Leu	Pro	245	250	255	
Ser	Asn	Ala	Arg	Phe	His	Ile	Ile	Asp	Leu	His	Pro	Glu	Gly	Gly	Tyr	260	265	270	
Gln	Ile	Ala	Thr	Ala	Ala	Leu	Thr	Asn	Leu	Lys	Glu	Thr	Ser	Thr	Pro	275	280	285	
Leu	Thr	Ile	Ser	Ile	Glu	Glu	Asn	Thr	Ile	Ser	Leu					290	295	300	

## (2) INFORMATIONS POUR LA SEQ ID NO: 642:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 627822..628124

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 642:

```

Pro Phe Leu Ser Lys Lys Ile Pro Ser Leu Tyr Lys Ser Ser Ala Leu
1      5      10      15
Asn Leu Arg Ile Thr Asn Leu Glu Gly Leu Pro Met Lys Glu Lys Lys
20     25     30
Val Leu Glu Leu Ser Pro Glu Ala Thr Leu Leu Lys Lys Leu Arg Asp
35     40     45
Arg Ala Ile Ser Gln Gln Glu Thr Gln Lys Arg Lys Ala Trp Val Glu
50     55     60
Lys Leu Ala Ala Met Pro Glu Ser Thr Arg Asp Tyr Leu Glu Pro Gln
65     70     75     80
Ala His Leu Glu Pro Ser Gln Leu Phe Arg Lys Val Ala Glu Arg Leu
85     90     95
Leu Glu Glu Gly Ala
100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 643:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(628146..628715)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 643:

```

Met Val Arg Val Ser Thr Ser Glu Phe Arg Val Gly Leu Arg Val Glu
1      5      10      15
Ile Asp Gly Gln Pro Tyr Val Ile Leu Gln Asn Asp Phe Val Lys Pro
20     25     30
Gly Lys Gly Gln Ala Phe Asn Arg Ile Lys Val Lys Asn Phe Leu Thr
35     40     45
Gly Arg Val Ile Glu Lys Thr Phe Lys Ser Gly Glu Ser Ile Glu Thr
50     55     60
Ala Asp Val Arg Glu Gln Met Arg Leu Leu Tyr Thr Asp Gln Glu
65     70     75     80
Gly Ala Thr Phe Met Asp Asp Glu Thr Phe Glu Gln Glu Leu Ile Phe
85     90     95
Trp Asp Lys Leu Glu Asn Val Arg Gln Trp Leu Leu Glu Asp Thr Ile
100    105    110
Tyr Thr Leu Val Leu Tyr Asn Gly Asp Val Ile Ser Val Glu Pro Pro
115    120    125
Ile Phe Met Glu Leu Thr Ile Ala Glu Thr Ala Pro Gly Val Arg Gly
130    135    140
Asp Thr Ala Ser Gly Arg Val Leu Lys Pro Ala Thr Thr Asn Thr Gly
145    150    155    160

```

(2) INFORMATION POUR LA SEQ ID NO: 644:

(A) LONGUEUR: 290 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 628932..629801

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 644:

[illegible]

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 645:

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 646:

Lys Phe Leu Ala Ser Pro Arg Arg Lys Val Phe Arg Ser Ser Ala Val  
1 5 10 15

```

Lys Met Phe Phe Ala Ala Lys Gln Gln Glu Gly Lys Lys Leu Gln Glu
      20      25      30
Glu Trp Gln Glu Arg Phe Arg Val Trp Ser Lys Gln Ala Pro Glu Gln
      35      40      45
His Gln Glu Tyr Leu Arg Leu Ile Gln Glu Ile Ser Ile Gln Glu Leu
      50      55      60
Glu Glu Ile Leu Asn Leu Ile Asp Met Pro Glu Ser Ile Ala Gly Arg
      65      70      75      80
Ala Ala Ser Asn Lys Val Ile Gln Val Leu Ala Glu Asp Ile Pro Ser
      85      90      95
Leu Val Gly Gly Ser Ala Asp Leu Ser Ser Ser Asp Gly Thr Trp Ile
      100      105      110
Ala Lys Glu Gly Thr Ile Ser Ala Ser Asp Phe Leu Gly Arg Asn Ile
      115      120      125
Arg Tyr Gly Val Arg Glu Phe Gly Met Gly Thr Ile Met Asn Gly Leu
      130      135      140
Ala Tyr Ser Gln Val Phe Arg Pro Phe Gly Gly Thr Phe Leu Val Phe
      145      150      155      160
Ser Asp Tyr Leu Arg Ser Ala Ile Arg Leu Ala Ala Leu Ser Lys Leu
      165      170      175
Pro Val Ile Tyr Gln Phe Thr His Asp Ser Ile Phe Val Gly Glu Asp
      180      185      190
Gly Pro Thr His Gln Pro Ile Glu Gln Ile Met Ser Leu Arg Ala Ile
      195      200      205
Pro Gly Leu Arg Val Ile Arg Leu Arg Met Arg Met Lys
      210      215      220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 647:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 287 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(630915..631775)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 647:

```

Ile Asp Ile Leu Glu Lys Ile Ala Gly Thr Ile Lys Gln Leu Ser Ile
1      5      10      15
Glu Ser Ile Gln Lys Ala Ser Ser Gly His Pro Gly Met Pro Leu Gly
      20      25      30
Cys Ala Glu Leu Ala Ala Tyr Leu Tyr Gly Tyr Val Leu Arg Tyr Asn
      35      40      45
Ser Lys Asp Ser Arg Trp Val Asn Arg Asp Arg Phe Val Leu Ser Ala
      50      55      60
Gly His Gly Ser Ala Leu Tyr Ser Cys Leu His Leu Ala Gly Phe
      65      70      75      80
Asp Val Asn Leu Glu Asp Leu Gln Gln Phe Arg Gln Leu Gln Ser Arg
      85      90      95
Thr Pro Gly His Pro Glu Phe Arg Glu Thr Asp Gly Val Glu Ala Thr
      100      105      110
Thr Gly Pro Leu Gly Gln Gly Val Gly Asn Ala Val Gly Met Ala Leu
      115      120      125
Ser Leu Lys Met Leu Gly Ala Arg Phe Asn Gln Pro Ala Asn Ser Ile

```

130		135		140											
Phe	Asp	Ala	Lys	Val	Tyr	Cys	Leu	Ala	Gly	Asp	Gly	Cys	Phe	Met	Glu
145					150					155					160
Gly	Val	Ser	His	Glu	Ala	Cys	Ser	Phe	Ala	Gly	Ser	Leu	Gly	Leu	Asp
				165						170					175
Asn	Leu	Val	Leu	Ile	Tyr	Asp	Tyr	Asn	Glu	Ile	Ile	Leu	Asp	Gly	Thr
				180						185				190	
Leu	His	Asp	Val	Ser	Ile	Glu	Asp	Thr	Lys	Gln	Arg	Phe	Leu	Ala	Tyr
		195					200					205			
Gly	Trp	Asp	Val	Phe	Glu	Thr	Asp	Gly	His	Asp	Phe	Glu	Ser	Leu	His
	210						215					220			
Gln	Val	Phe	Thr	Gln	Ile	Lys	Lys	Ser	Gln	Cys	Lys	Pro	Thr	Leu	Ile
225					230					235					240
Ile	Ala	His	Thr	Ile	Ile	Gly	His	Gly	Ser	Pro	Lys	Glu	Gly	Thr	Asn
				245					250					255	
Lys	Ala	His	Gly	Ser	Pro	Leu	Gly	Glu	Asp	Gly	Val	Ala	Gln	Thr	Lys
			260					265					270		
Ser	Phe	Trp	His	Leu	Pro	Glu	Glu	Lys	Phe	Phe	Val	Leu	Arg	Gln	
		275					280						285		

(2) INFORMATIONS POUR LA SEQ ID NO: 648:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 637635..638084

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 648:

Met	Leu	Ser	Asn	Thr	Leu	Arg	Ser	Asn	Phe	Leu	Lys	Phe	Tyr	Ala	Asn
1				5					10					15	
Arg	Asn	His	Thr	Pro	Val	Ala	Ser	Ser	Pro	Val	Phe	Pro	His	Asn	Asp
			20					25					30		
Pro	Ser	Ile	Leu	Phe	Thr	Asn	Ala	Gly	Met	Asn	Gln	Phe	Lys	Asn	Ile
		35					40					45			
Phe	Leu	Gly	Lys	Glu	Gln	Thr	Ser	Tyr	Thr	Arg	Ala	Thr	Thr	Ser	Gln
	50					55				60					
Lys	Cys	Ile	Arg	Ala	Gly	Gly	Lys	His	Asn	Asp	Leu	Glu	Asn	Val	Gly
65				70					75					80	
His	Thr	Ser	Arg	His	Leu	Thr	Phe	Phe	Glu	Met	Leu	Gly	Asn	Phe	Ser
			85						90					95	
Phe	Gly	Asp	Tyr	Phe	Lys	Gln	Asp	Ala	Ile	Ser	Phe	Ala	Trp	Glu	Val
			100					105					110		
Ser	Leu	Ser	Val	Phe	Asn	Phe	Asp	Pro	Asp	Phe	Ile	Tyr	Ala	Thr	Val
		115					120					125			
His	Glu	Lys	Asp	Asp	Glu	Xaa	Ser	Leu	Phe	Gly	Lys	Asn	Ile	Phe	Arg
	130					135					140				
Gln	Thr	Glu	Phe	Phe	Val										
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 649:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 724 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 638036..640207

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 649:

Xaa	Phe	Ala	Leu	Trp	Glu	Lys	Tyr	Leu	Pro	Thr	Asp	Arg	Ile	Phe	Arg	1	5	10	15
Leu	Thr	Asp	Lys	Asp	Asn	Phe	Trp	Ser	Met	Ala	Asp	Thr	Gly	Pro	Cys	20	25	30	
Gly	Phe	Cys	Ser	Glu	Leu	Leu	Phe	Asp	Arg	Gly	Glu	Lys	Phe	Gly	Lys	35	40	45	
Ala	Ala	Ser	Pro	Leu	Glu	Asp	Val	Asp	Gly	Glu	Arg	Phe	Leu	Glu	Tyr	50	55	60	
Trp	Asn	Leu	Val	Phe	Met	Glu	Phe	Asn	Arg	Thr	Ser	Asp	Gly	Thr	Leu	65	70	75	80
Leu	Ala	Leu	Gln	Lys	Lys	Cys	Val	Asp	Thr	Gly	Ala	Gly	Leu	Glu	Arg	85	90	95	
Leu	Val	Ser	Leu	Leu	Ala	Glu	Thr	Lys	Thr	Val	Phe	Glu	Ala	Asp	Val	100	105	110	
Leu	Arg	His	Leu	Ile	Ser	Lys	Ile	Glu	Asn	Leu	Ser	Gly	Thr	Thr	Tyr	115	120	125	
Ser	Pro	Thr	Glu	Ala	Lys	Gly	Ala	Ala	Phe	Arg	Val	Ile	Ala	Asp	His	130	135	140	
Ile	Arg	Ser	Leu	Ser	Phe	Ala	Ile	Ala	Asp	Gly	Leu	Leu	Pro	Gly	Asn	145	150	155	160
Thr	Glu	Arg	Gly	Tyr	Val	Leu	Arg	Lys	Ile	Leu	Arg	Arg	Ala	Val	Asn	165	170	175	
Tyr	Gly	Lys	Arg	Leu	Gly	Phe	Asn	Arg	Pro	Phe	Leu	Ala	Asp	Val	Val	180	185	190	
Pro	Ser	Leu	Val	Asp	Val	Met	Gly	Glu	Ala	Tyr	Pro	Glu	Leu	Ser	Ala	195	200	205	
Ser	Val	Thr	Gln	Ile	Gln	Glu	Val	Leu	Thr	Thr	Glu	Glu	Glu	His	Phe	210	215	220	
Phe	Lys	Thr	Leu	Gln	Arg	Gly	Gly	Asn	Leu	Leu	Gln	Gln	Val	Val	Lys	225	230	235	240
Ser	Ser	Ala	Ser	Ser	Ala	Lys	Ile	Ser	Gly	Glu	Asp	Ala	Phe	Lys	Leu	245	250	255	
Lys	Asp	Thr	Tyr	Gly	Leu	Pro	Ile	Asp	Glu	Ile	Ala	Leu	Leu	Ala	Lys	260	265	270	
Asp	Tyr	Asn	Tyr	Ala	Ile	Asp	Met	Asp	Thr	Phe	Glu	Lys	Leu	Glu	Val	275	280	285	
Glu	Ala	Lys	Glu	Arg	Ser	Arg	Lys	Asn	Thr	Lys	Lys	Thr	Lys	Asn	Asp	290	295	300	
Ser	Asp	Ser	Val	Phe	Gln	Asp	Leu	Asp	Pro	Thr	Asn	Thr	Ser	Glu	Phe	305	310	315	320
Ile	Gly	Tyr	Asp	Thr	Leu	Ser	Cys	Asp	Thr	Phe	Ile	Glu	Gly	Ile	Ile	325	330	335	
Lys	Tyr	Asn	Glu	Ile	Ala	Ser	Ser	Leu	Glu	Glu	Gly	Asp	Glu	Gly	Ala	340	345	350	
Ile	Ile	Leu	Arg	Thr	Thr	Pro	Phe	Tyr	Ala	Glu	Lys	Gly	Gly	Gln	Ile	355	360	365	
Gly	Asp	Ser	Gly	Glu	Ile	Phe	Cys	Glu	Ser	Gly	Thr	Phe	Leu	Val	Ser				

370		375		380
His Thr Ile Ala Pro	Lys Ala Gly Leu Ile Val	His Leu Gly Lys Leu		
385	390	395		400
Ser Gln Gly Ser Leu Thr Thr Thr Met Ala Val Thr Ala Gln Val Asn				
	405	410		415
Gln Asn Leu Arg Lys Lys Thr Ala Asn Asn His Thr Gly Cys His Leu				
	420	425		430
Leu His Lys Ala Leu Glu Met Thr Leu Gly Glu His Ile Arg Gln Pro				
	435	440		445
Gly Ser Tyr Val Asp Ser Gln Lys Ile Arg Leu Asp Phe Thr His Asn				
	450	455		460
Lys Ala Leu Ser Pro Glu Asp Leu Leu Ala Ile Glu Thr Leu Val Asn				
465	470	475		480
Glu Lys Ile Arg Glu Asn Asp Pro Val Thr Ile Arg Glu Val Leu Tyr				
	485	490		495
Ser Asp Val Met Ser Ser Ser Glu Ile Lys Gln Phe Cys Gly Asp Lys				
	500	505		510
Tyr Gly Asp Ile Val Arg Val Val Leu Ala Gly Phe Ser His Glu Leu				
	515	520		525
Cys Gly Gly Thr His Ala Gln Ala Thr Gly Asp Ile Gly Tyr Phe Arg				
	530	535		540
Ile Thr Lys Glu His Ala Val Ala Thr Gly Ile Arg Arg Ile Glu Ala				
545	550	555		560
Thr Thr Gly Glu Asp Ala Glu Asn Ile Ala Arg Gly Gln Asp Val Asp				
	565	570		575
Leu Asn Glu Ile Ala Thr Val Ile Gln Ser Pro Lys Asp Gln Ile Leu				
	580	585		590
Val Lys Ile Arg Ser Val Met Glu Glu Lys Lys Asp Leu Ala Lys Gln				
	595	600		605
Val Ala Asp Leu Glu Asn Gln Leu Val Gln Gln Gln Val Lys Thr Leu				
	610	615		620
Leu Thr Ser Cys Glu Lys Ile Cys Asp Thr Ser Tyr Leu Val Tyr Tyr				
625	630	635		640
Leu Thr Glu Glu Glu Gly Gln Arg Ile Gln His Tyr Ala Asn Ala Ile				
	645	650		655
His Lys Glu Ile Pro Thr Asn Phe Ile Ser Leu Trp Ile Thr Glu Lys				
	660	665		670
Asn Gly Arg Tyr Ile Val Leu Ser Arg Val Ser Asp Asp Leu Thr Lys				
	675	680		685
Arg Gly Val Gln Ala His Thr Leu Leu Ala Glu Leu Leu Ala Pro Tyr				
	690	695		700
Gly Gly Arg Cys Gly Gly Lys Ala Ile Ser Ala Gln Gly Ser Ser Ala				
705	710	715		720
Glu Tyr Leu Lys				

(2) INFORMATIONS POUR LA SEQ ID NO: 650:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1084 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 640221..643472



## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 650:

Gln	Asn	Phe	Lys	Thr	Met	Asp	Phe	Asp	Pro	Thr	Ser	Ile	Asp	Phe	Ser	1	5	10	15
Ser	Phe	Pro	Leu	Leu	Lys	Asp	Thr	Lys	Leu	Pro	Ser	Leu	Val	Glu	Asn	20	25	30	
Leu	His	Ser	Gly	Ala	Arg	Ser	Phe	Val	Ile	Ala	Lys	Leu	Phe	Lys	Glu	35	40	45	
Leu	Lys	Arg	Ser	Ile	Val	Val	Ile	Thr	Thr	Pro	Ala	Lys	Leu	Asp	Asp	50	55	60	
Leu	Phe	Glu	Asp	Leu	Thr	Thr	Leu	Leu	Ala	Glu	Ser	Pro	Leu	Glu	Phe	65	70	75	80
Pro	Ala	Ser	Glu	Ile	Asp	Leu	Ser	Pro	Lys	Leu	Val	Asn	Val	Asp	Ala	85	90	95	
Val	Gly	Lys	Arg	Asp	His	Ile	Leu	Tyr	Ser	Leu	Gln	Lys	Gln	Ser	Ala	100	105	110	
Pro	Val	Ile	Cys	Val	Thr	Thr	Leu	Lys	Ala	Leu	Leu	Glu	Arg	Thr	Pro	115	120	125	
Ser	Pro	Glu	Ser	Met	Ile	Arg	Asp	His	Leu	Glu	Leu	Arg	Val	Gly	Glu	130	135	140	
Glu	Leu	Asp	Pro	Asp	Thr	Leu	Leu	Asp	Leu	Cys	Lys	Ser	Leu	Gly	Tyr	145	150	155	160
Arg	His	Glu	Ala	Leu	Ala	Arg	Glu	Lys	Gly	Asp	Phe	Ala	Phe	Arg	Gly	165	170	175	
Gly	Ile	Val	Asp	Ile	Phe	Pro	Leu	Ser	Ser	Pro	Glu	Pro	Phe	Arg	Ile	180	185	190	
Glu	Phe	Trp	Gly	Asp	Arg	Val	Ser	Ser	Ile	Arg	Ser	Tyr	Asn	Pro	Ser	195	200	205	
Asp	Gln	Leu	Ser	Thr	Gly	Lys	Leu	Ser	Gln	Ile	Thr	Ile	Ser	Pro	Ala	210	215	220	
Thr	Ala	Ile	Ile	Pro	Thr	Asp	Lys	Leu	Ser	Tyr	Ser	Leu	Leu	Asp	Tyr	225	230	235	240
Phe	Lys	Ala	Phe	Pro	Leu	Cys	Ile	Phe	Asp	Gly	Leu	Ser	Ser	Leu	Glu	245	250	255	
Asp	Asn	Phe	Ser	Asp	Ile	Ala	Gly	Ile	Leu	Ala	Ser	Leu	Pro	Lys	Arg	260	265	270	
Phe	Met	Pro	Ile	Gln	Asp	Leu	Cys	Gln	Arg	Ile	Leu	Lys	Glu	Phe	Thr	275	280	285	
Pro	Leu	Phe	Phe	Glu	Glu	Lys	Thr	Phe	Pro	Asn	Leu	Ile	Ser	His	Lys	290	295	300	
Asp	Thr	Gly	Phe	Ser	Ile	Glu	Ala	Phe	His	Lys	Lys	Ile	Ser	Val	Gln	305	310	315	320
Arg	Val	Ser	Leu	Pro	Phe	Ile	Tyr	Pro	Pro	Ala	Leu	Ile	Glu	Thr	Ser	325	330	335	
Gly	Glu	Gln	Asn	Pro	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Phe	Gln	Asp	Phe	340	345	350	
Cys	Ala	Gly	Arg	Thr	Leu	Ser	Leu	Ala	Leu	Tyr	Cys	Ser	Asn	Thr	Lys	355	360	365	
Ser	Leu	Lys	Glu	Ala	His	Asp	Leu	Ala	Ala	Ala	Cys	Ile	Pro	Asn	Thr	370	375	380	
Gln	Ile	Tyr	Asp	His	Pro	Thr	Thr	Leu	Ser	Ser	Ser	Phe	Ala	Leu	Val	385	390	395	400
Glu	Ala	Gly	Phe	Ala	Ala	Val	Ser	Leu	Ser	Glu	Phe	Ala	Ala	Ser	Lys	405	410	415	
Val	Leu	Arg	Arg	Gln	Lys	Gln	Arg	Asn	Tyr	Phe	Ser	Thr	Thr	Thr	Glu	420	425	430	
Glu	Val	Tyr	Ile	Pro	Val	Pro	Gly	Glu	Thr	Val	Val	His	Leu	His	Asn	435	440	445	
Gly	Ile	Gly	Lys	Phe	Ile	Gly	Ile	Glu	Lys	Lys	Pro	Asn	His	Leu	Asn				

450		455		460
Ile Glu Thr Asp Tyr	Leu Val Leu Glu Tyr	Ala Asp Lys Ala Arg Leu		
465	470	475		480
Tyr Val Pro Ser Asp	Gln Ala Tyr Leu Ile Ser Arg Tyr Val Gly Ala			
	485	490		495
Ser Glu Lys Ala Pro Asp	Leu His His Leu Asn Gly Ala Lys Trp Arg			
	500	505		510
Arg Ser Arg Glu Leu Ser Glu	Asn Ser Val Ile Leu Tyr Ala Glu Lys			
	515	520		525
Leu Ile Gln Met Glu Ala Gln	Arg Ser Thr Ala Asn Ser Phe Ile Tyr			
	530	535		540
Pro Pro His Gly Glu Glu Val	Ile Lys Phe Ala Glu Ser Phe Pro Tyr			
545	550	555		560
Glu Glu Thr Pro Asp Gln	Leu Lys Ala Ile Asp Gln Ile Tyr Ala Asp			
	565	570		575
Met Met Ser Asp Lys Leu Met	Asp Arg Leu Ile Cys Gly Asp Ala Gly			
	580	585		590
Phe Gly Lys Thr Glu Ile Ile	Met Arg Ala Ala Val Lys Ala Val Cys			
	595	600		605
Asp Gly His Lys Gln Val Ile	Val Met Val Pro Thr Thr Ile Leu Ala			
	610	615		620
Asn Gln His Phe Glu Thr Phe	Ser Gln Arg Met Ala Gly Leu Pro Ile			
625	630	635		640
Thr Ile Gly Leu Leu Ser Arg	Phe Ser Gln Gly Lys Thr Met Lys Lys			
	645	650		655
Thr Leu Glu Asp Ile Ala Gln	Gly Arg Ile Asp Ile Leu Ile Gly Thr			
	660	665		670
His Lys Val Ile Asn Lys Ala	Ile Glu Phe His Asn Pro Gly Leu Leu			
	675	680		685
Ile Ile Asp Glu Glu Gln Arg	Phe Gly Val Lys Ala Lys Asp Ser Leu			
	690	695		700
Lys Glu Arg Phe Pro Thr Ile	Asp Cys Leu Thr Val Ser Ala Thr Pro			
705	710	715		720
Ile Pro Arg Thr Leu Tyr Leu	Ser Leu Ser Gly Ala Arg Asp Leu Ser			
	725	730		735
Leu Ile Thr Met Pro Pro Leu	Asp Arg Leu Pro Val Ser Thr Phe Val			
	740	745		750
Met Glu His Ser Glu Glu Thr	Leu Ser Ala Ala Ile Arg His Glu Leu			
	755	760		765
Leu Arg Gly Gly Gln Val Tyr	Val Ile His Asn Arg Ile Glu Ser Ile			
	770	775		780
Phe Arg Leu Gly Glu Thr Ile	Arg Thr Leu Ile Pro Glu Ala Arg Ile			
785	790	795		800
Gly Val Ala His Gly Gln Met	His Ala Asp Glu Leu Ala Ser Ile Phe			
	805	810		815
Tyr Lys Phe Lys Thr Gln Gln	Thr Asn Val Leu Val Ala Thr Ala Leu			
	820	825		830
Ile Glu Asn Gly Ile Asp Ile	Pro Asn Ala Asn Thr Ile Leu Ile Asp			
	835	840		845
His Ala Asp Lys Phe Gly Met	Ala Asp Leu Tyr Gln Met Lys Gly Arg			
	850	855		860
Val Gly Arg Trp Asn Lys Lys	Ala Tyr Cys Tyr Xaa Leu Val Pro His			
865	870	875		880
Leu Asp Arg Leu Ser Gly Pro	Thr Ser Lys Arg Leu Glu Ala Leu Asn			
	885	890		895
Lys Gln Glu Tyr Gly Gly Gly	Met Lys Ile Ala Leu His Asp Leu Glu			
	900	905		910
Ile Arg Gly Ala Gly Asn Ile	Leu Gly Thr Asp Gln Ser Gly His Ile			
	915	920		925

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Ser Ala Val Gly Phe Asn Leu Tyr Cys Lys Leu Leu Lys Lys Ala Val
 930                      935                      940
Ala Ala Leu Lys His Lys Gln Lys Pro Met Leu Phe His Asp Asp Ile
945                      950                      955                      960
Lys Ile Glu Phe Pro Tyr His Ala Arg Ile Pro Glu Asp Tyr Ile Asp
                      965                      970                      975
Leu Ala Ser Met Arg Ile Glu Phe Tyr Gln Lys Ile Gly Asn Ala Glu
                      980                      985                      990
Ser Glu Glu Glu Leu Glu Ala Ile Glu Glu Glu Leu Arg Asp Arg Phe
 995                      1000                      1005
Gly Pro Ser Pro Glu Ala Ile Ser Trp Leu Phe Ala Leu Ala Arg Ile
1010                      1015                      1020
Arg Leu Ile Ala Gln Glu Tyr His Leu Ser Ser Ile Lys Gly Thr Gly
1025                      1030                      1035                      1040
Asn Ala Leu Tyr Ile Gln Gln Tyr His Asp Lys Asp Lys Gln Ile Gln
                      1045                      1050                      1055
Lys Thr Leu Pro Tyr Ser Leu Ser Pro Thr Pro Glu Leu Leu Val Lys
                      1060                      1065                      1070
Glu Val Gln Glu Ser Val Glu Lys Ala Phe Pro Lys
                      1075                      1080

```

(2) INFORMATIONS POUR LA SEQ ID NO: 651:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(640220..640627)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 651:

```

Ser Arg Ile Ile Asp Ser Gly Glu Gly Val Leu Ser Asn Lys Ala Phe
 1                      5                      10                      15
Ser Val Val Thr Gln Ile Thr Gly Ala Leu Cys Phe Cys Arg Glu Tyr
 20                      25                      30
Arg Ile Trp Ser Leu Phe Pro Thr Ala Ser Thr Phe Thr Ser Leu Gly
 35                      40                      45
Asp Lys Ser Ile Ser Glu Ala Gly Asn Ser Arg Gly Asp Ser Ala Asn
 50                      55                      60
Arg Val Val Lys Ser Ser Asn Lys Ser Ser Ser Phe Ala Gly Val Val
 65                      70                      75                      80
Ile Thr Thr Ile Glu Arg Leu Ser Ser Leu Asn Ser Phe Ala Met Thr
 85                      90                      95
Lys Asp Leu Ala Pro Glu Trp Arg Phe Ser Thr Lys Asp Gly Ser Phe
100                      105                      110
Val Ser Phe Asn Lys Gly Lys Leu Glu Lys Ser Met Leu Val Gly Ser
115                      120                      125
Lys Ser Ile Val Leu Lys Phe Cys
130                      135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 652:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 643485..644495

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 652:

Arg	Met	Pro	Met	Thr	Gly	Phe	Tyr	Glu	Thr	Ile	Ser	Pro	Arg	Asp	Gln
1				5					10					15	
Gln	Arg	Pro	Pro	Ile	Trp	Phe	Leu	Arg	Gln	Val	Gly	Arg	Tyr	Ile	Pro
			20					25					30		
Gln	Tyr	Gln	Glu	Leu	Lys	Arg	Asn	Arg	Ser	Leu	Lys	Asp	Phe	Phe	Leu
		35				40						45			
Asp	Thr	Glu	Ser	Ile	Val	Glu	Ala	Thr	Leu	Leu	Gly	Pro	Ser	Leu	Leu
	50					55					60				
Gly	Val	Asp	Ala	Ala	Ile	Val	Phe	Ala	Asp	Ile	Leu	Ser	Ile	Leu	Glu
65					70					75					80
Gly	Phe	Ser	Val	Asp	Tyr	Arg	Phe	Ala	Pro	Gly	Pro	Glu	Val	Ser	Tyr
			85						90					95	
Ser	Pro	His	Glu	Pro	Leu	Ile	Phe	Thr	Lys	Asp	Pro	Gln	Glu	Thr	Phe
			100					105					110		
Ser	Phe	Leu	Leu	Glu	Ala	Ile	Gln	Gln	Leu	Thr	Lys	Arg	Leu	Thr	Val
		115					120					125			
Pro	Leu	Ile	Ala	Phe	Ala	Ala	Ser	Pro	Phe	Thr	Leu	Ala	Ser	Tyr	Leu
	130					135					140				
Ile	Glu	Gly	Gly	Ala	Ser	Arg	Asp	Tyr	Pro	Lys	Thr	Ile	Ala	Phe	Leu
145					150					155					160
Tyr	Gln	Tyr	Pro	Asp	Arg	Phe	Lys	Ala	Leu	Leu	Asp	Glu	Ile	Thr	Leu
			165						170					175	
Gly	Thr	Ala	Thr	Tyr	Leu	Gln	Met	Gln	Val	Gln	Ala	Gly	Ala	Ala	Ala
			180					185					190		
Ile	Gln	Leu	Phe	Glu	Ser	Ser	Ser	Leu	Arg	Leu	Pro	Pro	His	Leu	Phe
		195					200					205			
Ala	Lys	Tyr	Val	Val	Ala	Pro	Asn	Thr	Lys	Leu	Ile	Arg	Gln	Ile	Lys
	210					215						220			
Gln	Thr	Gly	Asn	Pro	Pro	Ile	Ser	Leu	Phe	Cys	Arg	Cys	Phe	Tyr	Gln
225				230						235					240
Glu	Phe	Leu	Ser	Leu	Tyr	Ala	Ile	Gly	Ala	Asp	Thr	Leu	His	Pro	Asp
			245						250					255	
Tyr	His	Val	Glu	Leu	Pro	Glu	Val	Tyr	Arg	Gln	Ile	His	Ser	Pro	Gly
		260					265						270		
Ser	Ile	Gln	Gly	Asn	Phe	Asp	Pro	Ala	Leu	Leu	Leu	Leu	Pro	Gln	Asp
		275				280						285			
Ala	Leu	Ile	Ala	His	Leu	Glu	Ala	Tyr	Leu	Ala	Pro	Leu	Lys	Gln	Gln
	290					295					300				
Ser	His	Tyr	Ile	Phe	Asn	Leu	Gly	His	Gly	Ile	Leu	Pro	Gln	Thr	Pro
305					310					315					320
Ile	Glu	Asn	Val	Gln	Ala	Val	Val	Ser	Cys	Leu	Thr	Ser	Ile	Ser	Thr
			325						330					335	
Ser															

(2) INFORMATIONS POUR LA SEQ ID NO: 653:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 644471..645430

Met	Phe	Asn	Ile	Asn	Phe	Asn	Phe	Leu	Lys	Gly	Leu	His	Gln	Pro	Ala
1				5					10					15	
Pro	Arg	Tyr	Thr	Ser	Tyr	Pro	Thr	Ile	Val	Asp	Trp	Glu	Ser	Ser	Ser
			20					25					30		
Asp	Tyr	Gly	Tyr	Thr	Ala	Leu	Glu	Arg	Leu	Ala	Gln	Glu	Gln	Asp	Pro
		35				40						45			
Leu	Ser	Leu	Tyr	Phe	His	Ile	Pro	Phe	Cys	Gln	Ser	Met	Cys	Leu	Tyr
	50					55					60				
Cys	Gly	Cys	Thr	Val	Val	Leu	Asn	Arg	Lys	Ala	Glu	Ile	Val	Asp	His
65				70						75					80
Tyr	Ile	Glu	Thr	Leu	Ile	Gln	Glu	Met	Arg	Leu	Ala	Phe	Ser	Leu	Leu
				85					90					95	
Gly	Gly	Lys	Lys	Pro	Val	Ser	Arg	Ile	His	Phe	Gly	Gly	Gly	Thr	Pro
			100					105					110		
Ser	Arg	Leu	Ser	Arg	Ala	Gln	Phe	Glu	Arg	Leu	Phe	Thr	His	Ile	His
		115					120					125			
Arg	Phe	Phe	Asp	Leu	Ser	Asn	Ile	Glu	Glu	Leu	Ala	Ile	Glu	Phe	Asp
	130					135					140				
Pro	Arg	Ser	Leu	Arg	Glu	Asp	Ala	Asp	Lys	Pro	Phe	Leu	His	Asn	
145				150						155				160	
Leu	Gly	Phe	Asn	Arg	Val	Ser	Leu	Gly	Ile	Gln	Asp	Thr	Gln	Trp	Glu
			165						170					175	
Val	Gln	Glu	Ala	Val	Arg	Arg	Arg	Gln	Ser	Tyr	Glu	Glu	Ser	Leu	Leu
			180					185					190		
Ala	Tyr	Gln	Leu	Phe	Arg	Asp	Leu	Lys	Phe	Thr	Gly	Ile	Asn	Ile	Asp
		195					200					205			
Leu	Ile	Tyr	Gly	Leu	Pro	Lys	Gln	Thr	Gln	Ser	Ser	Phe	Lys	Gln	Thr
	210					215					220				
Ile	Glu	His	Ile	Leu	Asp	Met	Arg	Pro	Asp	Arg	Leu	Ala	Leu	Phe	Ser
225				230						235					240
Phe	Ala	His	Val	Pro	Trp	Ala	Lys	Pro	His	Gln	Lys	Ala	Leu	Arg	Thr
			245						250					255	
Lys	Asp	Leu	Pro	Ser	Met	Glu	Glu	Lys	Phe	Ala	Ile	Tyr	Ser	Gln	Ser
			260					265					270		
Arg	His	Thr	Leu	Ile	Gln	Glu	Gly	Tyr	Gln	Ala	Ile	Gly	Leu	Asp	His
		275					280					285			
Phe	Ser	Leu	Pro	Asp	Asp	Pro	Leu	Thr	Ile	Ala	Leu	Lys	Asn	Lys	Thr
	290					295					300				
Leu	Ile	Arg	Asn	Phe	Gln	Gly	Thr	Leu	Phe	Leu	Lys	Lys	Ile	Phe	
305				310						315				320	

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 645394..645840

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 654:

Phe	Pro	Arg	Tyr	Ser	Leu	Pro	Pro	Glu	Glu	Asp	Leu	Leu	Gly	Phe	Gly
1				5				10					15		
Ile	Ser	Ala	Thr	Ser	Phe	Ile	Arg	Gly	Ile	Tyr	Leu	Gln	Asn	Val	Lys
			20					25				30			
Asp	Leu	Arg	Glu	Tyr	Ser	Glu	Thr	Ile	Gln	Ala	Ser	Lys	Leu	Ala	Thr
		35					40					45			
Val	Lys	Gly	Lys	Ile	Leu	Ser	Gln	Asp	Asp	Lys	Ile	Arg	Lys	Trp	Val
	50					55					60				
Ile	His	Thr	Leu	Met	Cys	Ser	Phe	Ser	Leu	Ser	Lys	Leu	Glu	Phe	Glu
65					70					75					80
Gln	Arg	Phe	His	Glu	Arg	Phe	Asp	Arg	Tyr	Phe	Ala	Asp	Ser	Tyr	Asp
				85					90					95	
Arg	Leu	Cys	Gly	Met	Glu	Ser	Ala	Gly	Leu	Ile	Arg	Gln	Asp	Ser	Ser
			100					105					110		
Ser	Leu	Gln	Val	Thr	Pro	Leu	Gly	Glu	Leu	Phe	Val	Arg	Val	Ile	Ala
		115					120					125			
Thr	Ala	Phe	Asp	His	Tyr	Phe	Leu	Lys	Asn	Ile	Val	Glu	Lys	Pro	Leu
	130						135					140			
Phe	Ser	Lys	Ser	Ile											
145															

(2) INFORMATIONS POUR LA SEQ ID NO: 655:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 424 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 645840..647111

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 655:

Met	Lys	His	Ala	Leu	Ile	Val	Gly	Ser	Gly	Ile	Ala	Gly	Leu	Ser	Ala
1				5					10					15	
Ala	Trp	Trp	Leu	His	Lys	Arg	Phe	Pro	His	Val	Gln	Leu	Ser	Ile	Leu
			20					25					30		
Glu	Lys	Glu	Ser	Arg	Ser	Gly	Gly	Leu	Ile	Val	Thr	Glu	Lys	Gln	Gln
		35					40					45			
Gly	Phe	Ser	Leu	Asn	Met	Gly	Pro	Lys	Gly	Phe	Val	Leu	Ala	His	Asp
	50					55					60				
Gly	Gln	His	Thr	Leu	His	Leu	Ile	Gln	Ser	Leu	Gly	Leu	Ala	Asp	Glu
65					70					75					80
Leu	Leu	Tyr	Ser	Ser	Pro	Glu	Ala	Lys	Asn	Arg	Phe	Ile	His	Tyr	Asn
			85						90					95	
Asn	Lys	Thr	Arg	Lys	Val	Ser	Pro	Trp	Thr	Ile	Phe	Lys	Gln	Asn	Leu
			100					105					110		

Pro Leu Ser Phe Ala Lys Asp Phe Phe Ala Arg Pro Tyr Lys Gln Asp  
 115 120 125  
 Ser Ser Val Glu Ala Phe Phe Lys Arg His Ser Ser Lys Leu Arg  
 130 135 140  
 Arg Asn Leu Leu Asn Pro Ile Ser Ile Ala Ile Arg Ala Gly His Ser  
 145 150 155 160  
 His Ile Leu Ser Ala Gln Met Ala Tyr Pro Glu Leu Thr Arg Arg Glu  
 165 170 175  
 Ala Gln Thr Gly Ser Leu Leu Arg Ser Tyr Leu Lys Asp Phe Pro Lys  
 180 185 190  
 Glu Lys Arg Thr Gly Pro Tyr Leu Ala Thr Leu Arg Ser Gly Met Gly  
 195 200 205  
 Met Leu Thr Gln Ala Leu His Asp Lys Leu Pro Ala Thr Trp Tyr Phe  
 210 215 220  
 Ser Ala Pro Val Ser Lys Ile Arg Gln Leu Ala Asn Gly Lys Ile Ser  
 225 230 235 240  
 Leu Ser Ser Pro Gln Gly Glu Ile Thr Gly Asp Met Leu Ile Tyr Ala  
 245 250 255  
 Gly Ser Val His Asp Leu Pro Ser Cys Leu Glu Glu Ile Pro Glu Thr  
 260 265 270  
 Lys Leu Ile Lys Gln Thr Thr Ser Ser Trp Asp Leu Ser Cys Val Ser  
 275 280 285  
 Leu Gly Trp His Ala Ser Leu Pro Ile Pro His Gly Tyr Gly Met Leu  
 290 295 300  
 Phe Ala Asp Thr Pro Pro Leu Leu Gly Ile Val Phe Asn Thr Glu Val  
 305 310 315 320  
 Phe Pro Gln Pro Glu Arg Pro Asn Thr Ile Val Ser Leu Leu Leu Glu  
 325 330 335  
 Gly Arg Trp His Gln Glu Glu Ala Tyr Ala Phe Ser Leu Ala Ala Ile  
 340 345 350  
 Ser Glu Tyr Leu Gln Ile Tyr Thr Pro Pro Gln Ala Phe Ser Leu Phe  
 355 360 365  
 Ser Pro Arg Glu Gly Leu Pro Gln His His Val Gly Phe Ile Gln Ser  
 370 375 380  
 Arg Gln Arg Leu Leu Ser Lys Leu Pro His Asn Ile Lys Ile Val Gly  
 385 390 395 400  
 Gln Asn Phe Ala Gly Pro Gly Leu Asn Arg Ala Thr Ala Ser Ala Tyr  
 405 410 415  
 Lys Ala Ile Ala Ser Leu Leu Pro  
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 656:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 856 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(647109..649676)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 656:

Lys Ile Leu His Arg Ser Phe Gln Asn Gly Leu Leu Arg Cys Pro His  
 1 5 10 15  
 Asp Glu Lys Ser Leu Gln Ser Ser Leu Lys Arg Asn Lys Gln Val Phe

			20					25					30			
Phe	His	Met	Asn	Ile	Tyr	Arg	Phe	Ile	Ser	Gly	Ser	Cys	Ser	Trp	Phe	
		35					40					45				
Leu	Ile	Gly	Trp	Gly	Ile	Cys	Phe	Gly	Ala	Asp	Val	Pro	Leu	Ser	Phe	
	50					55					60					
Gly	His	Gln	Cys	Ala	Asp	Val	Arg	Lys	Ala	Met	Gln	Glu	Gly	Lys	Pro	
65					70					75					80	
Leu	Leu	Pro	Ile	Phe	Asp	Ala	Phe	Ile	Arg	Arg	Ile	Val	Asn	Asp	Ser	
				85					90					95		
Ser	Ser	Leu	Ser	Glu	Lys	Asp	Trp	Glu	Thr	Ala	Thr	Trp	Leu	Ile	Cys	
			100					105					110			
Glu	Tyr	Ile	Arg	Gly	Ser	Leu	Lys	Arg	Gly	Glu	Gln	Glu	Leu	Cys	Ser	
	115						120					125				
Glu	Leu	Val	Lys	Pro	Leu	Phe	Ser	Leu	Ala	Val	Met	Pro	Pro	Gln	Ser	
	130					135					140					
Lys	Ala	Arg	Ile	Lys	Gln	Val	Trp	Gln	Val	Leu	Asn	Pro	Gln	Gly	Ala	
145					150					155					160	
Ser	Leu	Lys	Asp	Leu	Val	Arg	Leu	Leu	Glu	Ser	Ser	Gly	Cys	Ser	Ser	
			165						170					175		
Ser	Pro	Gln	Asp	His	Leu	Leu	Leu	Ser	Leu	Tyr	Asn	Met	Thr	Leu	His	
			180					185					190			
Ser	Ser	Tyr	Glu	Asn	Lys	Lys	Ala	Glu	Ile	Leu	Phe	Ala	Arg	Glu	Gln	
		195					200					205				
Lys	Asn	Tyr	Gln	Asp	Ala	Leu	Arg	Leu	Cys	Glu	Glu	Leu	Gln	Glu	Asn	
	210					215					220					
Leu	Thr	Ser	Gly	Leu	Cys	Ser	Pro	Leu	Ser	Thr	Val	Tyr	Glu	Val	Glu	
225					230					235					240	
Gln	Ala	Phe	Leu	Lys	Arg	Ile	Ser	Leu	Ala	Ile	Arg	Trp	Glu	Gln	Glu	
			245						250					255		
Lys	Glu	Leu	Gln	Gly	Ser	Pro	Ser	Ile	Glu	Leu	Leu	Leu	Ala	Tyr	Cys	
			260					265					270			
Ser	Ala	Glu	Glu	Ser	Tyr	Ala	Glu	Ala	Val	Glu	Gln	Leu	Ile	Lys	Lys	
		275					280					285				
Ile	Glu	Leu	Gly	Ser	Leu	Asp	Arg	Ser	Gln	Glu	Val	Asp	Ala	Ile	Leu	
	290					295					300					
Phe	Ala	His	Ala	Leu	Ser	Lys	Leu	Pro	Trp	Glu	Glu	Thr	Leu	Gly	Glu	
305					310					315					320	
His	Glu	Leu	Glu	Val	Leu	Ile	Ser	Gly	Gly	His	Tyr	Leu	Thr	Ser	Ile	
			325						330					335		
Tyr	Ser	Gln	His	Ala	Tyr	Phe	Ser	Leu	Leu	Glu	Gln	Tyr	Phe	Lys	Lys	
			340					345					350			
Ser	Gln	Ile	Glu	Glu	Ile	Ser	Arg	Leu	Leu	Asp	Phe	Gly	Lys	Thr	Val	
		355					360			</						



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Lys Glu Gly Ser Ser Phe Phe Lys Val Leu Gly Ser Ser Arg Xaa Leu
      500      505      510
Ser Glu Glu Glu Phe Tyr Gly Xaa Leu Leu Lys Glu Met Ile Ser Arg
      515      520      525
Xaa His Arg Glu Lys Leu Ser Cys Ser Pro Ile Gln Arg Leu Val Tyr
      530      535      540
Asp Gln Leu Asp Arg Glu Ile Gln Leu Arg Leu Thr Glu Thr Leu Ile
      545      550      555      560
Gln Thr Glu Asp Leu Leu Val Arg Arg Lys Leu Ser Leu Trp Arg Ala
      565      570      575
Leu Tyr Glu Gly Ser Phe Val Ser Trp Gly Ser Ala His Gln Asn Gln
      580      585      590
Thr Leu Phe Glu Lys Ser Ile Leu Gln Cys Phe Ser Ala Leu Ser Gln
      595      600      605
Gln Asp Pro Ser Ala Ile Gln Gln Ile Ala Glu Ala Phe Ser Ser Gly
      610      615      620
Ala Ser Leu Trp Gln Ser Ser Leu Arg Met Val Trp Ala Val Ser His
      625      630      635      640
Thr Ser Glu Asn Pro Ile Ser Lys Ala Tyr Ser Leu Gly Ile Ser Asp
      645      650      655
Arg Pro Trp Gly Asp Arg Leu Tyr Leu Leu Gln Tyr Ser Leu Glu Gln
      660      665      670
Tyr Leu Ser Gly Asp Thr Glu Leu Leu Glu Tyr Leu Thr Gln Phe Pro
      675      680      685
Glu Leu Phe Pro Asn Ser Pro Leu Leu Pro Leu Val Tyr Tyr Leu Gln
      690      695      700
Ala Arg Gly Glu Gly Asp Pro Ile Arg Lys Ile Ala Trp Leu Thr Lys
      705      710      715      720
Ala Leu Glu Thr Phe Thr Glu Asn Ser Leu Leu Ala Lys Glu Met Lys
      725      730      735
Ala Trp Ala Pro Leu Tyr Tyr Leu Met Arg Met Asp Leu Ala Glu Thr
      740      745      750
Tyr Leu Tyr Leu Gly Asn Val Ser Lys Ser Asp Thr Leu Phe Glu Ala
      755      760      765
Ile Gln Glu Glu Trp Asp Ala Pro His His Pro Tyr Val Lys Leu Ile
      770      775      780
Asp Pro Pro His Ile Arg Val Ser Leu Glu Met Arg Trp Val Ser Gly
      785      790      795      800
Leu Ala His Val Tyr Glu Ala Ile Gln Ala Thr Glu Gln Arg Asn Ala
      805      810      815
Leu Leu Ile Ser His Ile Glu Lys Arg Phe Phe Gln Thr Arg Pro Arg
      820      825      830
Gln Glu Tyr Ile Gly Lys Met Leu Thr Phe Thr Ser Ser Leu Cys Arg
      835      840      845
Glu Leu Leu Ala Asp Ala Ser Trp
      850      855

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(2) INFORMATIONS POUR LA SEQ ID NO: 657:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 649970..650344

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 657:

Met	Ala	Leu	Lys	Asp	Thr	Ala	Lys	Lys	Met	Thr	Asp	Leu	Leu	Glu	Ser
1			5					10						15	
Ile	Gln	Gln	Asn	Leu	Leu	Lys	Ala	Glu	Lys	Gly	Asn	Lys	Ala	Ala	Ala
			20					25					30		
Gln	Arg	Val	Arg	Thr	Glu	Ser	Ile	Lys	Leu	Glu	Lys	Thr	Ala	Lys	Val
		35					40					45			
Tyr	Arg	Lys	Glu	Ser	Ile	Lys	Ala	Glu	Lys	Met	Gly	Leu	Met	Lys	Lys
	50					55					60				
Ser	Lys	Ala	Ala	Ala	Lys	Lys	Ala	Lys	Ala	Ala	Lys	Lys	Pro	Val	
65					70				75					80	
Arg	Ala	Thr	Lys	Thr	Val	Ala	Lys	Lys	Ala	Cys	Thr	Lys	Arg	Thr	Cys
				85				90						95	
Ala	Thr	Lys	Ala	Lys	Val	Lys	Pro	Thr	Lys	Lys	Ala	Ala	Pro	Lys	Thr
			100					105					110		
Lys	Val	Lys	Thr	Ala	Lys	Lys	Thr	Arg	Ser	Thr	Lys	Lys			
		115					120					125			

(2) INFORMATIONS POUR LA SEQ ID NO: 658:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 435 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 650418..651722

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 658:

Ser	Leu	Leu	Phe	Phe	Leu	Leu	Ser	Phe	Pro	Phe	Ser	Gln	Arg	Gln	Val
1				5					10					15	
Leu	Ala	Asn	Lys	Ser	Thr	Thr	Ser	His	Leu	Leu	Trp	Arg	Lys	Asn	Leu
			20					25					30		
Ser	Leu	Ser	Leu	Gly	Phe	Lys	Leu	Ser	Cys	Tyr	Arg	Asn	Cys	Lys	
		35					40				45				
His	Phe	Gly	Val	Cys	Gly	Gly	Cys	Ser	Ser	Pro	Gln	Met	Glu	Tyr	Ala
	50					55					60				
Ser	Ser	Leu	Lys	Thr	Lys	Glu	Leu	Ala	Leu	His	Asn	Leu	Phe	Ala	Pro
65					70				75					80	
Leu	Ile	Pro	Ser	Gln	Asn	Ile	Leu	Pro	Val	Ile	Pro	Cys	Ser	Pro	Leu
				85				90						95	
Leu	Arg	Gly	Arg	Asn	Lys	Met	Glu	Phe	Ser	Phe	Tyr	Gln	Thr	Val	Asp
			100					105					110		
Gly	Glu	Lys	Thr	Leu	Gly	Phe	Ile	Ser	Pro	Ser	Lys	Pro	Lys	Lys	Gly
		115					120					125			
Ile	Pro	Ile	Thr	Glu	Cys	Leu	Met	Ile	Asp	Glu	Arg	Ala	Met	Asp	Ile
	130					135					140				
Leu	Asn	Ile	Thr	Arg	Ser	Trp	Trp	Thr	Ala	His	Pro	Asp	Leu	Ser	Ala
145					150				155					160	
Tyr	Tyr	Pro	Pro	Leu	Asn	Lys	Gly	Ser	Leu	Cys	Thr	Ile	Thr	Val	Arg
				165				170						175	
Val	Gly	Asn	Ile	Ser	Asn	Asp	Phe	Met	Ile	Ile	Leu	Thr	Thr	Ser	Gly
			180					185					190		

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Arg Glu Glu Phe Ala Val Pro Leu Asn Ile Ile Gln Glu Trp Gln Gln
    195                200                205
Ser Leu Leu Asp Ser Gly Leu Pro Ile Thr Ser Ile Phe Trp Glu Glu
    210                215                220
Lys Leu Ser Ala Arg Asn Ser Pro Thr Thr Phe Arg Thr Thr His Leu
    225                230                235                240
Tyr Gly Ala Pro Phe Leu Lys Gln Gln Leu Ser Ile Asp Gly Arg Ser
    245                250                255
Ser Leu Phe His Ile Arg Pro Arg Ser Phe Phe Gln Pro Gln Ser Leu
    260                265                270
Gln Ala Glu Lys Ile Ile Gln Thr Ile Lys Glu Phe Ile Asp Pro Cys
    275                280                285
Gly Glu Glu Thr Leu Leu Asp Leu Tyr Cys Gly Ala Gly Thr Ile Gly
    290                295                300
Ile Leu Leu Ala Pro Tyr Val Lys Lys Ile Ile Gly Val Glu Leu Val
    305                310                315                320
Pro Asp Ala Val Ala Ser Ala Gln Glu Asn Ile Gln Leu Asn Ser Val
    325                330                335
Asp Met Glu Val Phe Leu Glu Asp Ala Lys Gln Phe Cys Lys Arg Asn
    340                345                350
Glu Asn Leu Pro Ser Pro Asp Ile Val Val Ile Asp Pro Pro Arg Cys
    355                360                365
Gly Met Gln Asn Lys Ala Leu Lys Tyr Leu Leu Arg Met Ala Pro Lys
    370                375                380
Lys Ile Val Tyr Val Ser Cys Asn Pro Leu Thr Gln Ile Gln Glu Cys
    385                390                395                400
Ser Val Leu Val Glu Gln Gly Tyr Gln Leu Arg His Met Gln Pro Ile
    405                410                415
Asp Gln Phe Pro His Thr Asn His Leu Glu Asn Ile Val Leu Leu Glu
    420                425                430
Arg Leu Ser
    435

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(2) INFORMATIONS POUR LA SEQ ID NO: 659:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 162 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 651686..652171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 659:

```

Ser Phe Gly Lys Tyr Cys Ala Leu Arg Lys Ala Phe Leu Lys Gln Glu
1      5      10      15
Ser Leu Ile Pro Asn Ala Val Pro Ser Gly Lys Gly Leu Ile Pro Leu
    20      25      30
Ser Ser Cys Val Asn Leu Ser Phe Leu Thr Leu Ile Lys Gly Thr Ser
    35      40      45
Met Tyr Ser Arg Leu Phe Phe Ser Ile Leu Xaa Phe Leu Gly Cys Cys
    50      55      60
Pro Ala Leu Phe Ala Asp Thr Asp Ser Pro Gln Arg Ala Thr Phe Gly
    65      70      75      80
Gln Pro Ala Val Met Leu Gly Ile Ala Ile Val Phe Phe Tyr Phe Ile

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				85					90					95					
Leu	Trp	Arg	Pro	Glu	Gln	Xaa	Arg	Arg	Gln	Ala	Met	Glu	Lys	Arg	Lys				
			100						105					110					
Ser	Glu	Leu	Ala	Val	Gly	Asp	Lys	Val	Thr	Ala	Met	Gly	Ile	Val	Gly				
		115					120					125							
Thr	Ile	Ala	Glu	Ile	Arg	Glu	Xaa	Thr	Val	Ile	Leu	Asn	Ile	Ala	Ser				
	130					135				140									
Gly	Lys	Ile	Glu	Ile	Leu	Lys	Thr	Ala	Ile	Ser	Glu	Ile	Leu	Lys	Ala				
145					150					155					160				
Glu	Lys																		

(2) INFORMATIONS POUR LA SEQ ID NO: 660:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 131 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 652516..652908

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 660:

Ile	Ser	Gly	Ile	Ala	Ile	Pro	Ser	Pro	Cys	Gly	Gly	Lys	Ala	Ala	Cys				
1			5					10				15							
Lys	Gln	Cys	Lys	Val	Arg	Ile	Thr	Lys	Asn	Ala	Asp	Glu	Pro	Leu	Glu				
		20					25					30							
Thr	Asp	Arg	Ser	Thr	Phe	Ser	Lys	Gln	Gln	Leu	Glu	Gln	Gly	Trp	Arg				
		35				40					45								
Leu	Ser	Cys	Gln	Thr	Lys	Val	Gln	His	Asp	Leu	Cys	Leu	Glu	Val	Glu				
	50				55				60										
Asp	Arg	Tyr	Phe	Asn	Ala	Ser	Ser	Trp	Glu	Gly	Thr	Val	Val	Ser	Asn				
65				70				75						80					
Glu	Asn	Val	Ala	Thr	Phe	Ile	Lys	Glu	Leu	Val	Leu	Ser	Val	Asp	Pro				
			85				90					95							
Ser	Arg	Pro	Ile	Pro	Phe	Lys	Pro	Gly	Gly	Tyr	Leu	Gln	Ile	Thr	Val				
		100					105					110							
Pro	Pro	Tyr	Lys	Thr	Asn	Thr	Phe	Gly	Leu	Glu	Ala	Asp	Tyr	Gly	Ser				
		115				120						125							
Pro	Ile	Leu																	
130																			

(2) INFORMATIONS POUR LA SEQ ID NO: 661:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 265 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 652799..653593

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 661:

```

Ile Leu Arg Ala Leu Phe Leu Leu Asn Leu Glu Ala Ile Tyr Lys Leu
1           5           10           15
Pro Phe Leu Leu Ile Lys Pro Ile Leu Ser Asp Trp Lys Gln Thr Met
          20           25           30
Asp Pro Gln Tyr Tyr Ser Asp Trp Glu Thr Phe His Leu Phe Asp Gln
          35           40           45
Val Ile Asp Asn Leu Ser Leu Asp Thr Asp Ser Ala Asn Lys Ala Tyr
          50           55           60
Ser Leu Ala Ser Tyr Pro Ala Glu Leu Pro Leu Ile Lys Phe Asn Val
65          70          75          80
Arg Ile Ala Thr Pro Ser Phe Val Asp Gln Ala Pro Asp Pro Thr Ile
          85          90          95
Pro Trp Gly Val Cys Ser Ser Tyr Ile Phe Ser Leu Lys Pro Gly Asp
          100         105         110
Lys Val Met Val Ser Gly Pro Tyr Gly Glu Ser Phe Met Lys Glu Asn
          115         120         125
Asn Arg Pro Val Ile Phe Leu Ile Gly Gly Ala Gly Ser Ser Phe Gly
          130         135         140
Arg Ser His Ile Leu Asp Leu Leu Leu Asn Lys His Ser Asp Arg Glu
145         150         155         160
Leu Thr Leu Trp Tyr Gly Ala Arg Ser Leu Lys Glu Asn Ile Tyr Gln
          165         170         175
Glu Glu Tyr Glu Lys Leu Glu Lys Glu Phe Pro Asn Phe His Tyr His
          180         185         190
Leu Val Leu Ser Gln Pro Leu Gln Glu Asp Leu Asp Gln Gly Trp Asp
          195         200         205
Lys Asn Asp Pro Ile Lys Thr Asn Phe Leu Phe Lys Ala Phe Glu Leu
          210         215         220
Gly Gln Leu Ser His Leu Pro Asn Pro Glu Asp Tyr Leu Tyr Tyr Val
225         230         235         240
Cys Gly Pro Ala Leu His Asn Ser Ser Ile Leu Thr Val Leu Asp Asn
          245         250         255
Tyr Gly Val Ser Ala Leu Leu Leu Phe
          260         265

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 662:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 572 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: 660136..661851

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 662:

```

Met Lys Arg Thr Pro Ala Pro Leu Ala Phe Arg Lys Ala Ala Ala Phe
1           5           10           15
Gly Ala Ile Pro Val Cys Cys Ala Val Leu Leu Ser Met Ile Ser Pro
          20           25           30
Ala Gln Asn Leu Pro Gln Phe Leu Ala Thr Arg Val Pro Met Val Val
          35           40           45
Met Asp Leu Gln Pro Pro Lys Ala Tyr Leu Gly Gly Ile Pro Phe Tyr

```

50	55	60
Leu Leu Tyr Asp Gly	Asn Ser Phe Ser Leu Lys	Leu Leu Ile Gly Ala
65	70	75
Val Gly Thr Gly Leu	Ile Phe Leu Ala Ile Leu	Leu Cys Ala Ile Phe
	85	90
Tyr Leu Ile Pro Lys	Ser Phe Val Leu Lys	Lys Lys Ala Leu Leu Asp
	100	105
Asp Leu Leu Lys Phe	Leu Lys Asn Lys Phe Tyr	Ala Cys Trp Asn Ala
	115	120
Cys Lys Lys Leu Leu	Lys Asn Leu Val Asn Asn	Lys Lys Tyr Val Pro
	130	135
Glu Pro Ser Leu Arg	Val Pro Ser Ser Pro Ser	Val Ala Lys Lys Glu
145	150	155
Met Leu Lys Leu Pro	Thr Pro Val Ile Ser Leu	Pro Leu Glu Asn Lys
	165	170
Asp Leu His Asp Asp	Ser Ser Val Asn Arg Thr	Ile Phe Leu Thr Pro
	180	185
Pro His Pro Thr Lys	Arg Thr Leu Ser Pro Gln	Lys Arg Thr Asp Leu
	195	200
Pro Asn Leu Leu Pro	Lys Asp Ser Ala Ser Ala	Pro Ala Gln Thr Ser
	210	215
Tyr Lys Pro Leu Pro	Thr Pro Ser Pro Phe Val	Leu Ala Gly Asp Ala
225	230	235
Pro Asp Leu Pro Gln	Tyr His Leu Leu Ser Lys	Arg Asn Val Arg Arg
	245	250
Pro Glu Ser Leu Leu	Glu Glu Leu Lys Lys Lys	Ala Ala Ile Leu Gln
	260	265
Gln Thr Leu Ala Ser	Phe Gly Ile Glu Ala Ala	Ile Gly Asn Ile Cys
	275	280
Ser Gly Pro Thr Leu	Ala Ala Phe Glu Val Leu	Pro Asn Thr Gly Val
	290	295
Lys Val Gln Lys Ile	Lys Ala Leu Glu Asn Asp	Ile Ala Leu Asn Leu
305	310	315
Gln Ala Ser Ser Ile	Arg Ile Ile Ala Pro Ile	Pro Gly Lys Ala Ala
	325	330
Val Gly Ile Glu Ile	Pro Asn Pro Asp Pro Gln	Pro Val Asn Phe Arg
	340	345
Asp Leu Leu Glu Asp	Tyr Gln Lys Gly Thr Gln	Arg Leu Gln Val Pro
	355	360
Leu Leu Leu Gly Arg	Lys Ala Asn Gly Asp Asn	Phe Trp Thr Asp Leu
	370	375
Ala Thr Met Pro His	Leu Ile Ile Ala Gly Thr	Thr Thr Gly Ser Gly Lys
385	390	395
Ser Val Cys Ile Asn	Thr Ile Val Met Ser Leu	Ile Met Thr Ser Pro
	405	410
Pro Thr Asp Ile Lys	Leu Val Ile Val Asp Pro	Lys Lys Val Glu Leu
	420	425
Thr Gly Tyr Ser Gln	Leu Pro His Met Leu Thr	Pro Val Ile Thr Glu
	435	440
Ser Lys Glu Ala His	Ser Ala Leu Ile Trp Leu	Val Arg Glu Met Glu
	450	455
Leu Arg Tyr Glu Ile	Leu Arg Phe Leu Gly Leu	Arg Asn Ile Gln Ser
465	470	475
Phe Asn Ser Arg Thr	Arg Asn Val Asp Ile Glu	Ala Ser Tyr Asp Lys
	485	490
Glu Ile Pro Glu Lys	Met Pro Phe Ile Val Gly	Ile Ile Asp Glu Leu
	500	505
Ser Asp Leu Leu Ser	Ser Ser Ser His Asp Ile	Glu Thr Pro Ile Val
	515	520
		525

Arg Leu Ala Gln Met Ala Arg Ala Val Gly Ile His Leu Ile Leu Ala  
 530 535 540  
 Thr Gln Arg Pro Ser Arg Asp Val Ile Thr Gly Ile Ile Lys Ala Asn  
 545 550 555 560  
 Ser Leu Leu Glu Ser Pro Leu Lys Leu Pro Thr Lys  
 565 570

(2) INFORMATIONS POUR LA SEQ ID NO: 663:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 661740..662282

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 663:

Ser Cys Arg Asn Pro Pro Asn Leu Ser Asn Thr Thr Pro Phe Ser Arg  
 1 5 10 15  
 Cys Asp His Arg Asn Asn Gln Ser Lys Phe Pro Ser Arg Ile Ala Phe  
 20 25 30  
 Lys Val Ala Asn Lys Val Asn Ser Gln Ile Ile Ile Asp Glu Pro Gly  
 35 40 45  
 Ala Glu Asn Leu Met Gly Asn Gly Asp Met Leu Val Val Ser Pro Gly  
 50 55 60  
 Ser Phe Ala Pro Val Arg Val Gln Gly Ala Tyr Ile Cys Asp Asp Asp  
 65 70 75 80  
 Ile Asn Lys Val Ile Lys Asp Leu Cys Ser Arg Phe Pro Cys Lys Tyr  
 85 90 95  
 Val Ile Pro Ser Phe Asn Thr Tyr Asp Asp Pro Gly Ser Met Asp Pro  
 100 105 110  
 Glu Asp Leu Asp Pro Leu Phe Asn Gln Ala Lys Thr Leu Val Leu Gln  
 115 120 125  
 Thr Gly Asn Ala Ser Thr Thr Phe Leu Gln Arg Lys Leu Lys Ile Gly  
 130 135 140  
 Tyr Ala Arg Ala Ala Ser Ile Ile Asp Gln Leu Glu Glu Ala Arg Ile  
 145 150 155 160  
 Val Gly Pro Ser Glu Gly Ala Lys Pro Arg Gln Ile Leu Val Gln Leu  
 165 170 175  
 Ser Asn Gln Asp Asp  
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 664:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 263 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 662286..663074

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 664:

```

Ser Met Glu Gly Phe Cys Pro Ile Ala Ser Gly Ser Lys Gly Asn Cys
1      5      10      15
Ala Tyr Leu Gly Thr Arg Ser Cys Lys Leu Leu Ile Asp Leu Gly Ile
20      25      30
Ser Lys Gln Ala Val Thr Glu Ala Leu His Ser Met Gly Ile His Pro
35      40      45
Glu Asp Ile Gln Gly Ile Phe Val Thr His Glu His Ser Asp His Ile
50      55      60
Ala Gly Leu Arg Ser Phe Ile Lys Thr Tyr Arg Thr Pro Ile Ile Cys
65      70      75      80
Asn Ile Glu Thr Ala Arg Ser Leu Arg Gln Leu Leu Asp Leu Cys Pro
85      90      95
Thr Phe Lys Ile Phe Thr Thr Gly His Arg Phe Ser Leu Glu Asp Leu
100     105     110
Arg Val Gln Thr Phe Asn Val Pro His Asp Ala Val Asp Pro Val Gly
115     120     125
Phe Ile Phe Gln Tyr Ser Gly Met Lys Leu Gly Phe Cys Thr Asp Leu
130     135     140
Gly Trp Val Thr Ser Trp Ile Thr His Leu Leu Cys Asp Cys Asp Tyr
145     150     155     160
Leu Leu Ile Glu Ser Asn His Asp Pro Glu Met Val Leu Arg Ser Ser
165     170     175
Arg Pro Glu Ser Cys Lys Gln Arg Ile Leu Ser Lys Gln Gly His Ile
180     185     190
Ser Asn Ala Glu Cys Gly Ala Leu Leu Gln Arg Val Leu Thr Pro Arg
195     200     205
Ile Lys Lys Ile Tyr Leu Ala His Leu Ser Leu Glu Cys Asn Thr Ala
210     215     220
Glu Gln Ala Leu Asn Thr Val Thr Ser Ala Ile Gln Glu Ile Thr Asp
225     230     235     240
Val His Pro Val Ile Ala Gln Ser Ser Gly Ile Thr Asp Pro Ile Phe
245     250     255
Phe Ser Ala Pro Ser Leu Val
260

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 665:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé -

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 662951..663730

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 665:

```

Tyr Gly Arg Ala Ser Phe Glu Tyr Ser Asp Val Cys His Ser Arg Asp
1      5      10      15
His Arg Cys Ser Ser Arg Asn Cys Ser Lys Phe Trp His Tyr Arg Ser
20      25      30
Tyr Phe Leu Phe Cys Ser Glu Pro Cys Met Thr Thr Asn Ser Thr Gln
35      40      45

```



```

Asp Thr Leu Tyr Leu Ser Leu His Gly Gly Ile Asp Ser Ala Ile Pro
 50          55          60
Tyr Pro Val Arg Arg Val Glu Gln Leu Leu Gln Phe Ser Phe Leu Pro
 65          70          75          80
Glu Leu Gln Phe Gln Asn Ala Ala Val Lys Gln Arg Ile Gln Arg Leu
          85          90          95
Cys Tyr Arg Glu Glu Lys Arg Leu Ala Val Ser Ser Leu Ala Lys Trp
          100          105          110
Leu Gly Gln Leu His Lys Gln His Leu Arg Ala Pro Lys Asn Pro Pro
          115          120          125
Val Ala Ile Cys Trp Ile Asn Ser Tyr Val Gly Tyr Gly Val Phe Ala
          130          135          140
Arg Glu Ser Ile Pro Ala Trp Ser Tyr Ile Gly Glu Tyr Thr Gly Ile
          145          150          155          160
Leu Arg Arg Arg Gln Ala Leu Trp Leu Asp Glu Asn Asp Tyr Cys Phe
          165          170          175
Arg Tyr Pro Val Pro Arg Tyr Ser Phe Arg Tyr Phe Thr Ile Asp Ser
          180          185          190
Gly Met Gln Gly Asn Val Thr Arg Phe Ile Asn His Ser Asp Asn Pro
          195          200          205
Asn Leu Glu Ala Ile Gly Ala Phe Glu Asn Gly Ile Phe His Ile Ile
          210          215          220
Ile Arg Ala Ile Lys Asp Ile Leu Pro Gly Glu Glu Leu Cys Tyr His
          225          230          235          240
Tyr Gly Pro Leu Tyr Trp Lys His Arg Lys Lys Arg Glu Glu Phe Val
          245          250          255
Pro Gln Glu Glu
          260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 666:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 156 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(663745..664212)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 666:

```

Ile Gln Glu Thr Ser Ile Met Gln Leu Thr Ser Gln Ala Phe Ser Tyr
 1          5          10          15
Gly Arg Pro Ile Pro Lys Lys Tyr Ser Cys Gln Gly Val Gly Ile Ser
          20          25          30
Pro Pro Leu Ser Phe Ser Asp Val Pro Arg Glu Ala Lys Ser Leu Val
          35          40          45
Leu Ile Val Glu Asp Pro Asp Val Pro Pro Ser Val Arg Glu Asp Gly
          50          55          60
Leu Trp Ile His Trp Ile Val Tyr Asn Leu Ser Pro Val Val Ser Asn
          65          70          75          80
Leu Ala Glu Gly Ala Gln Ile Phe Ala Val Gln Gly Leu Asn Thr Ala
          85          90          95
Gly Glu Ile Gly Tyr Cys Pro Pro Cys Pro Pro Asp Ala Lys His Arg
          100          105          110
Tyr Tyr Phe Tyr Ala Tyr Ala Leu Asp Val Val Leu Ser Asp Glu Glu

```

	115		120		125
Gly	Val Thr Lys Glu Gln Leu Leu Glu Ala Met Asp Gly His Ile Ile				
	130		135		140
Ala	Thr Ala Glu Leu Met Gly Thr Tyr Glu Lys Asp				
145		150		155	

(2) INFORMATIONS POUR LA SEQ ID NO: 667:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 455 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(664255..665619)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 667:

Met	Leu	Gln	Phe	Leu	Lys	Gln	Ile	Asn	His	Phe	Leu	Thr	Ser	Phe	Cys
1				5					10					15	
Val	Phe	Pro	Leu	Ile	Leu	Cys	Leu	Gly	Gly	Ile	Leu	Thr	Trp	Lys	Leu
			20					25					30		
Arg	Gly	Leu	Gln	Phe	Thr	Ser	Leu	Gly	Met	Ser	Phe	Arg	Leu	Met	Leu
			35					40				45			
Asn	Asn	Gln	Gln	Glu	Gln	Ala	Gly	Ala	Glu	Gly	Glu	Gly	Val	Ser	Arg
	50					55					60				
Tyr	Glu	Ala	Val	Ala	Gly	Met	Leu	Ala	Gly	Asn	Phe	Gly	Thr	Gly	Asn
65					70					75				80	
Ile	Ala	Gly	Met	Ala	Ile	Ala	Val	Ala	Ser	Gly	Gly	Pro	Gly	Ala	Leu
				85					90					95	
Leu	Trp	Ile	Trp	Ile	Val	Thr	Leu	Phe	Ala	Ala	Ile	Val	Gln	Tyr	Ala
			100					105					110		
Gly	Ala	Phe	Leu	Gly	Cys	Lys	Tyr	Arg	Gln	Phe	Gln	Lys	Glu	Ser	Gln
		115					120					125			
Glu	Tyr	Ile	Gly	Gly	Pro	Ile	Ala	Cys	Leu	Gly	Tyr	Lys	Met	Gly	Ser
	130					135					140				
Arg	Phe	Xaa	Ala	Val	Ala	Xaa	Cys	Val	Ala	Ser	Leu	Ile	Thr	Ala	Phe
145					150					155					160
Ser	Ala	Gly	Ser	Leu	Val	Gln	Val	Asn	Ser	Ile	Ile	Ser	Leu	Cys	Ala
				165					170					175	
Asp	Gly	Val	Ser	Ala	Lys	Ile	Ala	Val	Gly	Ile	Leu	Leu	Ala	Leu	Ser
		180						185					190		
Val	Tyr	Pro	Ile	Leu	Ala	Gly	Gly	Asn	Thr	Arg	Val	Leu	Arg	Phe	Ser
		195					200						205		
Ala	Lys	Ala	Ile	Pro	Phe	Val	Ala	Gly	Phe	Tyr	Phe	Leu	Phe	Ser	Val
	210					215					220				
Ile	Val	Leu	Ala	Met	His	Cys	Asp	Lys	Ile	Leu	Pro	Ala	Leu	Gln	Leu
225					230					235					240
Val	Phe	Ser	Ser	Ala	Leu	Gly	Val	Lys	Ala	Gly	Ile	Ala	Gly	Val	Gly
			245						250					255	
Gly	Tyr	Thr	Leu	Gly	Gln	Val	Ile	Ser	Thr	Gly	Leu	Asn	Arg	Ala	Ile
		260						265					270		
Met	Ala	Thr	Asp	Gly	Gly	Ser	Gly	Met	Val	Ser	Ile	Leu	Gln	Ser	Asn
	275						280					285			
Ser	Lys	Ser	Thr	Asn	Pro	Val	Thr	Asp	Gly	Leu	Val	Thr	Leu	Leu	Pro
	290					295					300				

```

Pro Val Ile Val Ala Val Val Cys Ser Ile Thr Met Met Val Leu Leu
305                               310                     315           320
Val Thr Gly Ala Tyr Asp Ser Gly Glu Leu Gly Val Leu Met Val Met
                               325                     330           335
Asn Ala Phe Lys Ser Ser Leu Gly Met Leu Gly Gly Ser Val Val Leu
                               340                     345           350
Ile Ser Met Ile Leu Phe Gly Tyr Thr Thr Ala Leu Ser Trp Phe Ala
                               355                     360           365
Cys Ala Glu Lys Ser Leu Glu Tyr Met Ile Pro Gly Lys Arg Ala Asn
                               370                     375           380
Leu Leu Leu Lys Ala Ile Tyr Ile Ala Ile Ile Pro Met Gly Gly Val
385                               390                     395           400
Leu Gly Met Gln Phe Ile Trp Ala Leu Ser Asp Leu Gly Phe Cys Gly
                               405                     410           415
Met Val Ile Phe Asn Ser Ile Ser Leu Ile Ala Leu Phe Arg Glu Val
                               420                     425           430
Ile Ala Thr Arg Tyr Glu Val Ala Leu Leu Arg Lys Glu Ala Gln Ala
                               435                     440           445
Gln Ser Asp Pro Leu Arg Gln
                               450                     455

```

(2) INFORMATIONS POUR LA SEQ ID NO: 668:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(665727..666083)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 668:

```

Cys Leu Leu Leu Leu Ile Ser Leu Leu Leu Leu Trp Leu Trp Leu Arg
1                               5                     10           15
Gly Lys Leu Lys Ala His Tyr Arg Val Leu Glu Arg Ser Ile Leu Leu
                               20                     25           30
His Leu Leu Gln Ala Leu Ala Glu Asp Pro Ala Leu Ile Ala Gly Met
                               35                     40           45
Lys Lys Met Gln Gly Arg Asp Trp Val Trp Asn Ile Phe Ile Thr Glu
                               50                     55           60
Leu Ser Lys Val Phe Ser Gln Ala Ala Ser Leu Gly Leu Ser Ala Leu
65                               70                     75           80
Gln Thr Phe Ala Ala Phe Ala Ser Thr Leu Gly Leu Asp Ser Gly Thr
                               85                     90           95
Val Thr Ser Ile Val Asp Gly Glu Arg Trp Ala Glu Leu Ile Asp Val
                               100                    105          110
Val Ile Gln Asn Pro Ala Ile
                               115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 669:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(665782..666423)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 669:

```

Tyr Tyr Lys Phe Ile Phe Asn Phe Gly Arg Phe Met Lys Lys Phe Ile
1      5      10      15
Tyr Lys Tyr Ser Phe Gly Ala Leu Leu Leu Ser Gly Leu Ser Gly
      20      25      30
Leu Ser Ser Cys Cys Ala Asn Ser Tyr Gly Ser Thr Leu Ala Lys Asn
      35      40      45
Thr Ala Glu Ile Lys Glu Glu Ser Val Ile Leu Arg Glu Lys Pro Asp
      50      55      60
Ala Gly Cys Lys Lys Lys Ser Ser Cys Tyr Leu Arg Lys Phe Phe Ser
65      70      75      80
Arg Lys Lys Pro Lys Glu Lys Thr Glu Pro Val Leu Pro Asn Phe Lys
      85      90      95
Ser Tyr Ala Asp Pro Met Thr Asp Ser Glu Arg Lys Asp Leu Ser Phe
      100      105      110
Val Val Ser Ala Ala Ala Asp Lys Ser Ser Ile Ala Leu Ala Met Ala
      115      120      125
Gln Gly Glu Ile Lys Gly Ala Leu Ser Arg Ile Arg Glu Ile His Pro
      130      135      140
Leu Ala Phe Val Thr Ser Ser Cys Arg Arg Ser Cys Phe Asn Cys Trp
145      150      155      160
Asn Glu Lys Asp Ala Arg Thr Gly Leu Gly Leu Glu Tyr Leu Tyr His
      165      170      175
Arg Ile Lys Gln Ser Phe Phe Ser Ser Ile Phe Arg Ala Phe Ser
      180      185      190
Val Ala Asp Val Cys Arg Val Arg Val Asp Leu Arg Ile Arg Leu Gly
      195      200      205
Asp Arg Tyr Leu Asn Cys
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 670:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 429 acides aminés

(B) TYPE: acide aminé -

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 666831..668117

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 670:

```

Cys Pro Cys Phe Leu Ser Thr Ser Thr Ser Arg Asn Val Pro Ser Ser
1      5      10      15
Thr Thr Lys Ile Gly Ser Glu Val Trp Ile Glu Gln Lys Val Arg Gln
      20      25      30
Tyr Pro Glu Leu Leu Trp Leu Val Glu Pro Ser Ser Thr Gly Ala Ser
      35      40      45

```

Leu	Lys	Ser	Pro	Ser	Gly	Ala	Ile	Phe	Ser	Pro	Thr	Leu	Phe	Gln	Lys	50	55	60
Lys	Val	Pro	Ala	Phe	Asp	Ile	Ala	Val	Arg	Ser	Leu	Ile	His	Leu	His	65	70	75
Leu	Leu	Ile	Gln	Gly	Ser	Arg	Gln	Ala	Tyr	Ala	Gln	Leu	Ile	Gln	Leu	85	90	95
Gln	Thr	Ser	Glu	Ser	Pro	Leu	Thr	Phe	Lys	Gln	Phe	Leu	Ala	Leu	His	100	105	110
Lys	Gln	Leu	Thr	Leu	Phe	Leu	Asn	Ser	Pro	Lys	Glu	Phe	Tyr	Asp	Ser	115	120	125
Val	Lys	Val	Leu	Glu	Thr	Ala	Ile	Val	Leu	Arg	His	Leu	Gly	Cys	Ser	130	135	140
Thr	Lys	Ala	Val	Ala	Ala	Phe	Lys	Pro	Tyr	Phe	Ser	Glu	Met	Gln	Arg	145	150	155
Glu	Thr	Phe	Tyr	Thr	Lys	Ala	Leu	His	Val	Leu	His	Thr	Phe	Pro	Glu	165	170	175
Leu	Ser	Pro	Ser	Phe	Ala	Arg	Leu	Ser	Pro	Glu	Gln	Lys	Thr	Leu	Phe	180	185	190
Phe	Ser	Leu	Arg	Lys	Leu	Ala	Asn	Tyr	Asp	Glu	Leu	Leu	Ser	Leu	Thr	195	200	205
Asn	Thr	Pro	Ser	Phe	Gln	Leu	Leu	Ser	Ala	Gly	Arg	Ser	Gln	Arg	Ala	210	215	220
Leu	Leu	Ala	Leu	Asp	Leu	Tyr	Leu	Tyr	Ala	Leu	Asp	Ser	Cys	Gly	Glu	225	230	235
Gln	Gly	Met	Ser	Ser	Gln	Phe	His	Thr	Asn	Phe	Ala	Pro	Leu	Gln	Ser	245	250	255
Met	Leu	Gln	Gln	Tyr	Ala	Thr	Val	Glu	Glu	Ala	Phe	Ser	Arg	Tyr	Phe	260	265	270
Thr	Tyr	Arg	Ala	Asn	Arg	Leu	Gly	Phe	Asp	Gly	Ser	Ser	Arg	Ser	Glu	275	280	285
Met	Ala	Leu	Val	Arg	Met	Ala	Thr	Leu	Met	Asn	Leu	Ser	Pro	Ser	Glu	290	295	300
Ala	Ala	Ile	Leu	Thr	Thr	Ser	Phe	Lys	Thr	Leu	Pro	Thr	Glu	Glu	Ala	305	310	315
Asp	Thr	Leu	Val	Asn	Ser	Phe	Tyr	Thr	Asn	Lys	Gly	Asp	Ser	Leu	Ala	325	330	335
Leu	Ser	Leu	Arg	Gly	Leu	Pro	Thr	Leu	Val	Ser	Glu	Leu	Thr	Arg	Thr	340	345	350
Ala	Arg	Gly	Asn	Thr	Asn	Ala	Glu	Ala	Arg	Ser	Gln	Gln	Ile	Tyr	Ala	355	360	365
Thr	Thr	Leu	Ser	Leu	Val	Ala	Lys	Ser	Leu	Lys	Ala	His	Lys	Glu	Met	370	375	380
Leu	Asn	Lys	Gln	Ile	Leu	Ser	Lys	Glu	Ile	Val	Leu	Asp	Phe	Ser	Glu	385	390	395
Thr	Ala	Ala	Ser	Cys	Gln	Gly	Leu	Asp	Ile	Phe	Ser	Glu	Asn	Val	Ala	405	410	415
Val	Gln	Ile	His	Leu	Asn	Gly	Thr	Val	Ser	Ile	His	Leu				420	425	

(2) INFORMATIONS POUR LA SEQ ID NO: 671:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 668121..668375

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 671:

Ser	Lys	Lys	Thr	Pro	Asp	Leu	Ile	Arg	Arg	Ser	Ser	Phe	Ser	Thr	Pro
1				5				10					15		
Phe	Tyr	Ser	Phe	Pro	Ile	Arg	Glu	Asn	Asn	Asp	Ala	Ile	Ser	Lys	Ala
			20				25					30			
Val	Phe	Met	Pro	Glu	Ala	Pro	Lys	Leu	Gly	Pro	Leu	Ile	Pro	Ala	Arg
		35					40					45			
Ser	Gln	Ala	Ala	Ser	Ile	Leu	Gly	Ala	Val	Ile	Thr	Glu	Asn	Val	Ile
	50					55				60					
Gly	Arg	Gln	Lys	Ser	Lys	Asp	Arg	Arg	Leu	Thr	Pro	Ala	Ala	Thr	Leu
65					70				75						80
Ser	Ala	Ile	Cys	Ser											
					85										

(2) INFORMATIONS POUR LA SEQ ID NO: 672:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(668174..668470)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 672:

Ile	Pro	Cys	Ala	Ile	Lys	Lys	Leu	Leu	Ser	Thr	Ser	Gly	Gln	Phe	His
1				5				10					15		
Ala	Val	Val	Ala	Cys	Gly	Val	Leu	Ile	Gln	Gly	Glu	Thr	Ser	His	Tyr
			20				25					30			
Glu	His	Ile	Ala	Asp	Ser	Val	Ala	Ala	Gly	Val	Ser	Arg	Leu	Ser	Leu
		35				40					45				
Asp	Phe	Cys	Leu	Pro	Ile	Thr	Phe	Ser	Val	Ile	Thr	Ala	Pro	Asn	Met
	50					55				60					
Glu	Ala	Ala	Trp	Glu	Arg	Ala	Gly	Ile	Lys	Gly	Pro	Asn	Leu	Gly	Ala
65				70				75							80
Ser	Gly	Met	Lys	Thr	Ala	Leu	Glu	Met	Ala	Ser	Leu	Phe	Ser	Leu	Ile
				85				90						95	
Gly	Lys	Glu													

(2) INFORMATIONS POUR LA SEQ ID NO: 673:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 306 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(668616..669533)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 673:

```

Ser Gly Ser Asp Ser Glu Ser Phe Val Arg Pro Gly His Val Phe Pro
1      5      10      15
Leu Ile Ser Gln Pro Gly Gly Val Val Gln Arg Pro Gly His Thr Glu
      20      25      30
Ala Ala Met Asp Leu Met Arg Leu Ala Gly Met Gln Pro Cys Gly Ile
      35      40      45
Phe Ala Glu Leu Val Asn Pro Asp His Ser Met Met Arg Gln Gln Gln
50      55      60
Val Leu Ala Phe Ala Glu Gln His Asp Leu Thr Val Ile Thr Val Asp
65      70      75      80
Asp Leu Ile Thr Tyr Arg Tyr Thr Tyr Asp Ser Leu Val Thr Lys Ile
      85      90      95
Ser Ser Ala Arg Leu Pro Thr Lys Tyr Gly Asp Phe Ser Ile Tyr Val
      100     105     110
Tyr Glu Ser Ile Ile Asp Gly Thr Gln His Phe Ala Leu Val Lys Gly
      115     120     125
Asp Ile His Glu Gln Glu Ala Val Pro Val Arg Val His Ser Glu Cys
130     135     140
Leu Thr Gly Asp Ile Leu Gly Ser Cys Arg Cys Asp Cys Gly Ala Gln
145     150     155     160
Leu Asp Met Ala Met Arg Tyr Ile Ala Glu Glu Gly Leu Gly Val Ile
      165     170     175
Val Tyr Leu Arg Gly Gln Glu Gly Arg Gly Ile Gly Phe Gly His Lys
      180     185     190
Ile Arg Ala Tyr Ala Leu Gln Asp Leu Gly Tyr Asp Thr Val Asp Ala
      195     200     205
Asn Leu Gln Leu Gly Phe Pro Ile Asp Ala Arg Glu Tyr Gly Met Ala
210     215     220
Ala Gln Val Leu Lys Asp Leu Gln Leu Thr Ser Val Arg Leu Ile Thr
225     230     235     240
His Asn Pro Arg Lys Phe Phe Glu Leu Gln Arg Leu Gly Ile His Val
      245     250     255
Leu Asp Arg Ile Ile Leu Pro Val Ser Ile Ser Thr Glu Asn Glu Gly
      260     265     270
Tyr Leu Arg Thr Lys Lys Glu Arg Met Gly His Trp Leu Asp Leu Pro
      275     280     285
Val Leu Asp Asp Val Glu Glu Tyr Glu Thr Val Glu Arg Met Ser
290     295     300
Cys Arg
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 674:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(669485..669868)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 674:

```

Gly Ile Ala Ser Val Gln Gln Ala Ile Lys Asp Val Ala Glu Gly Lys
1           5           10           15
Phe Val Ile Val Ile Asp Ala Ala Ser Arg Glu Asn Glu Gly Asp Leu
           20           25           30
Ile Leu Ala Gly Glu Lys Val Ser Thr Glu Lys Met Ser Phe Leu Leu
           35           40           45
Ser His Thr Thr Gly Ile Val Cys Ala Ser Leu Ser Arg Glu Gln Ala
50           55           60
Lys Ser Leu Asp Leu Pro Ala Met Val Gln Asp Asn Gln Cys Ala Phe
65           70           75           80
Lys Thr Ala Phe Thr Val Ser Val Asp Ala Ser Ser Gly Val Thr Thr
           85           90           95
Gly Val Ser Ala Ser Asp Arg Thr Arg Thr Val Gln Leu Leu Ala Asp
           100           105           110
Pro Ala Ala Thr Ala Ser Pro Leu Phe Asp Gln Gly Met Phe Ser Leu
           115           120           125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 675:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(669998..670780)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 675:

```

Lys Arg Arg Thr Arg Leu Gln Ala Ala Gly Ile Pro Val Tyr Val Gly
1           5           10           15
Val Gly Ser Gln Glu Ala Lys Thr Ser Leu Gln Pro Tyr Leu Tyr Gln
           20           25           30
Arg Glu Arg Gly Leu Pro Trp Val Met Lys Thr Ala Ala Ser Leu
           35           40           45
Asp Gly Gln Thr Ala Asp Arg Gly Gly Ser Ser Gln Trp Ile Ser Gly
50           55           60
Glu Leu Ala Arg Ala Asp Val Gly Lys Leu Arg Ala Glu Ser Gln Ala
65           70           75           80
Ile Ile Val Gly Ala Arg Thr Val Cys Leu Asp Asn Pro Arg Leu Ser
           85           90           95
Ala Arg Phe Pro His Gly Asp Leu Tyr Glu Arg Gln Pro Leu Arg Val
           100           105           110
Val Val Asp Ser Arg Gly Thr Val Pro Leu Glu Ser Arg Val Phe Asp
           115           120           125
Leu Ser Ser Gly Ser Thr Leu Phe Ala Thr Thr Gln Gln Cys Pro Lys
130           135           140
Glu Tyr Ile Gln Lys Leu Lys Asp Leu Gly Val Glu Val Trp Glu Ser
145           150           155           160
Ser Ser His Gln Val Asp Leu Lys Gly Leu Leu Arg Tyr Leu Ala Glu
           165           170           175
Arg Gly Cys Leu Gln Val Leu Val Glu Gly Gly Ala Gln Leu His Ser
180           185           190
Ala Phe Trp Gln Gln Lys Leu Val Asn Ala Gly Val Ile Tyr Trp Gly
195           200           205

```



```

Pro Lys Phe Leu Gly Asp Gln Gly Gln Pro Met Leu Arg Asp Leu Gln
  210                215                220
Leu Ser Leu Val Thr Ala Glu His Val Arg Ile Thr Glu Thr Ser Leu
225                230                235                240
Val Arg Asp Ser Val Lys Thr Cys Phe Glu Cys Leu Glu Gln Glu Ser
                245                250                255
Val Asp Lys Lys Gly
                260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 676:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(670732..671241)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 676:

```

Arg Asn Xaa Xaa Xaa Leu Phe Phe Glu Asp Gly Phe Arg Thr Leu Leu
1          5          10          15
Val Pro Cys Val Leu Ile Val Tyr Pro Thr Ser Leu His Leu Phe Arg
          20          25          30
Tyr Leu Ile Phe Gln Val Glu Tyr Met Glu Val Leu Ser Glu Gln Gln
          35          40          45
Leu Phe Phe Met Arg Lys Ala Val Ala Leu Gly Glu Lys Gly Arg Ile
50          55          60
Phe Ala Pro Pro Asn Pro Trp Val Gly Cys Val Ile Val Lys Asn Gly
65          70          75          80
Cys Val Ile Gly Glu Gly Trp His Gln Gly Ile Gly Ser Pro His Ala
          85          90          95
Glu Val Cys Ala Val Gln Asp Gln Lys Cys Ser Leu Glu Gly Ala Glu
          100         105         110
Val Tyr Val Thr Leu Glu Pro Cys Cys His Phe Gly Arg Thr Pro Pro
          115         120         125
Cys Val Asp Leu Leu Ile Lys Ser Lys Val Ala Ala Val Tyr Val Gly
130          135         140
Leu Leu Asp Pro Asp Pro Arg Val Cys Lys Lys Gly Val Pro Val Cys
145          150         155         160
Lys Gln Gln Gly Phe Pro Phe Met Leu Gly
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 677:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 422 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 671182..672447

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 677:

Tyr Ala Arg Asn Gln Lys Ser Ala Lys Ala Val Phe Lys Lys Lys Xaa  
 1 5 10 15  
 Xaa Xaa Ile Ser Leu Glu Arg Leu Leu Asp Leu Asp Lys Thr Val Arg  
 20 25 30  
 Gln Leu Lys Ala Asp Ser Glu Ala Leu Leu Ala Lys Arg Lys Val Leu  
 35 40 45  
 Ser Gly Gln Ile His Lys Ala Lys Val Ala Asn Glu Asn Ala Asp Ala  
 50 55 60  
 Leu Ile Gln Glu Val Asn Thr Ile Ala Asp Gln Leu Val Ala Phe Glu  
 65 70 75 80  
 Thr Thr Leu Gln Glu Gln Glu Ala Leu Leu Glu Asp Leu Met Ala Arg  
 85 90 95  
 Leu Pro Asn Tyr Pro Asp Glu Asp Val Pro Val Ser Pro Asp Lys Thr  
 100 105 110  
 Gly Asn Gln Met Ile Lys Ser His Gly Glu Val Pro Thr Phe Pro Phe  
 115 120 125  
 Pro Pro Lys His His Met Gln Leu Asn Glu Ala Leu Gln Ile Leu Asp  
 130 135 140  
 Phe Lys Leu Pro Ala Lys Thr Thr Gly Ser Gly Trp Pro Ala Tyr Cys  
 145 150 155 160  
 Asn Glu Gly Val Leu Leu Glu Trp Ala Leu Leu Thr Tyr Leu Leu Asn  
 165 170 175  
 Lys Gln Gln Ala His Gly Phe Gln Leu Trp Leu Pro Pro Leu Leu Val  
 180 185 190  
 Lys Arg Asp Ile Leu Phe Gly Ser Gly Gln Ile Pro Lys Phe Asp Gly  
 195 200 205  
 Gln Tyr Tyr Arg Val Glu Asp Gly Asp Arg Ser Leu Phe Leu Ile Pro  
 210 215 220  
 Thr Ala Glu Val Val Leu Asn Gly Phe His Ser Gln Glu Ile Leu Asn  
 225 230 235 240  
 Glu Gln Asp Leu Pro Leu Cys Tyr Ala Ala Phe Thr Pro Cys Phe Arg  
 245 250 255  
 Arg Glu Ala Gly Ala Gly Gly Ala His Glu Arg Gly Leu Val Arg Val  
 260 265 270  
 His Gln Phe His Lys Val Glu Met Phe Ala Phe Thr Thr Pro Glu Gln  
 275 280 285  
 Glu Glu Val Val Tyr Gln Lys Met Leu His Val Val Glu Glu Ile Leu  
 290 295 300  
 Ser Glu Leu Gln Leu Pro Tyr Gln Leu Ser Leu Leu Ser Thr Gly Asp  
 305 310 315 320  
 Met Ser Phe Thr Ala Lys Lys Thr Ile Asp Ala Glu Val Trp Leu Pro  
 325 330 335  
 Gly Gln Lys Ala Phe Tyr Glu Val Ser Ser Ile Ser Lys Cys Gly Asp  
 340 345 350  
 Phe Gln Ala Arg Arg Ser Glu Thr Arg Tyr Arg Asp Ala Gln Gly Lys  
 355 360 365  
 Leu His Phe Val Asn Thr Leu Asn Gly Ser Gly Leu Ala Thr Pro Arg  
 370 375 380  
 Leu Leu Val Ala Ile Leu Glu Asn Tyr Gln Gln Ala Asp Gly Ser Val  
 385 390 395 400  
 Val Ile Pro Ser Val Leu Arg Pro Tyr Met Asn Asn Gln Glu Ile Leu  
 405 410 415  
 Leu Pro Lys Thr Val Arg  
 420

## (2) INFORMATIONS POUR LA SEQ ID NO: 678:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 180 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 672692..673231

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 678:

```

Pro Leu Met Glu Lys Ser Tyr Ser Gln Leu Gly Ser Val Gly Phe Phe
1      5      10      15
Ile Pro Ala Val Ser Glu Ala Gln Ala Ala Trp Ala Tyr Ile Glu Leu
20      25      30
Thr His Arg Asn Met Leu Gln Glu Lys Lys Glu Ile Glu Thr Asn Pro
35      40      45
Glu Gln Glu Arg Ile Glu Leu Ala Val Leu Tyr Ala Asn Gln Gly Phe
50      55      60
Gln Glu Pro Leu Ile Ser Gln Met Leu Asp Phe Val Cys Ser Asp Ser
65      70      75      80
Ser Leu Leu Leu Ser Thr Met Leu Arg Glu Glu Leu His Ile Gln Leu
85      90      95
Glu Asp Tyr Pro His Pro Leu Lys Gln Gly Asn Val Lys Ala Leu Gly
100     105     110
Gly Ile Leu Gly Leu Leu Leu Phe Ala Pro Ile Thr Leu Ala Val Ser
115     120     125
Tyr Thr Ile Ala Ala Ile Leu Ala Ser Phe Met Ile Gly Val Leu Phe
130     135     140
Ala Val Lys Thr Arg Leu Ile Lys Asn Ala Ile Thr Pro Ala Ile Val
145     150     155     160
Trp Gly Val Gly Met Phe Ile Thr Ala Ile Ser Leu Cys Cys Ser Leu
165     170     175
Ile Arg Leu Phe
180

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 679:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 453 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 673204..674562

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 679:

```

Pro Leu Leu Leu Phe Asp Pro Ile Ile Leu Val His Thr Leu Ser Arg
1      5      10      15
Trp Pro Met Ser Pro Gln Leu Phe Ser Ser Pro Phe Ser Arg Glu Leu
20      25      30
Leu Ser Asp Phe Phe Glu Ser Gly Met Ala Glu Glu Asn Ser Pro Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 680:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 207 acides aminés

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 680:

(2) INFORMATIONS POUR LA SEQ ID NO: 681:

(A) LONGUEUR: 379 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 681:

Met	Lys	Lys	Thr	Lys	Tyr	Leu	Arg	Gln	Val	Asn	Leu	Trp	Val	Phe	Val
1				5					10					15	
Val	Ile	Ile	Leu	Leu	Met	Ser	Ile	Ser	Val	Ile	Val	Ile	Ser	Ser	Gln
			20					25					30		
Asp	Pro	Ser	Ser	Met	Leu	Val	His	Thr	Ser	Arg	Gly	Leu	Phe	Ser	Ala
		35					40					45			
Lys	Ser	Lys	Lys	Gln	Leu	Asp	His	Phe	Ala	Leu	Gly	Trp	Cys	Ala	Tyr

50					55					60					
Phe	Ile	Cys	Leu	Tyr	Val	Asp	Tyr	His	Gln	Phe	Lys	Arg	Trp	Ala	Trp
65					70					75					80
Val	Leu	Tyr	Ser	Leu	Ile	Leu	Phe	Ser	Leu	Ile	Gly	Leu	Phe	Phe	Val
				85					90					95	
Pro	Ala	Val	Gln	Asn	Val	His	Arg	Trp	Tyr	Arg	Ile	Pro	Ile	Ile	Asn
			100					105					110		
Leu	Ser	Val	Gln	Pro	Ser	Glu	Tyr	Ala	Lys	Leu	Ala	Val	Val	Ile	Met
		115					120					125			
Leu	Ser	Tyr	Ile	Leu	Glu	Met	Arg	Lys	Ala	Arg	Ile	Ser	Ser	Lys	Thr
	130					135					140				
Thr	Ala	Phe	Val	Ala	Cys	Ile	Ile	Val	Gly	Ile	Pro	Phe	Leu	Leu	Ile
145					150					155					160
Leu	Lys	Glu	Pro	Asp	Leu	Gly	Thr	Ala	Leu	Val	Leu	Cys	Pro	Ile	Ala
				165					170					175	
Leu	Thr	Ile	Phe	Tyr	Leu	Gly	Asn	Ile	Tyr	Pro	Pro	Leu	Val	Lys	Val
			180				185						190		
Cys	Ser	Val	Leu	Val	Ala	Leu	Gly	Met	Phe	Cys	Ser	Leu	Leu	Ile	Phe
		195					200					205			
Ser	Gly	Ile	Ile	Pro	His	Asp	Lys	Val	Lys	Pro	Tyr	Ala	Leu	Lys	Val
	210					215					220				
Leu	Lys	Glu	Tyr	Gln	Tyr	Glu	Arg	Leu	Ser	Pro	Ser	Asn	His	His	Gln
225					230					235					240
Arg	Ala	Ser	Leu	Ile	Ser	Ile	Gly	Val	Gly	Gly	Leu	Lys	Gly	Gln	Gly
				245					250					255	
Trp	Lys	Ser	Gly	Glu	Phe	Ala	Gly	Arg	Gly	Trp	Leu	Pro	Tyr	Gly	Tyr
			260					265					270		
Thr	Asp	Ser	Val	Phe	Pro	Ala	Ile	Gly	Glu	Glu	Phe	Gly	Leu	Leu	Gly
		275					280					285			
Leu	Leu	Phe	Val	Leu	Trp	Leu	Phe	Tyr	Asn	Leu	Val	Cys	Phe	Gly	Cys
	290					295					300				
Arg	Thr	Val	Ala	Val	Ala	Val	Asp	Asp	Phe	Gly	Arg	Phe	Leu	Ala	Gly
305					310					315					320
Gly	Val	Thr	Val	His	Leu	Val	Met	His	Val	Leu	Ile	Asn	Val	Ser	Met
				325					330					335	
Met	Ser	Gly	Leu	Leu	Pro	Ile	Thr	Gly	Val	Pro	Leu	Val	Leu	Ile	Ser
			340					345					350		
Tyr	Gly	Gly	Ser	Ser	Val	Ile	Ser	Thr	Met	Ala	Ser	Leu	Gly	Ile	Leu
		355					360					365			
Gln	Ser	Ile	Tyr	Ser	Arg	Arg	Phe	Ala	Lys	Tyr					
	370					375									

(2) INFORMATIONS POUR LA SEQ ID NO: 682:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(676476..677003)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 682:

Ala	Arg	Thr	Glu	Ser	Thr	Asn	Thr	Thr	Ala	Lys	Glu	Gly	Leu	Ser	Leu
1				5					10				15		

Trp	Asp	Pro	Tyr	Ala	Leu	Thr	Val	Ile	Thr	Thr	Arg	Glu	Gln	Thr	Ala
			20					25					30		
Gly	Arg	Gly	Lys	Phe	Gly	Arg	Val	Trp	His	Ser	Thr	Asp	Gln	Asp	Leu
		35					40					45			
Leu	Ala	Ser	Phe	Cys	Phe	Phe	Leu	Ser	Val	Asn	Asn	Val	Asp	Ser	Ala
	50					55				60					
Leu	Leu	Phe	Arg	Ile	Gly	Thr	Glu	Ala	Val	Met	Arg	Leu	Gly	Glu	Ser
65					70					75					80
Leu	Gly	Ile	Gln	Glu	Ala	Val	Met	Lys	Trp	Pro	Asn	Asp	Val	Leu	Val
			85						90					95	
Gln	Gly	Gln	Lys	Leu	Ser	Gly	Val	Leu	Cys	Glu	Thr	Ile	Pro	Val	Lys
			100					105					110		
Thr	Gly	Thr	Cys	Val	Ile	Ile	Gly	Ile	Gly	Val	Asn	Gly	Asn	Val	Gly
		115					120					125			
Ala	Asp	Glu	Leu	Leu	Gly	Ile	Asn	Gln	Pro	Ala	Thr	Ser	Leu	Gln	Glu
	130					135					140				
Leu	Ile	Gly	Arg	Pro	Val	Asp	Met	Glu	Glu	Gln	Leu	Lys	Arg	Leu	Thr
145					150					155					160
Lys	Glu	Ile	Lys	His	Leu	Ile	Gln	Thr	Leu	Pro	Leu	Trp	Gly	Arg	Glu
				165					170					175	

(2) INFORMATIONS POUR LA SEQ ID NO: 683:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 241 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(677700..678422)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 683:

Met	Ala	Lys	Val	Arg	Leu	Asn	Lys	Phe	Leu	Ala	Ser	Ala	Gly	Val	Ala
1				5				10						15	
Ser	Arg	Arg	Lys	Cys	Asp	Glu	Ile	Ile	Phe	Ala	Gly	Ser	Val	Thr	Val
		20						25					30		
Asn	Gly	Arg	Val	Ala	Thr	Gly	Pro	Phe	Val	Thr	Val	Asp	Glu	Glu	Phe
		35				40						45			
Asp	Ser	Val	Glu	Val	Gly	Gly	Gln	Arg	Ile	Gly	Ala	Glu	Lys	Lys	Val
	50				55					60					
Tyr	Phe	Met	Val	His	Lys	Pro	Leu	Gly	Tyr	Leu	Cys	Ser	Ser	Glu	Arg
65				70					75						80
Lys	Phe	Pro	Gly	Ser	Lys	Leu	Val	Ile	Asp	Leu	Leu	Ser	His	Cys	Pro
			85					90					95		
Tyr	Arg	Leu	Phe	Thr	Val	Gly	Arg	Leu	Asp	Lys	Glu	Thr	Ser	Gly	Leu
		100						105					110		
Ile	Leu	Val	Thr	Asn	Asp	Gly	Glu	Phe	Ala	Asn	Arg	Val	Ile	His	Pro
		115				120						125			
Ser	Phe	Gly	Ile	Thr	Lys	Glu	Tyr	Leu	Leu	Lys	Val	Ser	Arg	Asp	Val
	130					135				140					
Thr	Ala	Arg	Asp	Leu	Glu	Thr	Leu	Met	Ala	Gly	Thr	Val	Ile	Asp	Gly
145					150					155					160
Lys	Val	Val	Arg	Pro	Val	Ser	Val	Lys	Lys	Val	Arg	Arg	Gly	Thr	Ile
				165				170					175		
Lys	Ile	Ile	Val	Asn	Glu	Gly	Lys	Lys	His	Glu	Ile	Arg	Leu	Phe	Ala

(2) INFORMATION POUR LA SEO ID NO: 684:

(A) LONGUEUR: 264 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 678717..679508

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 684:

[illegible]



## (2) INFORMATIONS POUR LA SEQ ID NO: 685:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 382 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 679357..680502

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 685:

Arg	Asp	Lys	Asn	Ser	Arg	Asn	Thr	Leu	Leu	Leu	Leu	Val	Asn	Asn	Gln	1	5	10	15
Gln	Ala	Ile	Pro	Pro	Ser	Glu	Met	Val	Lys	Glu	Ala	Phe	Gln	Arg	Tyr	20	25	30	
Ala	Asp	Val	Phe	Ser	Tyr	Ser	Ala	Asn	Thr	Ser	Ile	Leu	Thr	Leu	Gln	35	40	45	
Ala	Glu	Ala	Glu	Ala	Ser	Ala	Arg	Lys	Leu	Thr	Gly	Cys	Gln	Glu	Lys	50	55	60	
Ala	Phe	Thr	Phe	His	Phe	Ile	Leu	His	Tyr	Pro	Asn	Val	Thr	Ala	Ile	65	70	75	80
Ile	Val	Ala	Ala	Leu	Leu	Glu	Asn	Gln	Asn	Ala	Phe	Gln	Gly	Arg	Asn	85	90	95	
His	Leu	Leu	Val	Pro	Ser	Cys	Glu	Gln	Gln	Phe	Ile	Ile	Asn	Ala	Leu	100	105	110	
Cys	Arg	Arg	Gln	Asn	Leu	Gly	Thr	Thr	Tyr	Asp	Trp	Val	Thr	Ser	Lys	115	120	125	
Asn	Gly	Arg	Val	Lys	Glu	Ser	Asp	Leu	Ala	Glu	Ala	Leu	Ser	Pro	Arg	130	135	140	
Thr	Leu	Leu	Phe	Ser	Ile	Ser	Ala	Ala	Asn	Gly	Met	Thr	Gly	Phe	Leu	145	150	155	160
Glu	Ala	Ile	Pro	Glu	Leu	Ala	Ala	Leu	Cys	Lys	Glu	Arg	Gly	Val	Ile	165	170	175	
Phe	His	Ile	Asp	Leu	Ser	Asp	Ile	Leu	Gly	Arg	Cys	Ala	Leu	Pro	Ala	180	185	190	
Glu	Leu	Tyr	Gln	Ala	Asp	Ile	Leu	Thr	Phe	Ser	Ser	Gln	Ser	Leu	Gly	195	200	205	
Gly	Ile	Gly	Pro	Ser	Gly	Ala	Met	Phe	Ile	Ser	Pro	Ala	Leu	Thr	Lys	210	215	220	
Tyr	Phe	Ser	Leu	Trp	Leu	Pro	Ser	Asn	Pro	Gln	Val	Pro	Thr	Cys	Leu	225	230	235	240
Ser	Ser	Leu	Ala	Ala	Phe	Ser	Leu	Ala	Cys	Gln	Glu	Arg	Thr	Thr	Ala	245	250	255	
Phe	Ser	Ser	Leu	Val	Leu	Ser	Ala	Ile	Ser	Ser	Arg	Ala	Ala	Leu	Lys	260	265	270	
Gln	Ala	Leu	Ser	Ala	Ile	Pro	Gln	Val	Glu	Phe	Leu	Leu	Glu	Asp	Ser	275	280	285	
Ala	Pro	Arg	Leu	Pro	Asn	Val	Ala	Val	Phe	Ala	Ile	Pro	Gly	Ile	Pro	290	295	300	
Ala	Glu	Ser	Leu	Gly	Phe	Phe	Leu	Ser	Gln	Lys	Asn	Ile	Phe	Val	Gly	305	310	315	320
Leu	Gly	Tyr	Glu	Arg	Phe	Gln	Pro	Leu	Ser	Gln	Ile	Leu	Gln	Ser	Ser	325	330	335	
Gly	Ile	Ser	Pro	Phe	Leu	Cys	His	Ser	Ala	Leu	His	Val	Ser	Phe	Thr				

			340					345				350	
Glu	Arg	Thr	Pro	Thr	Thr	His	Phe	Ser	Ala	Leu	Ala	Thr	Ala
			355						360			365	
Glu	Gly	Ile	Ser	His	Leu	Gln	Pro	Leu	Val	Thr	Gln	Ser	Leu
		370					375				380		

(2) INFORMATIONS POUR LA SEQ ID NO: 686:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 680579..681280

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 686:

Thr	Trp	Arg	Thr	Leu	Ser	His	Asp	Gln	Glu	Asp	Glu	Glu	Ile	Gln	Leu
1				5					10					15	
Val	Ile	Gly	Lys	Gln	Gly	His	Leu	Leu	Met	Gly	Asn	Thr	Leu	Leu	Phe
			20					25					30		
Tyr	Trp	Leu	Val	Asp	Lys	Thr	Asn	Gly	Ile	Ile	Arg	Glu	Ala	Lys	Phe
		35				40					45				
Gln	Tyr	Phe	Gly	His	Pro	Tyr	Leu	Leu	Val	Leu	Ala	Glu	Ala	Thr	Cys
	50				55						60				
Ser	Leu	Val	Ile	Gly	Lys	Thr	Phe	Ala	Glu	Ala	Tyr	Lys	Ile	Thr	Ile
65					70					75					80
Asn	Asp	Leu	Asp	Gln	Glu	Val	Arg	Gly	His	Ala	Asn	Pro	Ser	Ile	Phe
				85					90					95	
Leu	Glu	Asp	Leu	Ser	Pro	Leu	Tyr	His	Leu	Val	Ile	Asp	Ala	Leu	Asp
			100					105					110		
Ile	Ala	Ile	Glu	Gln	Cys	Val	Asp	Ile	Pro	Val	Asn	Asp	Ser	Pro	Phe
		115					120					125			
Pro	Phe	Lys	Asp	Ala	Leu	Ser	Gln	Leu	Ser	Glu	Gly	Asn	Pro	Tyr	Ser
	130				135						140				
Thr	Glu	Glu	Trp	Gly	Ala	Leu	Ser	His	Asp	Glu	Gln	Leu	Ser	Ala	Leu
145					150					155					160
Asn	Thr	Met	Met	Lys	Glu	Lys	Ile	Ala	Pro	Leu	Val	Ala	Val	Asp	Ser
				165					170					175	
Gly	Asp	Val	Arg	Ile	Val	His	Phe	Glu	Gly	Leu	Thr	Val	Thr	Ile	Ala
			180					185					190		
Tyr	Ser	Gly	Asn	Cys	Ser	Ser	Cys	Leu	Ser	Ser	Val	Gly	Ser	Thr	Leu
		195					200					205			
Asn	Ser	Ile	Gly	Gln	Leu	Phe	Arg	Ala	His	Val	Tyr	Pro	Leu	Leu	Glu
	210					215					220				
Ile	Lys	Val	Asp	Glu	Gln	Ser	Leu	Leu	Phe						
225						230									

(2) INFORMATIONS POUR LA SEQ ID NO: 687:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 340 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 681539..682558

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 178 acides aminés  
(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 682554..683087

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 688:

Glu	His	Lys	His	Leu	Glu	Asp	Tyr	Val	Ala	Ser	Pro	His	Leu	Arg	Ser
1				5					10					15	
Leu	Ala	Cys	Leu	Asp	Asn	Ser	Gln	Leu	Pro	Ile	Glu	Thr	Pro	Leu	Phe
			20					25					30		
Glu	Gln	Lys	Ala	Leu	Ser	His	Glu	Leu	Leu	Ser	Leu	Ile	Gln	Val	Phe
		35					40					45			
Arg	Lys	Leu	Ser	Val	His	Leu	Leu	Ser	Glu	Ile	Glu	Lys	Leu	Ser	Gln
	50					55					60				
Lys	Leu	Lys	Pro	Glu	Leu	Leu	Glu	Leu	Ala	Val	Leu	Val	Cys	Glu	Lys
65				70					75					80	
Phe	Leu	Tyr	Arg	Lys	Leu	Ala	Cys	Thr	Glu	Glu	Leu	Ala	Leu	Leu	Ile
			85						90					95	
Ser	Ala	Ala	Leu	Gln	His	His	Leu	Ala	Thr	Tyr	Ala	Val	Ser	Pro	Ile
			100					105					110		
Lys	Ile	Gly	Leu	His	Pro	Glu	Asp	Leu	Ser	Asn	Leu	Ser	Lys	Trp	Leu
		115					120					125			
Ile	Leu	His	Asp	Val	Pro	Leu	Leu	Lys	Asn	Ile	Glu	Phe	Ile	Ala	Asp
	130					135					140				
Pro	Leu	Cys	Lys	Lys	Ala	Ser	Tyr	Lys	Ile	Glu	Leu	Pro	Ser	Gly	Ile
145				150					155					160	
Leu	Arg	Gln	Asp	Ile	Gly	Glu	Glu	Leu	Ser	His	Leu	Leu	Ser	Val	Leu
			165						170					175	
Thr	Pro														

(2) INFORMATIONS POUR LA SEQ ID NO: 689:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 434 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 683164..684465

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 689:

Met	Thr	His	Leu	Gln	Glu	Glu	Thr	Leu	Leu	Ile	His	Gln	Trp	Arg	Pro
1			5						10					15	
Tyr	Arg	Glu	Cys	Gly	Ile	Leu	Ser	Arg	Ile	Ser	Gly	Ser	Leu	Leu	Glu
			20					25					30		
Ala	Gln	Gly	Leu	Ser	Ala	Cys	Leu	Gly	Glu	Leu	Cys	Gln	Ile	Ser	Leu
		35					40					45			
Ser	Arg	Ser	Asp	Pro	Ile	Leu	Ala	Glu	Val	Ile	Gly	Ile	His	Asn	Arg
	50					55					60				
Thr	Thr	Leu	Leu	Leu	Ala	Leu	Thr	Pro	Ile	Tyr	Tyr	Leu	Ala	Ile	Gly
65				70					75					80	

Ala	Glu	Val	Val	Pro	Leu	Arg	Arg	Pro	Ala	Ser	Leu	Pro	Leu	Ser	Asn	
				85					90					95		
His	Leu	Leu	Gly	Arg	Val	Leu	Asp	Gly	Phe	Gly	Asn	Pro	Leu	Asp	Gly	
			100					105					110			
Gly	Ser	Gln	Leu	Pro	Lys	Thr	Asn	Leu	Ser	Pro	Leu	Phe	Ser	Ser	Pro	
		115					120					125				
Ser	Ser	Pro	Met	Ser	Arg	Thr	Pro	Ile	Gln	Glu	Val	Phe	Pro	Thr	Gly	
		130				135					140					
Ile	Arg	Ala	Ile	Asp	Ala	Leu	Leu	Thr	Ile	Gly	Glu	Gly	Gln	Arg	Val	
145					150					155					160	
Gly	Ile	Phe	Ser	Glu	Pro	Gly	Gly	Gly	Lys	Ser	Ser	Leu	Leu	Ser	Thr	
				165					170						175	
Ile	Ala	Lys	Gly	Ser	Gln	Gln	Thr	Ile	Asn	Val	Ile	Ala	Leu	Ile	Gly	
			180					185					190			
Glu	Arg	Gly	Arg	Glu	Val	Arg	Asp	Tyr	Val	Asn	Gln	His	Lys	Glu	Gly	
		195					200					205				
Leu	Ala	Ala	Gln	Arg	Thr	Val	Ile	Ile	Ala	Ser	Thr	Ala	Tyr	Glu	Thr	
		210				215					220					
Ala	Ala	Ser	Lys	Val	Ile	Ala	Gly	Arg	Ala	Ala	Ile	Thr	Ile	Ala	Glu	
225					230					235					240	
Tyr	Phe	Arg	Asp	Gln	Gly	Ala	Arg	Val	Leu	Phe	Thr	Met	Asp	Ser	Leu	
				245					250					255		
Ser	Arg	Trp	Ile	Glu	Ser	Leu	Gln	Glu	Val	Ala	Ile	Ala	Arg	Gly	Glu	
			260					265					270			
Thr	Leu	Ser	Thr	His	His	Tyr	Ala	Ala	Ser	Val	Phe	His	His	Val	Ala	
		275					280					285				
Glu	Phe	Leu	Glu	Arg	Ala	Gly	Asn	Asn	Asp	Lys	Gly	Ser	Ile	Thr	Ser	
	290					295					300					
Phe	Tyr	Ala	Ile	Leu	His	Tyr	Ala	Asn	His	Pro	Asp	Ile	Phe	Thr	Asp	
305					310					315					320	
Tyr	Val	Lys	Ser	Leu	Leu	Asp	Gly	His	Phe	Phe	Leu	Ser	Pro	Gln	Glu	
				325					330					335		
Lys	Ser	Phe	Ser	Ser	Pro	Pro	Ile	Asn	Val	Leu	Thr	Ser	Leu	Ser	Arg	
			340					345					350			
Ser	Ser	Arg	Gln	Leu	Ala	Leu	Pro	His	His	Tyr	Ala	Ala	Ala	Gln	Glu	
		355					360					365				
Leu	Leu	Ser	Leu	Leu	Lys	Ala	Tyr	His	Glu	Ala	Ile	Asp	Ile	Ile	Gln	
		370				375					380					
Leu	Gly	Ala	Tyr	Val	Ser	Gly	Gln	Asp	Ala	His	Leu	Asp	Arg	Ala	Ile	
385					390					395					400	
Arg	Leu	Leu	Pro	Ser	Val	Lys	Gln	Phe	Leu	Ser	Gln	Pro	Tyr	Ser	His	
				405					410					415		
Tyr	Ser	Ala	Ile	His	Glu	Thr	Ile	Glu	Gln	Leu	Cys	Gln	Leu	Leu	Lys	
			420			-		425					430			
His	Glu															

(2) INFORMATIONS POUR LA SEQ ID NO: 690:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(684418..684774)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 690:

Phe	Phe	Phe	Gly	Leu	Val	Val	Phe	Val	Cys	Arg	His	Lys	His	Leu	Ser
1				5					10					15	
Lys	Thr	Phe	Ser	Gly	Pro	Asp	Ala	Val	Tyr	Ile	Glu	Lys	Phe	Ala	Leu
			20					25					30		
Phe	Val	Asn	Val	Leu	Asn	Val	Gly	His	Ile	His	Gly	Tyr	Met	Thr	Asp
		35					40					45			
Ile	Gly	Ile	Val	Cys	Ala	Leu	Leu	Arg	Lys	Phe	Ser	Arg	Cys	Ala	Pro
	50					55					60				
Val	Phe	Val	Val	Ser	Arg	Cys	Ser	Ile	Val	Glu	Ser	Ala	Phe	Phe	Thr
65					70					75					80
Val	Ser	Asn	Arg	Val	Arg	Phe	Leu	Lys	Ser	Ser	Ile	Val	Ser	Ser	Leu
			85					90						95	
Asp	Arg	Ser	Trp	Ser	Phe	Leu	Phe	Met	Phe	Gln	Gln	Leu	Ala	Gln	Leu
			100					105					110		
Phe	Asn	Ser	Phe	Met	Asn	Ser									
			115												

(2) INFORMATIONS POUR LA SEQ ID NO: 691:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 449 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 684857..686203

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 691:

Val	Asp	Leu	Ser	Phe	Leu	Leu	Asp	Gln	Leu	Leu	Pro	Ile	Gln	Gln	Glu
1				5					10					15	
His	Leu	Leu	Glu	Tyr	Trp	Pro	Ser	Leu	Ser	Pro	Gln	Gln	Arg	Leu	Arg
			20					25					30		
Leu	Gly	Thr	Gln	Ile	Ala	Gln	Ile	Asp	Ile	Pro	Phe	Phe	Leu	Arg	Gln
		35					40					45			
Gln	Ala	Leu	Leu	Gln	Asn	Pro	Gln	Ala	Ser	His	Gln	Glu	Tyr	Thr	Pro
	50					55					60				
Leu	Ser	Pro	Val	His	Tyr	Ala	Gly	Asp	Asn	Pro	Ala	Tyr	Ala	Gln	Leu
65					70					75					80
Gly	Phe	Gln	Leu	Leu	Gln	Arg	Gly	Lys	Val	Gly	Cys	Val	Val	Leu	Ala
			85					90						95	
Gly	Gly	Gln	Gly	Ser	Arg	Leu	Lys	Phe	Asp	Gly	Pro	Lys	Gly	Leu	Tyr
			100					105					110		
Pro	Val	Ser	Val	Lys	Lys	Lys	Lys	Pro	Leu	Tyr	Gln	Leu	Val	Ala	Glu
		115					120					125			
Lys	Val	Ala	Ala	Ala	Ser	Lys	Trp	Val	Gly	Arg	Pro	Leu	Pro	Leu	Ala
	130					135					140				
Ile	Met	Thr	Ser	Pro	Leu	Asn	His	Lys	Gln	Thr	Leu	Ser	Tyr	Phe	Ala
145					150					155					160
Thr	Asn	Asp	Tyr	Phe	Asn	Leu	Ser	Pro	Ser	Gln	Val	Asp	Phe	Phe	Cys
			165					170						175	
Gln	Pro	Leu	Trp	Pro	Leu	Leu	Ser	Leu	Ser	Gly	Asp	Leu	Phe	Leu	Glu
			180					185						190	

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 692:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 336 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: 686197..687204

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 692:

Gly	Leu	Met	Lys	Glu	Thr	Ile	Ala	Tyr	Leu	Gly	Met	Gly	Met	Trp	Gly
1				5					10					15	
Phe	Ser	Leu	Ala	Asn	Leu	Leu	Ala	Asn	Asn	Gly	His	Arg	Val	Val	Gly
			20					25					30		
Trp	Ala	Arg	Asn	Pro	Ala	Leu	Ile	Glu	Gln	Leu	Ser	Val	Gln	Arg	Arg
		35					40					45			
His	Pro	Ala	Ala	Pro	His	Ile	Ser	Ile	Pro	Gln	Asn	Leu	Ser	Phe	Thr
	50					55					60				
Tyr	His	Met	Glu	Glu	Ala	Leu	Asp	Gly	Ala	Thr	Met	Ile	Val	Glu	Gly

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65          70          75          80
Val Thr Ser Ala Gly Met Arg Pro Val Leu Thr Gln Leu Lys Ala Leu
85          90          95
Thr Glu Leu Arg Val Pro Leu Val Ile Thr Ser Lys Gly Ile Glu Gln
100         105         110
Asn Thr Gly Leu Leu Leu Ser Glu Ile Ala Leu Glu Ile Phe Gly Arg
115         120         125
Pro Ala Ala Gln His Leu Gly Tyr Leu Ser Gly Pro Ser Ile Ala Ser
130         135         140
Glu Val Leu Arg Gly Cys Pro Cys Ser Val Val Ile Ser Ala Tyr Asn
145         150         155
Pro Asp Thr Leu Lys Gln Ile His Arg Ala Phe Leu Thr Pro Thr Phe
165         170         175
Arg Val Tyr Pro Asn Ser Asp Leu Lys Gly Val Ala Leu Gly Gly Ala
180         185         190
Leu Lys Asn Val Ile Ala Ile Ala Cys Gly Ile Ser Asp Gly Phe Arg
195         200         205
Phe Gly Asp Asn Ala Lys Ser Gly Leu Val Thr Arg Gly Leu His Glu
210         215         220
Ile Arg Lys Phe Ala Thr Ile Met Gly Cys Arg Pro Asp Thr Leu Asn
225         230         235
Gly Leu Ala Gly Leu Gly Asp Leu Cys Thr Thr Cys Phe Ser Ala Phe
245         250         255
Ser Arg Asn Thr Leu Phe Gly Lys Leu Leu Ala Glu Gly Leu Thr Pro
260         265         270
Glu Gln Ala Lys Thr Lys Ile Gly Met Val Val Glu Gly Val Tyr Thr
275         280         285
Ala Leu Ser Ala His Gln Ile Ala Thr His His Arg Ile Asp Met Pro
290         295         300
Ile Thr Thr Ser Val Tyr Arg Val Leu Tyr Glu Asn Leu Asp Ile Gln
305         310         315
Glu Gly Ile Ala Gln Leu Leu Gln Arg Asp Thr Lys Glu Glu Tyr Leu
325         330         335

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(2) INFORMATIONS POUR LA SEQ ID NO: 693:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 340 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 687341..688360

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 693:

```

Met Ser Ser Lys Leu Val Asn Tyr Leu Arg Leu Thr Phe Leu Ser Phe
1          5          10          15
Leu Gly Ile Ala Ser Thr Ser Leu Asp Ala Met Pro Ala Gly Asn Pro
20         25         30
Ala Phe Pro Val Ile Pro Gly Ile Asn Ile Glu Gln Lys Asn Ala Cys
35         40         45
Ser Phe Asp Leu Cys Asn Ser Tyr Asp Val Leu Ser Ala Leu Ser Gly
50         55         60
Asn Leu Lys Leu Cys Phe Phe Gly Asp Tyr Ile Phe Ser Glu Glu Ala
65         70         75         80

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Gln Val Lys Asp Val Pro Val Val Thr Ser Val Thr Thr Ala Gly Ile  
                   85                  90                  95  
 Gly Pro Ser Pro Asn Ile Thr Ser Thr Thr Lys Thr Arg Asn Phe Asp  
                   100                  105                  110  
 Leu Val Asn Cys Asn Leu Asn Ala Asn Cys Val Ala Ala Ala Phe Ser  
                   115                  120                  125  
 Leu Pro Asp Arg Ser Leu Ser Ala Ile Pro Leu Phe Asp Val Ser Phe  
                   130                  135                  140  
 Glu Val Lys Val Gly Gly Leu Lys Gln Tyr Tyr Arg Leu Pro Met Asn  
                   145                  150                  155                  160  
 Ala Tyr Arg Asp Phe Thr Ser Glu Pro Leu Asn Ser Glu Ser Glu Val  
                   165                  170                  175  
 Thr Asp Gly Met Ile Glu Val Gln Ser Asn Tyr Gly Phe Val Trp Asp  
                   180                  185                  190  
 Val Ser Leu Lys Lys Val Ile Trp Lys Asp Gly Val Ser Phe Val Gly  
                   195                  200                  205  
 Val Gly Ala Asp Tyr Arg His Ala Ser Cys Pro Ile Asp Tyr Ile Ile  
                   210                  215                  220  
 Ala Asn Ser Gln Ala Asn Pro Glu Val Phe Ile Ala Asp Ser Asp Gly  
                   225                  230                  235                  240  
 Lys Leu Asn Phe Lys Glu Trp Ser Val Cys Val Gly Leu Thr Thr Tyr  
                   245                  250                  255  
 Val Asn Asp Tyr Val Leu Pro Tyr Leu Ala Phe Ser Ile Gly Ser Val  
                   260                  265                  270  
 Ser Arg Gln Ala Pro Asp Asp Ser Phe Lys Lys Leu Glu Asp Arg Phe  
                   275                  280                  285  
 Thr Asn Leu Lys Phe Lys Val Arg Lys Ile Thr Ser Ser His Arg Gly  
                   290                  295                  300  
 Asn Ile Cys Ile Gly Ala Thr Asn Tyr Ile Ala Asp Asn Phe Phe Tyr  
                   305                  310                  315                  320  
 Asn Val Glu Gly Arg Trp Gly Ser Gln Arg Ala Val Asn Val Ser Gly  
                   325                  330                  335  
 Gly Phe Gln Phe  
                   340

(2) INFORMATIONS POUR LA SEQ ID NO: 694:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 80 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(688193..688432)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 694:

Leu Asp Met Arg Gly Asn Leu Leu Leu Ile Ser Leu Glu Gly Glu Val  
 1                  5                  10                  15  
 Lys Arg Arg Gly Phe Gly Gly Leu Glu Leu Glu Ser Ser Gly Asp Val  
                   20                  25                  30  
 His Ser Ala Leu Ala Ser Pro Ser Ser Phe Tyr Val Val Glu Glu Val  
                   35                  40                  45  
 Ile Gly Asp Ile Val Cys Arg Ser Asp Ala Asp Val Ser Thr Met Arg  
                   50                  55                  60  
 Ala Gly Asn Phe Thr Asn Phe Lys Phe Glu Val Ser Glu Ala Ile Phe

65

70

75

80

(2) INFORMATIONS POUR LA SEQ ID NO: 695:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 395 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(688432..689616)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 695:

Arg	Ala	Lys	Thr	Ile	Met	Arg	Asn	His	Pro	Ile	Pro	Glu	Gly	Gln	Lys
1				5					10					15	
Tyr	Phe	Val	Pro	Thr	Ile	Glu	Thr	Ala	Ala	Pro	Arg	Glu	Arg	Arg	Val
			20					25					30		
Ser	Pro	Ala	Glu	Val	Ala	Ala	Asp	Tyr	Thr	Gln	Leu	His	Glu	Ala	Ala
		35					40					45			
Thr	Tyr	Leu	Gln	Val	Phe	Gln	Asp	Leu	Leu	Asn	Asp	Ala	His	Gln	Leu
	50					55				60					
Gly	Leu	Asn	Lys	Glu	Phe	Val	Glu	Ser	Leu	Arg	Gln	Asp	Phe	Leu	Lys
65					70				75					80	
Thr	Gly	Ser	Glu	Met	Ser	Leu	Met	Gln	Ala	Leu	Trp	Thr	Glu	Glu	Ser
				85					90					95	
Gln	Arg	Glu	Ala	Arg	Lys	Arg	Glu	Arg	Lys	Glu	Leu	Gln	Gln	Gln	Leu
			100					105					110		
Glu	Ser	Lys	Val	Leu	Gly	Pro	Gln	Ala	Leu	Thr	Thr	Ala	Lys	Glu	Leu
		115					120					125			
His	Pro	Val	Asp	Asp	Ser	Ile	Val	Asn	Lys	Met	Pro	Phe	Gln	Ser	Ala
	130					135					140				
Phe	Ala	Tyr	Ile	Leu	Leu	Asp	Lys	Tyr	Ile	Pro	Ala	Gln	Glu	Glu	Ala
145					150					155					160
Leu	Tyr	Ala	Leu	Ala	Arg	Glu	Leu	Asn	Phe	Ser	Gly	Tyr	Ala	Gln	Thr
			165						170					175	
Leu	Phe	Ser	Pro	Val	Leu	Glu	Leu	Val	Lys	Ser	Phe	Asn	Asn	Ala	Pro
			180					185					190		
Ile	Val	Tyr	Asn	Leu	Gly	Ser	Tyr	Ile	Gly	Gln	Thr	Ala	Gly	Thr	Ala
		195					200					205			
Asn	Phe	Lys	Tyr	Gly	Tyr	Gln	Met	Val	Leu	Asp	Arg	Tyr	Glu	Thr	Glu
	210					215					220				
Thr	Gly	Gln	Leu	Arg	Lys	Asp	Ile	Lys	Asn	Ala	Glu	Asn	Ala	Lys	Gln
225					230					235					240
Gln	Leu	Ala	Gln	Ile	Ile	Lys	Asn	Val	Glu	Ala	Asn	Asn	Ser	Leu	Thr
			245						250					255	
Thr	Glu	His	Lys	Thr	Gln	Leu	Lys	Asp	Met	Ala	Asn	Gly	Tyr	Ile	Gln
			260					265					270		
Thr	Leu	Asp	Val	Cys	Ile	Ser	Gln	Met	Gln	Glu	Leu	Ser	Thr	Gly	Leu
		275					280					285			
Arg	Gly	Leu	Ser	Phe	Ile	Pro	Gly	Arg	Asp	Glu	Tyr	Asn	Pro	Ala	Tyr
	290					295					300				
Glu	Ile	Met	Gly	Ser	Ser	Phe	Ser	Val	Val	Thr	Leu	Gln	Asn	Leu	Glu
305					310					315					320
Gly	Lys	Val	Val	Asp	Gly	Glu	Ile	Asn	Ile	Ser	Ser	Gly	Glu	Thr	Lys
				325					330					335	

Gly Gly Leu Leu Asn Phe Phe Thr Tyr Phe Leu Ala Asp Val Gln Asn  
                                   340                                  345                                  350  
 Phe Gly Asp Leu Ala Gln Thr Asn Gln Leu Met Leu Glu Leu Gln Met  
                                   355                                  360                                  365  
 Arg Ala Met His Gln Gln Trp Ser Leu Val Thr Ala Ser Leu Lys Leu  
                                   370                                  375                                  380  
 Leu His Asn Val Tyr Arg Thr Leu Ala Ser Ser  
 385                                  390                                  395

(2) INFORMATIONS POUR LA SEQ ID NO: 696:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(689631..689960)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 696:

Gly Thr Asp Phe Trp Arg Asn Met Pro Asp Glu Val Asp Glu Ala Phe  
 1                                  5                                  10                                  15  
 Thr Ala Lys Ile Gly Ser Lys Glu Phe Asp Thr Trp Ile Gln Gln Leu  
                                   20                                  25                                  30  
 Thr Thr Phe Glu Ser Ala Val Ile Glu Gly Gly Arg Asn Gly Val Met  
                                   35                                  40                                  45  
 Pro Gly Gly Glu Gln Gln Val Leu Gln Ser Leu Glu Ser Lys Gln Gln  
                                   50                                  55                                  60  
 Asp Tyr Thr Ser Phe Asn Gln Asn Gln Gln Leu Ala Leu Gln Met Glu  
 65                                  70                                  75                                  80  
 Ser Ala Ala Ile Gln Gln Glu Trp Thr Met Val Ala Ala Ala Leu Ala  
                                   85                                  90                                  95  
 Leu Met Asn Gln Ile Phe Ala Lys Leu Ile Arg Arg Phe Lys  
                                   100                                  105                                  110

(2) INFORMATIONS POUR LA SEQ ID NO: 697:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(689846..690487)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 697:

Lys Ser Glu Val Glu Pro Ser Ser Leu Asn Tyr Phe Asn Ala Met Val  
 1                                  5                                  10                                  15  
 Glu Ala Lys Lys Thr Phe Val Glu Thr Ser Pro Ile Gln Met Val Tyr  
                                   20                                  25                                  30  
 Ser Ser Leu Met Leu Asp Lys Tyr Leu Pro Asn Gln Gln Tyr Ile Leu

```

      35              40              45
Glu Thr Leu Gly Ser Gln Met Thr Phe Ser Asn Lys Ala Ala Arg Tyr
  50              55              60
Leu Asn Asp Ile Ile Ala His Ala Val Ser Phe Gln Thr Ala Asn Val
  65              70              75              80
Tyr Tyr Ser Leu Gly Met Tyr Leu Arg Gln Met Asn Gln Gln Glu Phe
      85              90              95
Pro Glu Val Ile Ser Arg Ala Asn Asp Thr Val Lys Lys Glu Ile Asp
      100              105              110
Arg Ser Arg Ala Asp Leu Phe His Cys Lys Lys Ala Ile Glu Lys Ile
      115              120              125
Lys Glu Leu Val Thr Ser Ile Asn Ala Asp Thr Glu Leu Thr Ser Ser
      130              135              140
Gln Arg Ala Glu Leu Leu Glu Thr Leu Ala Ser Tyr Ala Phe Glu Phe
  145              150              155              160
Glu Asn Leu Tyr His Asn Leu Ser Asn Val Tyr Val Met Val Ser Lys
      165              170              175
Val Gln Ile Ser Gly Val Thr Cys Leu Met Lys Trp Met Arg Leu Leu
      180              185              190
Leu Leu Arg Leu Asp Arg Arg Asn Ser Ile Leu Gly Phe Ser Ser Leu
      195              200              205
Gln His Leu Lys Val Leu
      210

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(2) INFORMATIONS POUR LA SEQ ID NO: 698:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(690463..690717)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 698:

```

Ala Phe Gly Asp Tyr Asn Gly Val Tyr Leu Phe Asp Asn Lys Gly Leu
  1              5              10              15
Ala Thr Asn Leu Phe Asn Pro Thr Phe Phe Phe Asp Val Val Ser Leu
      20              25              30
Met Thr Ala Asp Pro Thr Lys Thr Met Ser Arg Gln Asp Tyr Asn Lys
      35              40              45
Val Ile Thr Ala Ser Glu Ser Ser Ile Gln Lys Ile Asn Gln Ala Ile
  50              55              60
Thr Ala Trp Glu Leu Ala Ile Ala Glu Cys Gly Thr Lys Lys Ala Lys
  65              70              75              80
Ser Asn His Pro Val
      85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 699:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 699:

Pro 1	Glu	Ser	Arg	Ser 5	Met	Leu	Leu	Gln	Cys 10	Ile	Cys	Arg	Ser	Val 15	Phe
Phe	Phe	Gln	Gln	Leu 20	Asp	Glu	Lys	Ser 25	Lys	Gly	Leu	Lys	Arg 30	Ala	Leu
Gly	Leu	Leu	Glu	Glu 35	Val	Asp	Leu 40	Glu	Lys	Phe	Ile	Pro 45	Ser	Leu	Glu
Lys	Ser 50	Pro	Thr	Pro	Ile	Thr 55	Thr	Gly	Thr	Thr	Ser 60	Lys	Ile	Ser	Ala
Asp 65	Gly	Ile	Glu	Ile	Val 70	Gly	Glu	Leu	Ser	Ser 75	Glu	Thr	Ile	Leu	Ala 80
Asp	Pro	Asn	Lys	Ala 85	Ala	Ala	Gln	Val	Phe 90	Gly	Glu	Gly	Leu	Ala 95	Asp
Ser	Phe	Asp	Asp	Trp 100	Leu	Arg	Leu	Ser 105	Glu	Asn	Gly	Gly	Ile 110	Gln	Asp
Pro	Thr	Ala	Ile	Glu 115	Glu	Glu	Ile 120	Val	Thr	Lys	Tyr	Gln 125	Thr	Glu	Leu
Asn	Thr 130	Leu	Arg	Asn	Lys	Leu 135	Lys	Gln	Gln	Ser	Leu 140	Thr	Asp	Asp	Glu
Tyr 145	Thr	Lys	Leu	Tyr	Ala 150	Ile	Pro	Gln	Asn	Phe 155	Val	Lys	Glu	Ile	Glu 160
Ser	Leu	Lys	Asn	Glu 165	Asn	Asn	Val	Arg	Leu 170	Ile	Pro	Lys	Ser	Lys 175	Val
Thr	Asn	Phe	Trp 180	Gln	Asn	Ile	Met	Leu 185	Thr	Tyr	Asn	Ser	Val 190	Thr	Ser
Leu	Ser	Glu	Pro	Val 195	Ala	Asp	Ala 200	Met	Asn	Thr	Thr	Met 205	Thr	Glu	Tyr
Ser	Leu 210	Tyr	Ile	Glu	Arg	Ala 215	Thr	Glu	Ala	Ala	Lys 220	Leu	Ile	Arg	Glu
Ile 225	Thr	Asn	Thr	Ile	Lys 230	Asp	Ile	Phe	Asn	Pro 235	Val	Trp	Asp	Val	Arg 240
Glu	Gln	Thr	Gly	Ile 245	Phe	Arg	Leu	Lys	Gly 250	Ala	Glu	Tyr	Asn	Ala 255	Leu
Glu	Gly	Asn	Met 260	Ile	Gln	Ser	Leu	Leu 265	Ser	Phe	Ala	Gly	Leu 270	Phe	Arg
Gln	Leu	Met	Ser 275	Arg	Thr	Ala	Thr 280	Val	Asp	Glu	Ile	Gly	Ala 285	Leu	Tyr
Pro	Lys 290	Asn	Asp	Lys	Asn	Glu 295	Asp	Val	Ile	His	Thr 300	Ala	Ile	Asp	Asp
Tyr 305	Val	Asn	Ser	Leu	Ala 310	Asp	Leu	Lys	Ala	Asn	Glu 315	Gln	Val	Lys	Leu 320
Asn	Gly	Leu	Leu	Ser 325	Leu	Val	Tyr	Ala	Tyr 330	Tyr	Ala	Ser	Thr	Leu 335	Gly
Phe	Ala	Lys	Lys 340	Asp	Val	Phe	Asn	Asn 345	Ala	Gln	Ala	Ser	Phe 350	Thr	Asp
Tyr	Thr	Asn	Phe 355	Leu	Asn	Gln	Glu 360	Ile	Gln	Tyr	Trp	Arg	Pro 365	Arg	Glu
Thr	Ser 370	Ser	Phe	Asn	Ile	Ser 375	Asn	Gln	Ala	Leu	Arg 380	Thr	Phe	Lys	Asn
Lys 385	Pro	Ser	Val	Ile	Ile 390	Thr	Ala	Tyr	Ile	Phe 395	Leu	Ile	Ile	Lys	Asp 400

Met	Thr	Gly	Asp	Trp	Ile	Ser	Lys	Ile	Thr	His	Ser	Gly	Leu	Lys	Ser
1				5					10					15	
Trp	Ile	Glu	Glu	Val	Ile	Ala	Leu	Val	Ser	Pro	Asp	Asp	Val	Arg	Leu
		20						25					30		
Cys	Asp	Gly	Ser	Glu	Ala	Glu	Tyr	Gln	Gln	Leu	Cys	Gln	Gln	Met	Gln
		35					40					45			
Asp	Ala	Gly	Val	Met	Thr	Pro	Leu	Asn	Pro	Glu	Leu	His	Pro	Asn	Cys
	50					55					60				
Phe	Leu	Val	Arg	Ser	Ser	Pro	Ser	Asp	Val	Ala	Arg	Ala	Glu	Gln	Phe
65					70					75					80
Thr	Phe	Ile	Cys	Thr	Lys	Thr	Gln	Glu	Glu	Ala	Gly	Pro	Thr	Asn	Asn
			85						90					95	
Trp	Arg	Asp	Pro	Gln	Glu	Met	Arg	Ala	Glu	Leu	His	Ala	Leu	Phe	Arg
			100					105					110		
Gly	Cys	Met	Arg	Gly	Arg	Thr	Leu	Tyr	Ile	Val	Pro	Phe	Cys	Met	Gly
		115					120					125			
Pro	Leu	Asn	Ser	Pro	Phe	Ser	Leu	Ile	Gly	Val	Glu	Ile	Thr	Asp	Ser
	130					135					140				
Pro	Tyr	Val	Val	Cys	Ser	Met	Lys	Ile	Met	Thr	Arg	Met	Gly	Ala	Ser
145					150					155					160
Val	Leu	Ala	Met	Leu	Gly	Ser	Asn	Gly	Thr	Phe	Tyr	Lys	Cys	Leu	His
			165						170					175	
Ser	Val	Gly	Lys	Pro	Leu	Ala	Pro	Gly	Glu	Lys	Asp	Val	Ala	Trp	Pro
			180					185					190		
Cys	Asp	Pro	Glu	His	Met	Arg	Ile	Val	His	Phe	Gln	Asp	Asp	Ser	Ser
		195					200					205			
Val	Met	Ser	Phe	Gly	Ser	Gly	Tyr	Gly	Gly	Asn	Ala	Leu	Leu	Gly	Lys
	210					215					220				
Lys	Cys	Xaa	Thr	Leu	Arg	Leu	Ala	Ser	Tyr	Leu	Gly	His	Gln	Gln	Gly
225					230					235					240
Trp	Leu	Ala	Glu	His	Met	Leu	Ile	Ile	Gly	Val	Thr	Asn	Pro	Glu	Gly
			245						250					255	
Arg	Lys	Lys	Tyr	Phe	Ala	Ala	Ala	Phe	Pro	Ser	Ala	Cys	Gly	Lys	Thr
			260					265					270		
Asn	Leu	Ala	Met	Leu	Met	Pro	Lys	Leu	Pro	Gly	Trp	Lys	Val	Glu	Cys
		275					280					285			
Ile	Gly	Asp	Asp	Ile	Ala	Trp	Ile	Arg	Pro	Gly	Asn	Asp	Gly	Arg	Leu
	290					295					300				
Tyr	Ala	Val	Asn	Pro	Glu	Phe	Gly	Phe	Phe	Gly	Val	Ala	Leu	Gly	Thr
305					310					315					320
Ser	Glu	Thr	Thr	Asn	Pro	His	Ala	Leu	Ala	Thr	Cys	His	Ala	Asp	Ser
			325						330					335	
Leu	Phe	Thr	Asn	Val	Ala	Leu	Thr	Ala	Asp	Gly	Asp	Val	Trp	Trp	Glu
			340					345					350		

Gly	Lys	Thr	Thr	Thr	Pro	Pro	Gln	Gly	Met	Ile	Asp	Trp	Lys	Gly	Arg
		355					360					365			
Ala	Trp	Val	Ser	Gly	Gly	Glu	Pro	Ala	Ala	His	Pro	Asn	Ala	Arg	Phe
	370					375					380				
Thr	Ala	Pro	Leu	Asp	His	Cys	Pro	Ser	Leu	Asp	Pro	Gln	Trp	Asn	Asn
385					390					395					400
Pro	Gln	Gly	Val	Pro	Leu	Glu	Ala	Val	Ile	Phe	Gly	Gly	Arg	Arg	Thr
				405					410					415	
Glu	Thr	Ile	Pro	Leu	Val	Tyr	Glu	Ala	Leu	Ser	Trp	Glu	His	Gly	Val
			420				425						430		
Met	Met	Gly	Ala	Gly	Met	Ser	Ser	Thr	Thr	Thr	Ala	Ala	Ile	Val	Gly
		435					440					445			
Glu	Leu	Gly	Lys	Leu	Arg	His	Asp	Pro	Phe	Ala	Met	Leu	Pro	Phe	Cys
	450					455					460				
Gly	Tyr	Asn	Met	Ala	Ala	Tyr	Phe	Glu	His	Trp	Leu	Ser	Phe	Ala	Thr
465					470					475					480
Lys	Gly	Leu	Gln	Leu	Pro	Arg	Ile	Phe	Gly	Val	Asn	Trp	Phe	Arg	Lys
			485						490					495	
Asp	Glu	His	Gly	Gln	Phe	Ile	Trp	Pro	Gly	Phe	Ser	Glu	Asn	Leu	Arg
			500					505					510		
Val	Leu	Glu	Trp	Ile	Phe	Arg	Arg	Thr	Asp	Gly	Glu	Asp	Ala	Ile	Ala
		515					520					525			
His	Arg	Thr	Pro	Val	Xaa	Tyr	Leu	Pro	Thr	Ala	Glu	Gly	Leu	Asn	Thr
	530					535					540				
Ser	Gly	Leu	Asp	Leu	Ser	Glu	Asp	Ala	Leu	Arg	Ala	Leu	Leu	Thr	Val
545					550					555					560
Asp	Ala	Gln	Gly	Trp	Lys	Ala	Glu	Val	Ser	Asn	Ile	Arg	Lys	Tyr	Cys
			565					570						575	
Ser	Ile	Phe	Gly	Ala	Asp	Met	Pro	Gln	Arg	Ile	Leu	Glu	Glu	Leu	Ser
			580					585					590		
Arg	Ile	Glu	Ser	Glu	Leu	Lys									
		595													

(2) INFORMATIONS POUR LA SEQ ID NO: 701:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(693837..694853)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 701:

Val	Phe	Asn	Phe	Phe	Ser	Gly	Asn	Val	Gly	Ile	Asp	Leu	Gly	Thr	Ala
1			5						10					15	
Asn	Thr	Leu	Val	Tyr	Val	Arg	Gly	Arg	Gly	Ile	Val	Leu	Ser	Glu	Pro
		20					25					30			
Ser	Val	Val	Ala	Val	Asp	Ala	Gln	Thr	His	Ala	Val	Leu	Ala	Val	Gly
		35				40						45			
His	Lys	Ala	Lys	Ala	Met	Leu	Gly	Lys	Thr	Pro	Arg	Lys	Ile	Val	Ala
	50				55					60					
Val	Arg	Pro	Met	Lys	Asp	Gly	Val	Ile	Ala	Asp	Phe	Glu	Ile	Ala	Glu
65				70					75					80	
Gly	Met	Leu	Lys	Ala	Leu	Ile	Lys	Arg	Val	Thr	Pro	Ala	Arg	Ser	Met

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      85      90      95
Phe Arg Pro Lys Ile Leu Ile Ala Val Pro Ser Gly Ile Thr Gly Val
      100      105      110
Glu Lys Arg Ala Val Glu Asp Ser Ala Leu His Ala Gly Ala Gln Glu
      115      120      125
Val Ile Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Val Asp Leu
      130      135      140
Pro Val His Glu Pro Ala Ala Ser Met Ile Ile Asp Ile Gly Gly Gly
145      150      155      160
Thr Thr Glu Ile Ala Ile Ile Ser Leu Gly Gly Ile Val Glu Ser Arg
      165      170      175
Ser Leu Arg Ile Ala Gly Asp Glu Phe Asp Glu Cys Ile Ile Asn Tyr
      180      185      190
Met Arg Arg Thr Tyr Asn Leu Met Ile Gly Pro Arg Thr Ala Glu Glu
      195      200      205
Ile Lys Ile Thr Ile Gly Ser Ala Tyr Pro Leu Gly Asp Gln Glu Leu
      210      215      220
Glu Met Glu Val Arg Gly Arg Asp Gln Val Ala Gly Leu Pro Ile Thr
225      230      235      240
Lys Arg Ile Asn Ser Val Glu Ile Arg Glu Cys Leu Ala Glu Pro Ile
      245      250      255
Gln Gln Ile Ile Glu Cys Val Arg Leu Thr Leu Glu Lys Cys Pro Pro
      260      265      270
Glu Leu Ser Ala Asp Leu Val Glu Arg Gly Met Val Leu Ala Gly Gly
      275      280      285
Gly Ala Leu Ile Lys Gly Leu Asp Lys Ala Leu Ser Lys Asn Thr Gly
      290      295      300
Leu Ser Val Ile Thr Ala Pro His Pro Leu Leu Ala Val Cys Leu Gly
305      310      315      320
Thr Gly Lys Ala Leu Glu His Leu Asp Gln Leu Lys Lys Arg Lys Glu
      325      330      335
Ser Leu Val

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(2) INFORMATIONS POUR LA SEQ ID NO: 702:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 774 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(694942..697263)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 702:

```

Tyr Ser Tyr Pro Gly Ser Ser Val Trp Phe Leu Leu Arg Glu Arg Phe
1      5      10      15
Ala Ser Ile Pro Lys Phe Ile Ala Glu Leu Ser Asn Val Glu Ala Leu
      20      25      30
Asn Val Phe Ser Thr Leu Pro Tyr Thr Glu Glu Leu Gln Gly Val Cys
      35      40      45
Asp Ile Ser Tyr Leu Asp Gly Glu Leu Glu Ala Arg Leu Phe Phe Leu
      50      55      60
Tyr Asp Gly Gln Lys Val Pro Ala Thr Ser Phe Ser Leu Gln Tyr Gln
65      70      75      80

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Glu	Val	Arg	Thr	Phe	Val	Arg	Pro	Asp	Gly	Ile	Leu	Ala	Arg	Asn	Leu
				85					90					95	
Val	Glu	Glu	Arg	Lys	Ile	Leu	Glu	Glu	Val	Phe	Ser	Gly	Phe	Val	Tyr
			100					105					110		
Asp	Glu	Arg	Asp	Gly	Ala	Phe	His	Val	Lys	Ser	Glu	Lys	Lys	Ile	Val
			115				120					125			
Glu	Phe	Met	Thr	Glu	Thr	Ile	Pro	Asn	Asn	Gln	His	Arg	Ile	Thr	Phe
			130			135					140				
Asn	Cys	Pro	Glu	Thr	Leu	Ser	Asp	Gln	Phe	Ile	Tyr	Asp	Glu	Thr	Val
145					150					155					160
Phe	Asp	Leu	Ile	Phe	Arg	Ala	Gly	Glu	Asp	Ile	Asn	Tyr	Tyr	Glu	Ala
				165					170						175
Glu	Leu	Lys	Val	His	Gly	Leu	Leu	Lys	Gly	Ile	Ser	Leu	Asp	Leu	Leu
			180					185					190		
Trp	Asp	Cys	Val	Ser	Ala	Lys	Lys	Arg	Phe	Leu	Glu	Leu	Pro	Lys	Lys
			195				200					205			
Gly	Gly	Gln	Leu	Lys	Lys	Ala	Arg	Arg	Gly	Lys	Ala	Ser	Ala	Ser	Lys
			210			215					220				
Leu	Pro	Cys	Ile	Leu	Val	Leu	Asp	Leu	Glu	Lys	Ile	Ala	Pro	Val	Ile
225					230					235					240
Gln	Ile	Phe	Asn	Glu	Ile	Gly	Phe	Gln	Val	Leu	Asp	Asp	Phe	Val	Asp
				245					250					255	
Gln	Cys	Pro	Leu	Trp	Ser	Leu	Ser	Gly	Ile	Ser	Pro	Glu	Ser	Phe	Lys
			260					265					270		
Asp	Leu	Pro	Val	Asn	Phe	Ser	Met	Thr	Glu	Asp	Leu	Ala	Glu	Ile	Gln
			275				280					285			
Lys	Gln	Ile	Arg	Gly	Glu	Val	Asp	Phe	Glu	Phe	Gln	Glu	Val	Pro	Ser
			290			295					300				
Gln	Ile	Gln	Ala	Thr	Leu	Arg	Gly	Tyr	Gln	Lys	Glu	Gly	Val	His	Trp
305					310					315					320
Leu	Glu	Arg	Leu	Arg	Lys	Met	His	Leu	Asn	Gly	Ile	Leu	Ala	Asp	Asp
				325					330					335	
Met	Gly	Leu	Gly	Lys	Thr	Leu	Gln	Thr	Ile	Ile	Ala	Val	Thr	Gln	Ser
			340					345					350		
Arg	Leu	Glu	Lys	Gly	Gly	Gly	Cys	Ser	Leu	Ile	Ile	Cys	Pro	Thr	Ser
			355				360					365			
Leu	Val	Tyr	Asn	Trp	Lys	Glu	Glu	Phe	Arg	Lys	Phe	Asn	Pro	Glu	Phe
			370			375					380				
Lys	Thr	Leu	Val	Val	Asp	Gly	Ile	Pro	Ser	Gln	Arg	Arg	Lys	Gln	Leu
385					390					395					400
Ala	Ser	Leu	Glu	Glu	Tyr	Asp	Val	Ala	Ile	Thr	Ser	Tyr	Asn	Leu	Leu
				405					410					415	
Gln	Lys	Asp	Ile	Asp	Ile	Tyr	Lys	Asp	Phe	Leu	Phe	Asp	Tyr	Val	Val
			420					425					430		
Leu	Asp	Glu	Ala	His	His	Ile	Lys	Asn	Arg	Thr	Thr	Arg	Asn	Ala	Lys
			435				440					445			
Ser	Val	Lys	Met	Ile	Arg	Ala	Cys	His	Arg	Leu	Ile	Leu	Thr	Gly	Thr
			450			455					460				
Pro	Ile	Glu	Asn	Ser	Leu	Glu	Glu	Leu	Trp	Ser	Leu	Phe	Asp	Phe	Leu
465					470					475					480
Met	Pro	Gly	Leu	Leu	Ser	Ser	Tyr	Asp	Arg	Phe	Val	Gly	Lys	Tyr	Ile
				485					490					495	
Arg	Ile	Gly	Asn	Tyr	Met	Gly	Asn	Lys	Ala	Asp	Asn	Val	Glu	Ala	Leu
			500					505					510		
Arg	Arg	Lys	Val	Ala	Pro	Phe	Ile	Leu	Arg	Arg	Met	Lys	Glu	Asp	Val
			515				520					525			
Leu	Glu	Asp	Leu	Pro	Pro	Val	Ser	Glu	Ile	Leu	Tyr	His	Cys	His	Leu
			530			535					540				
Thr	Glu	Ser	Gln	Arg	Glu	Leu	Tyr	Gln	Ser	Tyr	Ala	Ala	Ser	Ala	Arg

```

545          550          555          560
Gln Glu Leu Ser Arg Leu Val Lys Gln Glu Gly Phe Glu Arg Ile His
          565          570          575
Ile His Val Leu Ala Thr Leu Thr Arg Leu Lys Gln Ile Cys Cys His
          580          585          590
Pro Ala Ile Phe Ala Lys Asp Thr Pro Glu Pro Gly Asp Ser Ala Lys
          595          600          605
Tyr Asp Met Leu Met Asp Leu Leu Ser Ser Leu Val Asp Ser Gly His
          610          615          620
Lys Thr Val Val Phe Ser Gln Tyr Thr Lys Met Leu Gly Ile Ile Arg
625          630          635          640
Gln Asp Leu Glu Ala Lys Gly Ile Pro Phe Val Tyr Leu Asp Gly Ser
          645          650          655
Thr Lys Asn Arg Leu Glu Ile Val Gln Gln Phe Asn Glu Asp Pro Gly
          660          665          670
Leu Leu Val Phe Leu Val Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn
          675          680          685
Leu Val Gly Ala Asp Thr Val Ile His Tyr Asp Met Trp Trp Asn Pro
          690          695          700
Ala Val Glu Asn Gln Ala Thr Asp Arg Val His Arg Ile Gly Gln Ser
705          710          715          720
Arg Ser Val Ser Ser Tyr Lys Leu Val Thr Leu Asn Thr Ile Glu Glu
          725          730          735
Lys Ile Leu Ser Leu Gln Asn Arg Lys Lys Gly Leu Val Lys Lys Val
          740          745          750
Ile Asn Ser Asp Asp Glu Val Val Ser Lys Leu Thr Trp Glu Glu Val
          755          760          765
Leu Glu Leu Leu Gln Ile
          770

```

(2) INFORMATIONS POUR LA SEQ ID NO: 703:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 305 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(697170..698084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 703:

```

Gly Ile Thr Arg Asp Phe Cys Arg Cys Ser Asp Ser Arg Gly Gly Thr
1          5          10          15
Lys Arg Ser Gly Thr Pro Lys Arg Asn Leu Arg Glu Tyr Asn His Ala
          20          25          30
Ala Asn Val Leu Ser Glu Asn Pro Phe Phe Leu Pro Leu Glu Tyr Ser
          35          40          45
Glu Lys Asp Ser Ala Gly Leu Ala Val Leu Phe Val Pro Gln Lys Asn
          50          55          60
Glu Gly Glu Val Phe Ser Pro Asn Gln Pro Ile Glu Phe Gln Leu Val
65          70          75          80
Leu Arg Leu Pro Gly Arg Ser Lys Pro Phe Tyr Ile Ser Asn Ile Lys
          85          90          95
Thr Phe Leu Glu Gly Val Leu Tyr Gln Glu Pro Ile Val Phe Ser Gly
          100          105          110

```

```

Arg Arg Phe Phe Thr Leu Gln Ser Phe Ser Ala Ser Asp Arg Lys
      115      120      125
Leu Ile Asp Leu Leu Ile Arg Tyr Ala Arg Tyr Ala Thr Gly Ser Ser
      130      135      140
Glu Glu Lys Leu Leu Lys Ser Ala Phe Leu Thr Pro Ala Ser Leu Gly
145      150      155      160
Met Ile Leu Ser Lys Met Phe Glu His Gln Met Ala Glu Ser Gly Gly
      165      170      175
Ser Gln Leu Gly Glu Arg Glu Cys Phe Gln Gly Ile Phe Cys Gly Asn
      180      185      190
Leu Glu Glu Pro Leu Leu Trp Ser Val Ser Pro Ala Lys Met Lys Phe
      195      200      205
His Leu Asp Tyr Phe Asp Thr Pro Tyr Lys Ala Leu Leu Met Lys Pro
      210      215      220
Leu Ile Val Val Asp Glu Glu Glu Leu Gln Pro Glu Gln Ala Val Leu
225      230      235      240
Leu Glu Ser Asn Tyr Pro Gly Ile Ile His Lys Asn Val Tyr His His
      245      250      255
Phe Leu Pro Gln Ile Lys Arg Ala His Leu Arg Thr Phe Ala Gly Leu
      260      265      270
Arg Asp Ile Ala Ile Pro Glu Ala Leu Phe Gly Ser Phe Cys Glu Asn
      275      280      285
Ala Leu Pro Val Phe Arg Asn Leu Leu Arg Asn Cys Pro Met Ser Arg
      290      295      300
Leu
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 704:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(697979..698392)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 704:

```

His Thr Xaa Arg Leu Glu Lys Ser Tyr Phe Ala Gln Gly Ala Val Val
1      5      -      10      15
Ser Ala Lys Ile Leu Ser Met Asn Gly Glu Thr Val Cys Ile Ser Ala
      20      25      30
Gln Ile Arg Gly Ser Tyr Asp Asn Val Tyr Glu Cys Glu Ile Glu Val
      35      40      45
Asp Arg Ala Glu Ser Asp Thr Val Asp Ser Asn Cys Asp Cys Ser Tyr
      50      55      60
Asn Tyr Asp Cys Gln His Val Val Ala Leu Leu Phe Tyr Leu Glu Gln
65      70      75      80
Tyr Phe Asn Glu Met Val Val Thr Tyr Ser Lys Glu Ala Asp Leu Ser
      85      90      95
Ser Asn Glu Glu Val Ser Lys Glu Leu Gln Glu Thr Phe Val Val Ala
      100      105      110
Ala Ile Arg Glu Glu Glu Arg Arg Asp Arg Glu His Gln Lys Glu Ile
      115      120      125
Phe Gly Asn Thr Ile Met Leu Leu Met Phe

```

130

135

(2) INFORMATIONS POUR LA SEQ ID NO: 705:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 432 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 698822..700117

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 705:

Phe	Ser	Ile	Asn	Ile	Glu	Glu	Asn	Ala	Gly	Cys	Val	Val	Ser	Ala	Lys
1				5					10					15	
Val	Gln	Ala	Asn	Pro	Leu	Val	Thr	Gln	Lys	Cys	His	Lys	Glu	Ala	Leu
			20					25					30		
Lys	Thr	Val	Lys	Lys	Asn	Val	Val	Leu	Pro	Gly	Phe	Arg	Lys	Gly	Lys
		35					40					45			
Ala	Pro	Asp	Asn	Ile	Val	Glu	Ser	Arg	Tyr	Ser	Thr	Gln	Val	Glu	Gln
	50					55					60				
Glu	Leu	Arg	Arg	Leu	Phe	Leu	Arg	Ala	Ser	Phe	Glu	Ala	Leu	Ser	Gln
65					70					75					80
Met	Cys	Asp	Arg	Lys	Pro	Leu	Ser	Pro	Lys	Ala	Val	Arg	Ser	Ser	Ala
				85					90					95	
Ile	Asp	Thr	Cys	Asn	Pro	Val	Asn	Gly	Gly	Ser	Val	Ser	Phe	Leu	Tyr
			100					105					110		
Glu	Ala	Phe	Pro	Val	Ile	Pro	Ser	Leu	Pro	Trp	Glu	Gln	Leu	Ser	Leu
		115					120					125			
Pro	Asp	Pro	Glu	Pro	Val	Lys	Glu	Ile	Ser	Glu	Glu	Asp	Leu	Glu	Asn
	130					135					140				
Gly	Leu	Lys	Asn	Val	Ala	Tyr	Phe	Phe	Ala	Thr	Lys	Thr	Pro	Val	Thr
145					150					155					160
Arg	Pro	Ser	Gln	Glu	Gly	Asp	Phe	Ile	Ser	Leu	Ser	Leu	Tyr	Val	Ser
				165					170					175	
Lys	Arg	Gly	Asp	Glu	Asn	Ser	Thr	Pro	Val	Ala	Ile	Phe	Glu	Asn	Lys
			180					185					190		
Tyr	Phe	Lys	Ile	Ser	Glu	Glu	Asp	Met	Thr	Asp	Ser	Phe	Lys	Ala	Arg
		195					200					205			
Phe	Leu	Asn	Val	Ser	Thr	Gly	His	Arg	Val	Glu	Glu	Glu	Ile	Gly	Ser
	210					215					220				
Glu	Asp	Ile	Gln	Ser	Phe	Leu	Asn	Gly	Asp	Leu	Leu	Thr	Phe	Thr	Val
225					230					235					240
Asn	Ala	Val	Ile	Glu	Ile	Ser	Ser	Pro	Glu	Met	Asp	Asp	Glu	Lys	Ala
				245					250					255	
Arg	Glu	Leu	Gln	Ala	Glu	Ser	Leu	Glu	Asp	Leu	Lys	Lys	Lys	Leu	Arg
			260					265					270		
Ile	Gln	Leu	Glu	Asn	Gln	Ala	Lys	Glu	Ala	Gln	His	Gln	Lys	Arg	Phe
		275					280					285			
Ser	Asp	Ala	Glu	Asp	Ala	Leu	Ala	Gln	Leu	Ile	Asp	Phe	Asp	Leu	Pro
	290					295					300				
Glu	Ser	Leu	Leu	Arg	Glu	Arg	Glu	Glu	Leu	Leu	Ser	Arg	Glu	Lys	Leu
305					310					315					320
Leu	Asn	Ala	Arg	Leu	Val	Lys	Tyr	Cys	Ser	Asp	Ser	Glu	Leu	Glu	Glu
				325					330					335	

Gln	Lys	Gln	Ala	Leu	Leu	Glu	Glu	Ala	Lys	Ala	Asp	Ala	Arg	Lys	Ala
			340					345					350		
Val	Lys	Leu	Leu	Phe	Leu	Thr	Gln	Lys	Val	Phe	Ser	Glu	Lys	Gly	Leu
		355					360					365			
Ser	Ile	Ser	Arg	Glu	Glu	Leu	Gln	Tyr	Met	Met	Asp	Val	Cys	Ser	Arg
	370					375					380				
Glu	Arg	Phe	Gly	Gly	Tyr	Pro	Pro	Lys	Asp	Ile	Ser	Asn	Glu	Met	Ile
385					390					395					400
Gln	Glu	Leu	Val	Leu	Val	Ala	Arg	Asp	Arg	Leu	Thr	Tyr	Arg	Lys	Ala
			405					410						415	
Ile	Glu	Ala	Ile	Ser	Ser	Glu	Lys	Lys	Asp	Leu	Glu	Val	Val	Pro	Ser
			420					425					430		

(2) INFORMATIONS POUR LA SEQ ID NO: 706:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 700287..700895

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 706:

Met	Thr	Leu	Val	Pro	Tyr	Val	Val	Glu	Asp	Thr	Gly	Arg	Gly	Glu	Arg
1			5					10					15		
Ala	Met	Asp	Ile	Tyr	Ser	Arg	Leu	Leu	Lys	Asp	Arg	Ile	Val	Met	Ile
		20					25					30			
Gly	Gln	Glu	Ile	Thr	Glu	Pro	Leu	Ala	Asn	Thr	Val	Ile	Ala	Gln	Leu
	35						40				45				
Leu	Phe	Leu	Met	Ser	Glu	Asp	Pro	Thr	Lys	Asp	Ile	Gln	Ile	Phe	Ile
	50					55				60					
Asn	Ser	Pro	Gly	Gly	Tyr	Ile	Thr	Ala	Gly	Leu	Ala	Ile	Tyr	Asp	Thr
65				70					75					80	
Ile	Arg	Phe	Leu	Gly	Cys	Asp	Val	Asn	Thr	Tyr	Cys	Ile	Gly	Gln	Ala
			85					90					95		
Ala	Ser	Met	Gly	Ala	Leu	Leu	Leu	Ser	Ala	Gly	Thr	Lys	Gly	Lys	Arg
		100						105					110		
Tyr	Ala	Leu	Pro	His	Ser	Arg	Met	Met	Ile	His	Gln	Pro	Ser	Gly	Gly
	115						120					125			
Ile	Ile	Gly	Thr	Ser	Ala	Asp	Ile	Gln	Leu	Gln	Ala	Ala	Glu	Ile	Leu
	130					135					140				
Thr	Leu	Lys	Lys	His	Leu	Ser	Asn	Ile	Leu	Ala	Glu	Cys	Thr	Gly	Gln
145				150						155					160
Ser	Val	Glu	Lys	Ile	Ile	Glu	Asp	Ser	Glu	Arg	Asp	Phe	Phe	Met	Gly
			165					170						175	
Ala	Glu	Glu	Ala	Ile	Ala	Tyr	Gly	Leu	Ile	Asp	Lys	Val	Ile	Ser	Ser
			180					185					190		
Ala	Lys	Glu	Thr	Lys	Asp	Lys	Ser	Ile	Ala	Ser					
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 707:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 418 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 700912..702165

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 707:

Gln	Lys	Lys	Asn	Leu	Ala	Val	Cys	Ser	Phe	Cys	Gly	Arg	Ser	Glu	Lys	1	5	10	15
Asp	Val	Glu	Lys	Leu	Ile	Ala	Gly	Pro	Ser	Val	Tyr	Ile	Cys	Asp	Tyr	20	25	30	
Cys	Ile	Lys	Leu	Cys	Ser	Gly	Ile	Leu	Asp	Lys	Thr	Pro	Ala	Pro	Ala	35	40	45	
Thr	Gln	Glu	Ile	Ala	Thr	Ser	Ser	Thr	Ser	Ser	Pro	Thr	Ser	Leu	Arg	50	55	60	
Val	Leu	Thr	Pro	Lys	Glu	Ile	Lys	Arg	His	Ile	Asp	Ser	Tyr	Val	Ile	65	70	75	80
Gly	Gln	Glu	Arg	Ala	Lys	Lys	Thr	Ile	Ser	Val	Ala	Val	Tyr	Asn	His	85	90	95	
Tyr	Lys	Arg	Ile	Arg	Ala	Leu	Met	Gln	Asp	Lys	Gln	Val	Ser	Tyr	Gly	100	105	110	
Lys	Ser	Asn	Val	Leu	Leu	Leu	Gly	Pro	Thr	Gly	Xaa	Gly	Lys	Thr	Leu	115	120	125	
Ile	Ala	Lys	Thr	Leu	Ala	Lys	Ile	Leu	Asp	Val	Pro	Phe	Thr	Ile	Ala	130	135	140	
Asp	Ala	Thr	Thr	Leu	Thr	Glu	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Val	Glu	145	150	155	160
Asn	Ile	Val	Leu	Arg	Leu	Leu	Gln	Ala	Ala	Asp	Tyr	Asp	Val	Ala	Arg	165	170	175	
Ala	Glu	Arg	Gly	Ile	Ile	Tyr	Ile	Asp	Glu	Ile	Asp	Lys	Ile	Gly	Arg	180	185	190	
Thr	Thr	Ala	Asn	Val	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	195	200	205	
Gln	Gln	Ala	Leu	Leu	Lys	Ile	Ile	Glu	Gly	Thr	Val	Ala	Asn	Ile	Pro	210	215	220	
Pro	Lys	Gly	Gly	Arg	Lys	His	Pro	Asn	Gln	Glu	Tyr	Ile	Arg	Val	Asn	225	230	235	240
Thr	Glu	Asn	Ile	Leu	Phe	Ile	Val	Gly	Gly	Ala	Phe	Val	Asn	Leu	Asp	245	250	255	
Lys	Ile	Ile	Ala	Lys	Arg	Leu	Gly	Arg	Thr	Thr	Ile	Gly	Phe	Ser	Glu	260	265	270	
Glu	Thr	Asp	Leu	Ala	Val	Thr	Asn	Arg	Asp	His	Leu	Leu	Ala	Lys	Val	275	280	285	
Glu	Thr	Glu	Asp	Leu	Ile	Thr	Phe	Gly	Met	Ile	Pro	Glu	Phe	Ile	Gly	290	295	300	
Arg	Phe	Asn	Cys	Ile	Val	Asn	Cys	Glu	Glu	Leu	Thr	Leu	Asp	Glu	Leu	305	310	315	320
Val	Glu	Ile	Leu	Thr	Glu	Pro	Ala	Asn	Ala	Ile	Xaa	Lys	Gln	Tyr	Arg	325	330	335	
Glu	Leu	Phe	Glu	Glu	Glu	Asn	Val	Lys	Leu	Ile	Phe	Glu	Lys	Glu	Ala	340	345	350	
Leu	Tyr	Ala	Ile	Ala	Gln	Lys	Ala	Lys	Gln	Ala	Lys	Thr	Gly	Ala	Arg	355	360	365	
Ala	Leu	Gly	Met	Ile	Leu	Glu	Asn	Leu	Leu	Arg	Asp	Leu	Met	Phe	Glu	370	375	380	

Ile Pro Ser Asp Pro Thr Val Glu Ala Ile Arg Ile Glu Glu Asp Thr  
 385 390 395 400  
 Ile Thr Gln Asn Lys Pro Pro Val Ile Ile Gln Lys Ser Pro Glu Ala  
 405 410 415  
 Ile Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 708:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 410 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 702183..703412

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 708:

Met	Thr	Gln	Ser	Thr	Leu	Glu	Val	Ala	Lys	Lys	Ile	Val	Arg	Lys	Leu	1	5	10	15
Arg	Asn	Ala	Gly	Tyr	Gln	Ala	Tyr	Phe	Val	Gly	Gly	Ser	Val	Arg	Asp	20	25	30	
Met	Leu	Leu	Gly	Arg	Pro	Ile	Glu	Glu	Val	Asp	Ile	Ala	Thr	Asn	Ala	35	40	45	
Ser	Pro	Thr	Ile	Val	Thr	Thr	Ile	Phe	Pro	Asp	Thr	Leu	Ser	Ile	Gly	50	55	60	
Ala	Ala	Phe	Gly	Ile	Ile	Ala	Val	Lys	Glu	Asn	Gly	Gln	Leu	Phe	Glu	65	70	75	80
Val	Ala	Thr	Phe	Arg	Ser	Asp	Glu	Asp	Tyr	Glu	Asp	Gly	Arg	His	Pro	85	90	95	
Asn	Arg	Val	Val	Phe	Ala	Ser	Met	Lys	Asp	Asp	Ala	Ile	Arg	Arg	Asp	100	105	110	
Phe	Thr	Ile	Asn	Gly	Met	Tyr	Tyr	Asp	Pro	Phe	Leu	Glu	Lys	Leu	Phe	115	120	125	
Asp	Leu	Val	Glu	Gly	Arg	Ala	Asp	Leu	Glu	Arg	Xaa	Ile	Ile	Arg	Ala	130	135	140	
Ile	Gly	Asn	Pro	Lys	Gln	Arg	Phe	Leu	Glu	Asp	Lys	Leu	Arg	Ile	Leu	145	150	155	160
Arg	Ala	Ile	Arg	Phe	Ala	Ala	Thr	Leu	Gly	Phe	Ala	Leu	Asp	Pro	Gln	165	170	175	
Thr	Glu	Gln	Ala	Ile	Ile	Lys	Glu	Leu	Pro	Ser	Leu	Pro	Asn	Ser	Val	180	185	190	
Ala	Pro	Glu	Arg	Ile	Trp	Gln	Glu	Leu	Lys	Lys	Met	Leu	Arg	Thr	Ala	195	200	205	
Pro	Tyr	Glu	Ser	Leu	Gln	Leu	Leu	Thr	Lys	Leu	Lys	Val	Leu	Pro	Ile	210	215	220	
Leu	Phe	Pro	Glu	Leu	Lys	Val	Ser	Ser	Ser	Gly	Phe	Leu	Arg	Ser	Ala	225	230	235	240
Ile	Ala	Phe	Ala	Gln	Lys	Ile	His	Asp	Ser	Gln	Ile	Pro	Glu	Ile	Ala	245	250	255	
Leu	Leu	Leu	Pro	Leu	Phe	Arg	Glu	Val	Asp	Lys	Glu	Lys	Ala	Leu	Glu	260	265	270	
Ala	Phe	Ser	Arg	Leu	Arg	Val	Ser	Asn	Lys	Glu	Leu	Lys	Leu	Leu	Glu	275	280	285	
Asp	Trp	Tyr	Ala	Ala	Leu	Pro	Gln	Phe	Leu	Ser	Lys	Gln	Asn	Asp	Lys				

```

      290              295              300
Phe Phe Trp Ala His Phe Phe Ala Ser Glu Thr Ser Ser Leu Leu Leu
305              310              315              320
Ser Leu Phe Leu Ser Met Gln Arg Ser Pro Asp Glu Gln Glu Leu Phe
      325              330              335
Ile Ala Arg Ile His Asp Leu Lys Thr Arg Leu Ala Ala Phe Ile Glu
      340              345              350
Arg Ile Gln Ser Gly Ala Pro Leu Val Ser Ala Gln Asp Leu Ile Ala
      355              360              365
Lys Gly Ile Thr Pro Gly Arg Leu Leu Gly Glu Leu Leu Arg Glu Ala
      370              375              380
Glu Ala Leu Ser Ile Glu His Glu Cys Ser Asp Lys Glu Lys Ile Leu
385              390              395              400
Ser Leu Leu Lys Ser Lys Gly Phe Trp Lys
      405              410

```

(2) INFORMATIONS POUR LA SEQ ID NO: 709:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 493 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 703522..705000

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 709:

```

Ser Leu Phe Met Arg Ile Ala Ile Leu Gly Arg Pro Asn Val Gly Lys
1              5              10              15
Ser Ser Leu Phe Asn Arg Leu Cys Arg Arg Ser Leu Ala Ile Val Asn
      20              25              30
Ser Gln Glu Gly Thr Thr Arg Asp Arg Leu Tyr Gly Glu Ile Arg Ala
      35              40              45
Trp Asp Ser Ile Ile His Val Ile Asp Thr Gly Gly Val Asp Gln Glu
50              55              60
Ser Thr Asp Arg Phe Gln Lys Gln Ile His Gln Gln Ala Leu Ala Ala
65              70              75              80
Ala Glu Glu Ala Ser Val Leu Leu Leu Val Val Asp Ile Arg Cys Gly
      85              90              95
Ile Thr Lys Gln Asp Glu Glu Leu Ala Lys Arg Leu Leu Pro Leu Lys
      100              105              110
Lys Pro Leu Ile Leu Val Met Asn Lys Ala Asp Ser Gln Gln Asp Leu
      115              120              125
Gln Arg Ile His Glu Phe Tyr Gly Leu Gly Ile Ser Asp Met Ile Ala
      130              135              140
Thr Ser Ala Ser His Asp Lys His Ile Asp Leu Leu Leu Glu Arg Ile
145              150              155              160
Arg Gln Ile Ala Gln Ile Pro Val Pro Ser Val Glu Glu Gln Asp Val
      165              170              175
Val Gln Glu Asp Glu Leu Pro Ser Glu Glu Ala Ala Ile Ser Leu His
      180              185              190
Ala Phe Ala Asp Glu Thr Leu Phe Glu Asn Glu Ser Leu Ser Gln Glu
      195              200              205
Glu Ala Ser Phe Leu Glu Glu Leu Val Ala Gln Thr Ala Thr Pro Ala
210              215              220

```



```

Pro Val Asp Arg Pro Leu Lys Val Ala Leu Ile Gly His Pro Asn Val
225                230                235                240
Gly Lys Ser Ser Ile Ile Asn Ala Leu Leu Lys Glu Glu Arg Cys Ile
                245                250                255
Thr Asp Asn Ser Pro Gly Thr Thr Arg Asp Asn Ile Asp Val Ala Tyr
                260                265                270
Thr His Asn Asn Lys Glu Tyr Val Phe Ile Asp Thr Ala Gly Leu Arg
                275                280                285
Lys Thr Lys Ser Ile Lys Asn Ser Val Glu Trp Met Ser Ser Ser Arg
290                295                300
Thr Glu Lys Ala Ile Ser Arg Thr Asp Ile Cys Leu Leu Val Ile Asp
305                310                315                320
Ala Thr Gln Gln Leu Ser Tyr Gln Asp Lys Arg Ile Leu Ser Met Ile
                325                330                335
Ala Arg Tyr Lys Lys Pro His Val Ile Leu Val Asn Lys Trp Asp Leu
                340                345                350
Met Phe Gly Val Arg Met Glu His Tyr Val Gln Asp Leu Arg Lys Met
355                360                365
Asp Pro Tyr Ile Gly Gln Ala His Ile Leu Cys Ile Ser Ala Lys Gln
370                375                380
Arg Arg Asn Leu Leu Gln Ile Phe Ser Ala Ile Asp Asp Ile Tyr Thr
385                390                395                400
Ile Ala Thr Thr Lys Leu Ser Thr Ser Leu Val Asn Lys Val Leu Ala
                405                410                415
Ser Ala Met Gln Arg His His Pro Gln Val Ile Asn Gly Lys Arg Leu
                420                425                430
Arg Ile Tyr Tyr Ala Ile His Lys Thr Thr Thr Pro Phe Thr Phe Leu
435                440                445
Leu Phe Ile Asn Ser Asn Ser Leu Leu Thr Lys Pro Tyr Glu Leu Tyr
450                455                460
Leu Lys Asn Thr Leu Lys Ala Ala Phe Asn Leu Tyr Arg Val Pro Phe
465                470                475                480
Asp Leu Glu Tyr Lys Ala Lys Pro Ala Arg Lys Ser Asn
                485                490

```

(2) INFORMATIONS POUR LA SEQ ID NO: 710:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: 705011..705604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 710:

```

Lys Asn Lys Asn Leu Leu Leu Glu Ile Ile Lys Thr Lys Ile Ser Tyr
1          5          10          15
Phe Leu Glu Ile Leu Ile Pro Met His Tyr Glu Pro Tyr Asp Glu Phe
                20                25                30
Glu Pro Asp Asn Glu Leu Asp His Leu Ile Cys Glu Ser Asp Lys Thr
35          40          45
Lys Pro Leu Asp Ala Tyr His Asp Thr Gly Val Tyr Ile Glu Glu Asp
50          55          60
Asp Arg Glu Asn Gly Asp Leu Leu Ile Val Leu Gly Lys Ser Ile Leu

```

```

65          70          75          80
Asn Gly Ala Ile Arg Gln Phe Tyr Ile Ser Asp His Asn Tyr Ala Tyr
      85          90          95
Thr Arg Gly Tyr Tyr Gln Gly Cys Trp Glu Gly Trp Phe Asn Ile Pro
      100        105        110
Pro Lys Lys Ile Thr Thr Ala Glu Tyr Asp Cys Asp Gln Leu Leu Gln
      115        120        125
Pro Asp Leu Leu Leu Thr Thr Asn Val Glu Lys Leu Ile His Ala Pro
      130        135        140
Glu Asp Phe Pro Ala Gln Asn Ala Asn Leu Asp Asn Ile Ile Ile Cys
145      150      155      160
Met Thr Ala Leu Asn Gly Glu His Arg Val Gln Phe Leu Ile Gly Asp
      165      170      175
Asn His Arg Ser Phe Trp Ile Arg His His Asp Gly Glu Ser Trp Ser
      180      185      190
Lys Trp Ser Thr Phe Ile
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 711:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 152 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(705704..706159)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 711:

```

Cys Arg Cys Gly Thr Asp Tyr Ile Gly Asp Leu Leu Ile Glu Ala Phe
1      5      10      15
Asp Val Lys Phe Ser Ala Met Leu Ala Glu Phe Thr Glu Ile Ile Gly
      20      25      30
Ser Ala Ala Asn Ala Gln Gly Ile Cys Asn Asp Ile Leu Arg Ser Val
      35      40      45
Ile Ile Ser His Ile Asp Glu Trp Lys Val His Leu Val Asp Met
      50      55      60
Asp Leu Leu Arg Ser Glu Val Gly Leu Arg Ser Val Gly Gln Lys Asp
65      70      75      80
Pro Leu Ile Glu Phe Lys Asn Glu Ser Phe Leu Leu Phe Glu Gly Leu
      85      90      95
Ile Arg Asp Ile Arg Ile Ala Ile Val Lys His Leu Phe Ala Leu Glu
      100     105     110
Leu Ser Leu Thr Arg Ser Asp Arg Pro Asp Asn Ala Ile Pro Thr Val
      115     120     125
Ala Thr Ala Phe His Asn His Asp Asn Phe Arg Pro Met Glu Leu Thr
130      135      140
Ile Val Gly Glu Glu Glu Glu Ser
145      150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 712:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(706138..706521)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 712:

```

Phe Ala Ile Ser Gly Pro Pro Glu Gly Glu Ala Met Ser Asp Pro Met
1           5           10           15
Phe Asp Arg Leu Ile Glu Thr Ala Gln Lys Arg Val Glu Gly Arg Asn
          20           25           30
Tyr Thr Ile Arg Lys His Thr Leu Glu Tyr Asp Asp Val Met Asn Lys
          35           40           45
Gln Arg Gln Thr Ile Tyr Ala Phe Arg Asn Asp Val Leu His Ala Glu
          50           55           60
Asp Leu Phe Val Val Ala Lys Glu Gln Ile Glu His Val Ala Leu Ala
65           70           75           80
Leu Ala Phe Leu Ile Leu Lys Asp Ala His Ala Asp His Cys Ser Leu
          85           90           95
Pro Lys Ile Glu Glu Trp Leu Ser Tyr Ser Phe Pro Val Lys Leu Asp
          100          105          110
Asp Gln Glu Ile Arg Arg Leu Gly Asp Val Asp Ala Val Gln Thr Thr
          115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 713:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 536 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(706496..708103)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 713:

```

Ser Ala Gly Ser Pro Pro Glu Lys Arg Lys Ala Ile Tyr Gln Cys Asp
1           5           10           15
Val Val Tyr Gly Thr Ala Ser Gly Phe Gly Phe Asp Tyr Leu Arg Asp
          20           25           30
Asn Ser Ile Ala Thr Arg Lys Glu Gln Val Gly Arg Gly Phe Tyr
          35           40           45
Phe Ala Ile Ile Asp Glu Ile Asp Ser Val Leu Ile Asp Glu Ala Arg
          50           55           60
Thr Pro Leu Ile Ile Ser Gly Pro Gly Glu Lys His Asn Pro Val Tyr
65           70           75           80
Phe Glu Leu Lys Asp Arg Val Ala Glu Leu Val Tyr Phe Gln Arg Glu
          85           90           95
Met Cys Asn His Ile Ala Ile Glu Ala Arg Lys Val Leu Asp Pro Phe
          100          105          110
Leu Gly Thr Asp Val Leu Pro Lys Asp Lys Lys Val Met Glu Ala Ile
          115          120          125
Ser Glu Ala Cys Arg Ala Leu Trp Leu Val Ser Lys Gly Met Pro Leu

```

130		135		140
Asn Arg Val Leu Arg Arg Val Arg Glu His Pro Asp Leu Arg Ala Met				
145		150		155
Ile Asp Lys Trp Asp Val Phe Tyr His Ala Glu Gln Asn Lys Glu Glu				160
	165		170	175
Cys Leu Glu Lys Leu Ser Ser Leu Tyr Ile Val Val Asp Glu His Asn				
	180		185	190
Asn Asp Phe Glu Leu Thr Asp Lys Gly Met Leu Gln Trp Ile Glu Lys				
	195	200	205	
Ile Gly Gly Ala Ala Glu Asp Phe Val Met Met Asp Met Gly His Glu				
	210	215	220	
Tyr Ala Leu Ile Glu Glu Asp Ala Thr Leu Ser Pro Ala Asp Lys Leu				
225		230	235	240
Asn Arg Lys Ile Ala Val Ser Glu Lys Asp Thr Gln Arg Lys Ala Arg				
	245	250	255	
Ala His Gly Leu Arg Gln Leu Leu Arg Ala His Leu Leu Met Glu Lys				
	260	265	270	
Asp Ile Asp Tyr Ile Val Arg Asp Asp Gln Ile Val Ile Ile Asp Glu				
	275	280	285	
His Thr Gly Arg Pro Gln Pro Gly Arg Arg Phe Ser Glu Gly Leu His				
	290	295	300	
Gln Ala Ile Glu Ala Lys Glu His Val Thr Ile Arg Lys Glu Ser Gln				
305		310	315	320
Thr Phe Ala Thr Val Thr Leu Gln Asn Phe Phe Arg Leu Tyr Glu Lys				
	325	330	335	
Leu Ala Gly Met Thr Gly Thr Ala Ile Thr Glu Ser Arg Glu Phe Lys				
	340	345	350	
Glu Ile Tyr Ser Leu Tyr Val Leu Gln Val Pro Thr Phe Lys Pro Cys				
	355	360	365	
Leu Arg Ile Asp His Asn Asp Ala Phe Tyr Met Thr Glu Arg Glu Lys				
	370	375	380	
Tyr Gln Ala Ile Val Ala Glu Ile Ile Ser Ala His Arg Ser Gly Lys				
385		390	395	400
Pro Ile Leu Ile Gly Thr Glu Ser Val Glu Val Ser Glu Lys Leu Ser				
	405	410	415	
Arg Ile Leu Arg Gln Asn Arg Ile Asn His Thr Val Leu Asn Ala Lys				
	420	425	430	
Asn His Ala Gln Glu Ala Glu Ile Ile Ala Gly Ala Gly Lys Val Gly				
	435	440	445	
Ala Val Thr Val Ala Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys				
	450	455	460	
Leu Asp Glu Glu Ala Val Ala Ala Gly Gly Leu Tyr Val Ile Gly Thr				
465		470	475	480
Ser Arg His Gln Ser Arg Arg Ile Asp Arg Gln Leu Arg Gly Arg Cys				
	485	490	495	
Ala Arg Leu Gly Asp Pro Gly Ala Ala Lys Phe Phe Leu Ser Phe Glu				
	500	505	510	
Asp Arg Leu Met Arg Leu Phe Ala Ser Pro Lys Leu Asn Thr Leu Ile				
	515	520	525	
Arg His Phe Arg Ser Ser Arg Arg				
530		535		

(2) INFORMATIONS POUR LA SEQ ID NO: 714:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 714:

(2) INFORMATION POUR LA SEQ ID NO: 715:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(708248..708607)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 715:

(2) INFORMATIONN POUR LA SEQ ID NO: 716:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 469 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(708872..710278)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 716:

Glu	Asn	Val	Ser	Leu	His	Lys	Asn	Lys	Asp	Leu	Lys	Arg	Phe	Phe	Trp	1	5	10	15
Tyr	Cys	Lys	Arg	Glu	Lys	Thr	Gln	Lys	Leu	Cys	Ile	Met	Trp	Leu	Ile	20	25	30	
Val	Ala	Trp	Thr	Leu	Leu	Ala	Cys	Leu	Ala	Met	Ala	Leu	Val	Phe	Lys	35	40	45	
Ala	Tyr	Arg	His	Val	Ile	Ser	Phe	Arg	Ser	Tyr	Val	Asn	Gln	Val	Met	50	55	60	
Arg	Asp	Val	Arg	Leu	Ser	Val	Asp	Leu	Lys	Glu	Trp	Ala	Val	Ala	Glu	65	70	75	80
Met	Arg	Leu	Ala	Pro	Ile	Leu	Lys	Lys	Arg	Gln	Tyr	Arg	Arg	Lys	Tyr	85	90	95	
Leu	Phe	Glu	Tyr	Ile	Arg	Ile	Leu	Arg	Glu	Leu	Glu	Arg	Phe	Glu	Glu	100	105	110	
Ala	Glu	Lys	Leu	Leu	Gly	Glu	Ala	Lys	Lys	Leu	Lys	Leu	Ala	Gly	Ala	115	120	125	
His	Phe	Phe	Leu	Glu	Val	Ala	His	Lys	Ala	Phe	Arg	His	Gly	Ala	Tyr	130	135	140	
Lys	Glu	Ala	Ala	His	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Glu	Leu	Met	Gly	145	150	155	160
Glu	Arg	Glu	Val	Ala	Arg	Tyr	Thr	Ile	Ser	Leu	Val	Tyr	Leu	Gly	Glu	165	170	175	
Val	Asp	Ala	Ala	Cys	Arg	Ile	Ile	Glu	Pro	Trp	Ile	Gly	Pro	Leu	Ala	180	185	190	
His	Gln	Glu	Val	Phe	Ile	Ser	Val	Gly	His	Ile	Tyr	Phe	Ala	Thr	Lys	195	200	205	
Arg	Tyr	Ala	Asp	Ala	Ile	Asp	Phe	Tyr	Arg	Arg	Ala	Arg	Ser	Leu	Gly	210	215	220	
Ser	Cys	Pro	Ile	Asp	Val	Leu	Tyr	Asn	Leu	Ala	His	Ser	Leu	Arg	Ile	225	230	235	240
Cys	Gly	Gln	Tyr	Val	Asp	Ala	Gly	Met	Leu	Phe	Arg	Glu	Leu	Leu	Gly	245	250	255	
Asp	Pro	Val	Tyr	Lys	Asp	Glu	Ala	Met	Phe	Asn	Ile	Gly	Leu	Cys	Glu	260	265	270	
Gln	Lys	Leu	Gly	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Ile	Tyr	Gln	Asn	Ser	275	280	285	
Glu	Leu	Trp	Val	Arg	Gly	Asp	Ala	Leu	Met	Met	Arg	Tyr	Ala	Ala	Leu	290	295	300	
Ala	Ala	Ala	Asp	Gln	Gln	Asp	Tyr	Gln	Leu	Ala	Glu	His	Cys	Trp	Thr	305	310	315	320
Leu	Ala	Phe	Arg	Cys	Gln	Ser	Tyr	Ala	Asp	Asp	Trp	Asn	Cys	Cys	Val	325	330	335	
His	Tyr	Gly	Leu	Ala	Leu	Cys	His	Leu	Lys	Lys	Tyr	Ala	Glu	Ala	Glu	340	345	350	
Lys	Val	Tyr	Leu	Arg	Val	Ile	Gln	Lys	Thr	Pro	Asp	Cys	Leu	Val	Ala	355	360	365	
Cys	Lys	Ala	Leu	Ala	Trp	Leu	Ala	Gly	Val	Gly	His	Ala	Thr	Met	Ile	370	375	380	

Ser Ala Arg Glu Gly Ile Ala Tyr Ala Lys Arg Ala Leu Gln Ile Lys  
 385 390 395 400  
 Arg Ser Pro Glu Val Leu Glu Leu Ser Ala Cys Glu Ala Arg Glu  
 405 410 415  
 Gly Asn Phe Asp Val Ala Tyr Asp Ile Gln Ala Ile Leu Ala Glu Arg  
 420 425 430  
 Asp Thr Thr Ala Lys Glu Arg Glu Arg Arg Ser Gln Ile Leu Lys Asn  
 435 440 445  
 Leu Arg Gln Lys Leu Pro Ile Asp Gln Gln His Ile Val Glu Val Ser  
 450 455 460  
 Leu Leu Leu Ala Ala  
 465

(2) INFORMATIONS POUR LA SEQ ID NO: 717:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 301 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(710262..711164)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 717:

Met Ala Ala Arg Glu Met Leu Tyr Val Asn Arg Glu Thr Gly Lys Val  
 1 5 10 15  
 Glu Gln Glu Arg Ile Ile Cys Ser Ser Leu Val Lys Phe Phe Ile Glu  
 20 25 30  
 Thr Arg Ile Gly Arg Ala Leu Tyr Ser Val Leu Cys Lys Asn Ser Leu  
 35 40 45  
 Phe Ser Arg Ile Val Gly Trp Cys Gln Arg Leu Arg Val Thr Arg Tyr  
 50 55 60  
 Phe Ile Lys Pro Phe Val Thr Lys Tyr Arg Ile Cys Ile Glu Glu Ser  
 65 70 75 80  
 Ala Ser Pro Leu His Asp Tyr Ala Ser Phe Asn Asp Phe Phe Val Arg  
 85 90 95  
 Lys Leu Lys Pro Asp Ala Arg Pro Ile Cys Gln Gly Glu Asp Ile Cys  
 100 105 110  
 Val Thr Pro Ala Asp Gly Ala Tyr Leu Val Phe Pro Ser Met Ala Asp  
 115 120 125  
 Leu Ser Leu Phe Thr Ile Lys Asn Lys Pro Phe Ser Leu Glu Ser Phe  
 130 135 140  
 Leu Gly Asp Pro Gln Leu Ala His Gln Tyr Ala Gln Gly Ser Met Ala  
 145 150 155 160  
 Ile Ala Arg Leu Ala Pro Phe Asp Tyr His Arg Phe His Phe Pro Ile  
 165 170 175  
 Ala Gly Ile Ala Glu Ala Pro Arg Arg Ile Asn Gly His Leu Phe Ser  
 180 185 190  
 Ile His Pro Leu Met Leu Lys Arg Asn Phe Glu Val Phe Thr Glu Asn  
 195 200 205  
 Lys Arg Glu Ile Thr Ile Ile Thr Ser Lys Glu Phe Gly Glu Val Ala  
 210 215 220  
 Tyr Val Glu Val Gly Ala Leu Asn Val Gly Ser Ile His Gln Thr Phe  
 225 230 235 240  
 Ser Pro Gly Ser Tyr Val Lys Lys Gly Ala Glu Lys Gly Phe Phe Ala

				245					250					255	
Phe	Gly	Gly	Ser	Thr	Val	Val	Leu	Leu	Phe	Gln	Pro	Gln	Arg	Ile	Ile
			260					265					270		
Phe	Asp	Ala	Asp	Leu	Val	Gly	Tyr	Ser	Ala	Gln	Gly	Leu	Glu	Thr	Arg
		275					280					285			
Cys	Arg	Met	Gly	Gln	Ser	Leu	Gly	Lys	Arg	Phe	Ser	Ser			
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 718:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 444 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 711432..712763

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 718:

Met	Leu	Arg	Asn	Asp	Thr	Ile	Thr	Ala	Ile	Ala	Thr	Pro	Pro	Gly	Glu
1			5					10						15	
Gly	Ser	Ile	Ala	Ile	Val	Arg	Val	Ser	Gly	Pro	Asp	Ala	Ile	Ser	Ile
			20					25				30			
Ser	Asp	Arg	Ile	Phe	Ser	Gly	Asn	Ile	Ala	Gly	Tyr	Ala	Ser	His	Thr
		35				40					45				
Ala	His	Leu	Gly	Thr	Val	Ser	His	Asn	Ala	Val	Cys	Ile	Asp	Gln	Ala
	50					55				60					
Leu	Val	Leu	Val	Met	Arg	Ala	Pro	Arg	Ser	Phe	Thr	Gly	Glu	Asp	Ile
65				70				75						80	
Val	Glu	Phe	Gln	Cys	His	Gly	Gly	Tyr	Phe	Ala	Cys	Ser	Gln	Ile	Val
			85					90					95		
Asn	Ala	Leu	Leu	Ala	Glu	Gly	Ala	Arg	Ala	Ala	Leu	Pro	Gly	Glu	Phe
		100					105					110			
Ser	Gln	Arg	Ala	Phe	Leu	Asn	Gly	Lys	Ile	Asp	Leu	Ile	Gln	Ala	Glu
		115				120				125					
Ala	Ile	Gln	Gln	Leu	Ile	Ala	Ala	Asp	Asn	Ile	Asp	Ala	Phe	Arg	Ile
	130					135				140					
Ala	Gln	Asn	Gln	Phe	Gln	Gly	His	Thr	Ser	Gln	Ala	Ile	Ser	Ser	Ile
145				150				155						160	
Ser	Ser	Leu	Ile	Ile	Glu	Ala	Leu	Ala	Tyr	Ile	Glu	Val	Leu	Ala	Asp
			165					170					175		
Phe	Pro	Glu	Glu	Asp	Ile	Glu	Thr	Glu	Asp	Ser	Leu	Pro	Lys	His	Arg
		180				185						190			
Ile	Met	Glu	Ala	Leu	Ser	Ile	Thr	Asp	Glu	Leu	Leu	Ser	Ser	Phe	Asp
	195					200						205			
Glu	Gly	Gln	Arg	Leu	Ala	Gln	Gly	Thr	Ser	Ile	Val	Leu	Ala	Gly	Leu
	210					215				220					
Pro	Asn	Ala	Gly	Lys	Ser	Ser	Ile	Leu	Asn	Ala	Leu	Thr	Gln	Lys	Asn
225				230				235						240	
Arg	Ala	Ile	Val	Thr	Asp	Ile	Pro	Gly	Thr	Thr	Arg	Asp	Ile	Leu	Glu
			245					250					255		
Glu	Asn	Trp	Val	Leu	Gln	Gly	Lys	Asn	Leu	Arg	Leu	Ile	Asp	Ser	Ala
		260						265					270		
Gly	Leu	Arg	Glu	Thr	Glu	Asn	Leu	Val	Glu	Lys	Glu	Gly	Ile	Ala	Arg
	275					280						285			



```

Ala Arg Glu Ala Met Ser Gln Ala Glu Gly Ile Leu Trp Val Val Asp
290                               295                               300
Ala Ser Gln Pro Leu Pro Glu Phe Pro Thr Ile Leu Tyr Gln Lys Pro
305                               310                               315                               320
Thr Ile Leu Leu Trp Asn Lys Cys Asp Ile Val Ser Pro Pro Gln Ile
                               325                               330                               335
Glu Val Pro Phe Gln Gln Ile Ser Val Ser Ala Lys Thr Gly Glu Gly
                               340                               345                               350
Leu Leu Glu Leu Lys Gln Ala Leu Gln Lys Trp Leu Asn Thr Thr Gln
                               355                               360                               365
Leu Gly Lys Ser Ser Lys Ile Phe Leu Val Ser Ala Arg His His Ser
370                               375                               380
Leu Leu His Ser Val Tyr Thr Cys Leu Thr Ala Ala Leu Asn Gly Phe
385                               390                               395                               400
Thr Glu His Leu Pro Asn Glu Cys Ile Ala Leu Asp Leu Arg Gln Ala
                               405                               410                               415
Leu His Ser Ile Gly Asn Leu Ser Gly Ser Glu Val Thr Glu Asn Val
                               420                               425                               430
Leu Gly Glu Ile Phe Ser Lys Phe Cys Ile Gly Lys
                               435                               440

```

(2) INFORMATIONS POUR LA SEQ ID NO: 719:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 224 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 712767..713438

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 719:

```

Pro Leu Met Lys Ser Leu Asn Val Gln Ala Lys Arg Ala Phe Ile Ile
1                               5                               10                               15
Ser Thr Leu Asn Arg Leu Phe Pro Asn Pro Ala Pro Ser Leu Thr Gly
                               20                               25                               30
Trp Gln Thr Pro Phe Gln Leu Leu Ile Ala Ile Leu Leu Ser Gly Asn
                               35                               40                               45
Ser Thr Asp Lys Ala Val Asn Ser Val Thr Pro Ser Leu Phe Ala Lys
50                               55                               60
Ala Pro Asp Ala Gln Ser Met Ser Met Leu Ala Pro Ser Glu Ile Tyr
65                               70                               75                               80
Ser Leu Ile Ala Pro Cys Gly Leu Gly Glu Arg Lys Ala Ala Tyr Ile
                               85                               90                               95
His Ala Leu Ser His Ile Leu Val Asp Arg Tyr His Gln Glu Thr Pro
                               100                               105                               110
His Thr Leu Pro Glu Leu Thr Ala Leu Pro Gly Val Gly Arg Lys Thr
                               115                               120                               125
Ala Ser Val Phe Leu Ser Ile Tyr Tyr Gly Glu Asn Thr Phe Pro Val
130                               135                               140
Asp Thr His Ile Leu Arg Leu Ala His Arg Trp Gln Leu Ser Asn Glu
145                               150                               155                               160
Thr Glu Ser Phe Ser Cys Arg Lys Arg Phe Ser Thr Val Ile Trp Thr
                               165                               170                               175
Lys Ala Leu Ser Glu Ile Ala Phe Thr Thr His Leu Leu Cys Lys Ser

```

		180					185			190
Val	Leu	Ser	Ser	Ala	Pro	Pro	Gln	His	Arg	Cys
		195					200			205
Phe	Leu	Thr	Asp	Arg	Leu	Thr	Ser	Phe	Leu	Thr
	210					215				220
									Glu	Ser
									Ser	Ile
									Ser	Ser
										Leu
										Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 720:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(713651..714232)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 720:

Lys	Val	Ser	Tyr	Phe	Leu	Asn	Ala	Asn	Gly	Leu	Leu	Arg	Arg	Ser	Asn
1				5					10					15	
Arg	Leu	Pro	Ile	Leu	Phe	Tyr	Arg	Asp	Gln	Lys	Gly	Asn	Phe	Ser	Ser
			20					25					30		
Trp	Asp	Asp	Phe	Thr	His	Asp	Val	Gln	Thr	Gln	Lys	Ser	Gly	Arg	Glu
		35				40						45			
Thr	Asp	Met	Pro	Asp	Ser	Leu	Arg	Gly	Arg	Val	Glu	Glu	Asp	Ala	Ala
	50					55					60				
Ser	Gln	Met	Ile	Val	Glu	Val	Leu	Leu	Ala	Phe	Leu	Asp	Asn	Gln	Asp
65				70					75					80	
Met	Tyr	Leu	Ser	Val	Ser	Phe	Glu	Ile	Leu	Arg	Asn	Phe	Leu	Glu	Glu
				85					90					95	
Lys	Val	Leu	Ser	Lys	Arg	Ser	Leu	Ser	Pro	Arg	Ser	His	Glu	Ala	Ile
			100					105					110		
Lys	Lys	Ile	Lys	Asp	Leu	Tyr	Leu	Val	Ser	Pro	Glu	Asp	Phe	Gln	Thr
		115					120					125			
Phe	Ile	Gly	Gly	Val	Ile	Thr	Glu	Ser	Leu	Phe	Gln	Glu	Glu	Asp	Gln
	130					135					140				
Leu	Val	Val	Gly	Cys	Met	Ile	Phe	Ser	Gln	Glu	Gly	Arg	Glu	Leu	Phe
145					150					155				160	
Asp	Ser	Trp	Lys	Gly	Ile	Ser	Gln	Thr	Tyr	Pro	His	Asp	Met	Leu	Tyr
			165						170					175	
Thr	Gln	Ala	Phe	Leu	Ala	Glu	Val	Val	Leu	His	Val	Xaa	Asn	Thr	Thr
			180					185					190		
Phe	Ile														

(2) INFORMATIONS POUR LA SEQ ID NO: 721:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 721:

(2) INFORMATION POUR LA SEQ ID NO: 722:

(A) LONGUEUR: 253 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(714834..715592)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 722:

Ala	Ser	Ile	Trp	Lys	Arg	Arg	Val	Ala	Arg	Arg	Asn	Glu	Asn	Tyr	Asp
1				5		-			10					15	
Val	Lys	Lys	Ala	Glu	Glu	Gln	Gln	Gly	Ile	Val	Gln	Tyr	Leu	Gln	Asp
			20					25					30		
Ser	Lys	Met	Pro	Ala	Leu	Thr	Arg	Ala	Tyr	Arg	His	Leu	Arg	Ala	Phe
		35					40					45			
Asn	Ser	Ala	Cys	Leu	Arg	Thr	Ile	Arg	Glu	Phe	Phe	Ala	Thr	Ile	Phe
	50					55					60				
Arg	Ala	Leu	Arg	Asp	Ala	Tyr	Tyr	Arg	His	Cys	Thr	Arg	Ser	Gly	Ile
65				70						75				80	
Asn	Phe	Cys	Gly	Ala	Asp	Lys	Asp	Ser	Leu	Glu	Val	Leu	Val	Ala	Val
			85					90						95	
Gly	Leu	Leu	Leu	Arg	Met	Ala	Thr	Leu	Arg	Ser	Phe	Glu	His	Val	Gly
			100					105					110		
Gly	Asn	Tyr	Glu	Asp	Arg	Leu	Val	Asn	Asn	Asp	Ala	Pro	Val	Thr	Gly
		115					120					125			
Ala	Gly	Arg	Thr	Leu	Val	Tyr	Asp	Ala	Val	Asp	Asp	Ile	Glu	Ser	Ile

130		135		140
Leu Asn Thr Arg Thr Asn Trp Pro Gln His Val Met Ile Gly Phe Ser				
145		150		155
Arg Gly Leu Val Gln Leu Cys Ala Thr Pro Tyr Asn Ala Thr Ser Gln				
	165		170	175
Glu Cys Phe Lys Ser Ile Val Arg Leu Glu Lys Glu Asp Pro Ser Ser				
	180		185	190
Asp Tyr Ser Gln Ala Leu Leu Leu Ala Gly Ile Ile Asp Arg Leu Ala				
	195		200	205
Glu Lys Ala Pro Met Ala Ala Lys Tyr Val Leu Asp Ala Leu Arg Val				
	210		215	220
Arg Thr Ser Glu Leu Ile Gly Glu Leu Ile Ile Leu Asp Leu Leu Pro				
225		230		235
Pro Val Trp Lys Val Gly Arg Gly Xaa Tyr Ser Leu Leu				240
	245		250	

(2) INFORMATIONS POUR LA SEQ ID NO: 723:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(715558..715854)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 723:

Ala Leu Tyr Gly Gly Asn Ser Gly Pro Glu Gly Phe Ser Ser Ala Ser				
1	5	10	15	
Arg Gly Asp Glu Ile Asp Asp Val Pro Asp Ser Glu Glu Gly Glu Leu				
	20	25	30	
Glu Glu Arg Val Ser Asp His Ala Glu Ser Ile Ile Thr Glu Ser Ser				
	35	40	45	
Glu Thr Leu Phe Arg Thr Thr Ser Ser Ser Gly Val Ser Glu Asp Leu				
	50	55	60	
Gln Gln His Val Ser Leu Glu Glu Ser Pro Arg Gln Arg Gly Phe Leu				
65	70	75	80	
Gly Arg Ile Arg Asp Ala Val Xaa Phe Tyr Leu Glu Ala Ser Cys Cys				
	85	90	95	
Thr Lys Glu				

(2) INFORMATIONS POUR LA SEQ ID NO: 724:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(715921..716937)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 724:

Asn	Leu	Ile	Lys	Ile	Val	Gly	Ile	Lys	Ser	Tyr	Cys	Phe	Gly	Gly	Gly			
1				5					10					15				
Phe	Met	Ser	Ile	Arg	Pro	Thr	Asn	Gly	Ser	Gly	Asn	Gly	Tyr	Pro	Ser			
			20					25					30					
Ile	Asn	Pro	Ser	Asn	Asp	Asn	Gln	Asp	Gly	Leu	Val	Gln	Ser	Thr	Ser			
		35					40					45						
Gly	Pro	Asn	Tyr	Gly	Gly	His	Thr	Val	Ser	Ser	Arg	Gly	Gly	Phe	Gln			
	50					55					60							
Gly	Ile	Cys	Val	Arg	Ile	Ala	Asp	Leu	Phe	Arg	Asn	Cys	Phe	Ser	Arg			
65					70				75						80			
Asn	Arg	Gly	Thr	Thr	Thr	Pro	Ser	Arg	Pro	Val	Ile	Thr	Gln	Ala	Asp			
			85					90					95					
Ile	Tyr	His	Pro	Thr	Ile	Phe	Gly	Gln	Gly	Ala	Gln	Pro	Ile	Val	Ser			
			100				105					110						
Thr	Gly	Asp	Lys	Lys	Leu	Asp	Ser	Ala	Ile	Ile	Gln	Ala	Asp	Leu	Arg			
		115				120						125						
Ala	Gln	Asn	Lys	Gln	Thr	Leu	Ala	Thr	His	Ile	Gln	Ser	Lys	Leu	Gly			
	130					135					140							
Ser	Met	Glu	Gly	Gln	Ser	Pro	Gln	Asp	Tyr	Lys	Ala	Gly	Ala	Tyr	Ser			
145					150				155						160			
Ala	Leu	Arg	Leu	Met	Leu	Phe	Thr	Pro	Gly	Glu	Thr	Thr	Val	Ser	Ser			
			165					170					175					
Glu	Arg	Glu	Arg	Gln	Ala	Cys	Val	Thr	Gly	Arg	Asp	Leu	Trp	Glu	Gln			
			180					185				190						
Ala	Ala	Gly	Asp	Leu	Ala	Thr	Asn	Gly	Asn	Thr	Asp	Gly	Leu	Met	Leu			
	195					200					205							
Met	Ala	Asn	Leu	Ser	Val	Gly	Gly	Lys	His	Val	Pro	Ala	Gly	His	Leu			
	210					215					220							
Arg	Glu	Tyr	Met	Asn	Thr	Val	Lys	Gly	Thr	Phe	Thr	Asp	Glu	Asn	Glu			
225					230				235						240			
Ala	Thr	Asp	Pro	Thr	Val	Asp	Ala	Ile	Leu	Asp	Leu	Ala	Ala	Lys	Ile			
			245					250					255					
Asp	Ala	Thr	Glu	Phe	Ser	Ser	Pro	Gly	Ser	Gly	Pro	Val	Ile	Leu	Asn			
		260					265					270						
Tyr	Ile	Gly	Asn	Cys	Gly	Gln	Val	Val	Leu	Glu	Asn	Glu	Lys	Met	Asn			
	275					280						285						
Gln	Leu	Val	Leu	Glu	Asp	Gln	Asn	Gly	Gln	Asp	Pro	Gln	Arg	Val	Gln			
	290					295					300							
Asp	Asn	Ser	Lys	Glu	Leu	Gln	Lys	Leu	Leu	Glu	Asn	Ala	Arg	Lys	Thr			
305					310				315						320			
Asp	Pro	Glu	Leu	Tyr	Phe	Gln	Thr	Leu	Thr	Val	Ile	Thr	Ser	Ser	Val			
			325					330					335					
Phe	Leu	Asp																

## (2) INFORMATIONS POUR LA SEQ ID NO: 725:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 403 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(717149..718357)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 725:

Met	Asp	Lys	Leu	Ser	Ile	Arg	Asp	Leu	Ser	Leu	Glu	Gly	Lys	Lys	Val
1				5				10						15	
Leu	Val	Arg	Val	Asp	Phe	Asn	Val	Pro	Ile	Lys	Asp	Gly	Lys	Ile	Leu
		20					25						30		
Asp	Asp	Val	Arg	Ile	Arg	Ser	Ala	Met	Pro	Thr	Ile	His	Tyr	Leu	Leu
		35				40						45			
Lys	Gln	Asp	Ala	Ala	Val	Ile	Leu	Val	Ser	His	Leu	Gly	Leu	Pro	Lys
	50					55					60				
Gly	Gly	Val	Phe	Glu	Glu	Ala	Tyr	Ser	Leu	Ala	Pro	Ile	Val	Pro	Val
65				70					75					80	
Leu	Glu	Gly	Tyr	Leu	Gly	His	His	Val	Pro	Leu	Ser	Pro	Asp	Cys	Ile
				85				90						95	
Gly	Glu	Val	Ala	Arg	Gln	Ala	Val	Ala	Gln	Leu	Ser	Pro	Gly	Arg	Val
			100					105					110		
Leu	Leu	Leu	Glu	Asn	Val	Arg	Phe	His	Lys	Gly	Glu	Glu	His	Pro	Asp
		115				120						125			
Glu	Asp	Pro	Ser	Phe	Ala	Ile	Glu	Leu	Ala	Ala	Tyr	Ala	Asp	Phe	Tyr
	130					135					140				
Val	Asn	Asp	Ala	Phe	Gly	Thr	Ser	His	Arg	Lys	His	Ala	Ser	Val	Tyr
145				150					155					160	
Arg	Val	Pro	Gln	Leu	Phe	Pro	Asp	Arg	Ala	Ala	Ala	Gly	Phe	Leu	Met
			165					170						175	
Glu	Lys	Glu	Leu	Glu	Phe	Leu	Gly	Gln	His	Leu	Leu	Val	Glu	Pro	Lys
			180					185					190		
Arg	Pro	Phe	Thr	Ala	Ile	Leu	Gly	Gly	Ala	Lys	Met	Ser	Ser	Lys	Ile
		195				200						205			
Gly	Val	Ile	Glu	Ala	Leu	Leu	Ser	Cys	Val	Asp	His	Leu	Val	Leu	Ala
	210					215					220				
Gly	Gly	Met	Gly	Tyr	Thr	Phe	Leu	Arg	Ala	Met	Asn	Arg	Gln	Val	Gly
225				230					235					240	
Asn	Ser	Leu	Val	Glu	Glu	Ser	Gly	Ile	Pro	Leu	Ala	Lys	Lys	Val	Leu
			245					250						255	
Glu	Lys	Ala	Gln	Ala	Leu	Gly	Val	Lys	Ile	His	Leu	Pro	Val	Asp	Ala
			260					265					270		
Lys	Val	Ala	Lys	Gln	Cys	Asp	Ser	Gly	Glu	Asp	Trp	Arg	Glu	Leu	Ser
		275				280						285			
Ile	Gln	Glu	Gly	Ile	Pro	Glu	Gly	Leu	Ala	Gly	Phe	Asp	Ile	Gly	Ala
	290					295					300				
Gln	Thr	Ile	Glu	Leu	Phe	Ser	Lys	Val	Ile	Gln	Glu	Ser	Ala	Thr	Ile
305				310					315					320	
Phe	Trp	Asn	Gly	Pro	Val	Gly	Val	Tyr	Glu	Val	Pro	Pro	Phe	Asp	Gln
			325					330						335	
Gly	Ser	Lys	Ala	Ile	Ala	Gln	Cys	Leu	Ala	Ser	His	Ser	Ser	Ala	Val
			340					345					350		
Thr	Val	Val	Gly	Gly	Gly	Asp	Ala	Ala	Ala	Val	Val	Ala	Leu	Ala	Gly
		355				360						365			
Cys	Thr	Ser	Gln	Ile	Ser	His	Val	Ser	Thr	Gly	Gly	Gly	Ala	Ser	Leu
	370					375					380				
Glu	Phe	Leu	Glu	Lys	Gly	Ser	Leu	Pro	Gly	Thr	Glu	Ile	Leu	Ser	Pro
385				390					395						400
Ala	Gln	Ser													

## (2) INFORMATIONS POUR LA SEQ ID NO: 726:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 121 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 718500..718862

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 726:

Gln	Asn	Ser	Ala	Arg	Ser	Asn	Lys	Lys	Asn	Thr	Ile	Glu	Ser	Ala	Ala	1	5	10	15
Pro	Ala	Gly	Thr	Val	Ile	Asn	His	Glu	Ser	Thr	Ile	Ser	Leu	Met	Ile	20	25	30	
Arg	Lys	Leu	Met	Ala	Arg	Lys	Pro	Leu	Ala	Asn	Pro	Ile	Pro	Asn	Thr	35	40	45	
Asp	Pro	Thr	Thr	Thr	Cys	Val	Val	Asp	Ile	Gly	Asn	Pro	Lys	Glu	Glu	50	55	60	
Ala	Ala	Ala	Ile	Val	Ile	Ala	Glu	Leu	Ile	Pro	Thr	Glu	Lys	Pro	Arg	65	70	75	
Asp	Gly	Val	Asn	Ser	Val	Ile	Phe	Phe	Pro	Ile	Val	Ser	Ile	Thr	Arg	85	90	95	
Gln	Pro	His	Val	Ala	Asn	Pro	Gln	Thr	Lys	Pro	Ser	Pro	Pro	Lys	Asp	100	105	110	
Ile	Asn	Thr	Lys	Arg	Thr	Phe	Glu	Glu								115	120		

(2) INFORMATIONS POUR LA SEQ ID NO: 727:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 433 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(718499..719797)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 727:

Asp	Ala	Arg	Arg	Glu	Ile	Gly	Met	Trp	Leu	Leu	Leu	Val	Cys	Val	Val	1	5	10	15
Val	Gly	Gly	Phe	Tyr	Thr	Ala	Trp	Asn	Ile	Gly	Ala	Asn	Asp	Val	Ala	20	25	30	
Asn	Ala	Val	Gly	Pro	Ser	Val	Gly	Ala	Gly	Ala	Leu	Thr	Leu	Lys	Gln	35	40	45	
Ala	Val	Leu	Ile	Ala	Ala	Val	Phe	Glu	Phe	Leu	Gly	Ala	Val	Leu	Leu	50	55	60	
Gly	Asp	Arg	Val	Ile	Gly	Thr	Ile	Glu	Ser	Gly	Leu	Val	Ala	Pro	Ser	65	70	75	
Gly	His	Val	Leu	Ser	Ser	Gln	Asp	Tyr	Val	Phe	Gly	Met	Ala	Ala	Ala	85	90	95	
Leu	Leu	Ala	Thr	Gly	Val	Trp	Leu	Gln	Ile	Ala	Ser	Phe	Cys	Gly	Trp	100	105	110	
Pro	Val	Ser	Thr	Thr	His	Ala	Ile	Val	Gly	Ala	Val	Leu	Gly	Phe	Gly				

	115		120		125	
Ile	Ile	Leu	Lys	Glu	Asp	Ala
130						Val
Val	Phe	Val	Ser	Trp	Leu	Ala
145						Ser
Phe	Leu	Ile	Phe	Ser	Phe	Ile
						Arg
Pro	Val	Ser	Ala	Met	Val	Arg
						Ile
Ile	Phe	Ala	Leu	Gly	Leu	Val
						Leu
Val	Ile	Ser	Phe	Ser	Pro	Ala
						Leu
Phe	Ala	Phe	Phe	Phe	Thr	Ile
225						Trp
Ile	Leu	Pro	Gln	Glu	Val	Leu
						Pro
Ser	Lys	Ser	Thr	Asp	Tyr	Gly
						Arg
Phe	Ala	Tyr	Leu	Gln	Met	Ile
						Ile
Gly	Ser	Asn	Asp	Val	Ala	Asn
						Ala
Arg	Thr	Leu	Tyr	Pro	Gln	Ser
305						Tyr
Met	Ser	Leu	Gly	Gly	Leu	Gly
						Leu
Trp	Arg	Val	Ile	Asp	Thr	Ile
						Gly
Ser	Arg	Gly	Phe	Ser	Val	Gly
						Met
Ala	Ser	Ser	Leu	Gly	Phe	Pro
						Ile
Ser	Val	Leu	Gly	Ile	Gly	Phe
385						Ala
Arg	Ile	Ile	Lys	Asp	Ile	Val
						Leu
Gly	Ala	Ala	Leu	Ser	Ile	Val
						Phe
Cys						

(2) INFORMATIONS POUR LA SEQ ID NO: 728:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 164 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(719782..720273)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 728:

Trp	Tyr	Glu	Lys	Arg	Cys	Lys	Lys	Thr	Leu	Gly	Phe	Gly	Ser	Ile	Ser
1						5			10				15		



```

Ser Cys Ile Pro Arg Ser Ala Val Gly Asp His Phe Asp Thr Arg Phe
      20      25      30
Leu Ser Arg Xaa Ala Glu Asp Ile Ala Ile Leu Leu Thr Val Lys Glu
      35      40      45
Leu Gln Phe Tyr Pro Glu Phe Glu Glu Leu Phe Phe Glu Phe Leu Gln
      50      55      60
Lys Thr Val Gln Ser Phe Glu Ala Val Ala Lys Thr Ile Arg Glu Met
      65      70      75      80
Asp Arg Leu Leu Glu Ser Ser Phe Gly Gly Asn Arg Ala Asp Lys Thr
      85      90      95
Arg Val Leu Val Ser Glu Val Ser Asn Leu Glu His Glu Cys Asp Leu
      100      105      110
Leu Gln Arg Glu Leu Met Lys Val Phe Phe Ser Asp Asp Phe Ala Ile
      115      120      125
Gly Thr Lys Gly Phe Val Leu Trp Met Gln Ile Ile Lys Gly Ile Ser
      130      135      140
Gly Ile Ser Asn Asn Ser Glu Lys Leu Ala Tyr Arg Val Ser Met Thr
      145      150      155      160
Leu Glu Glu Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 729:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 103 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(720144..720452)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 729:

```

Met Gln Val Leu Ala Ser Leu Phe Gly Gln Ser Pro Phe Ala Pro Leu
1      5      10      15
Gln Ala His Leu Glu Leu Val Ser Ser Thr Ile Asn Val Leu Phe Pro
      20      25      30
Leu Phe Ser Ala Leu Lys Glu Gly Asp Tyr Glu Arg Val Gly Val Leu
      35      40      45
Ala Gln Leu Val Ser Ser Lys Glu Arg Gln Ala Asp Gly Met Lys Asn
      50      55      60
Asp Val Arg Arg His Leu Ala Ser Gly Val Phe Leu Pro Val Phe Arg
      65      70      75      80
Ala Ala Leu Leu Glu Ile Ile Ser Ile Gln Asp Ser Leu Ala Asp Xaa
      85      90      95
Leu Arg Ile Ser Gln Phe Cys
      100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 730:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 321 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 720613..721575

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 730:

```

Met Cys Ala Gln Pro Leu Leu Gln Val Lys Asn Leu Ser Val Ser Leu
1      5      10      15
Asn Arg Asn Arg Val Ser Phe Leu Ala Val Asp Ser Leu Ser Phe Asp
20      25      30
Val Phe Pro Gly Gln Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly
35      40      45
Lys Ser Ile Thr Ala Gln Ser Leu Met Gln Leu Leu Pro Glu Glu Ser
50      55      60
Phe Ser Leu Ser Gly Glu Ala Leu Phe Asn Lys Glu Asn Leu Leu Asp
65      70      75      80
Arg Lys Asn Thr Asn Ala Lys Val Leu Phe Gly Ser Lys Ile Ser Met
85      90      95
Ile Phe Gln Asn Pro Leu Ala Ser Phe Asp Pro Val Phe Thr Ile Glu
100     105     110
Gln Gln Phe His Glu Val Ile Arg Thr His Leu Gly Ile Ser Asn Lys
115     120     125
Met Ala His Glu Gln Met Leu Ala Val Leu Arg Glu Thr Gly Phe Gln
130     135     140
Asp Pro Glu Arg Cys Ile Lys Leu Tyr Pro His Glu Leu Ser Gly Gly
145     150     155     160
Met Leu Gln Arg Met Ala Ile Ala Met Thr Leu Leu Thr Ser Pro Asp
165     170     175
Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln
180     185     190
Tyr Gln Ile Leu Gln Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met
195     200     205
Ser Leu Leu Ile Ile Thr His Asp Met Gly Val Val Ala Glu Met Ala
210     215     220
Asp Asp Val Phe Val Leu Tyr Ala Gly Arg Met Glu Glu Tyr Ser Ser
225     230     235     240
Val Gln Glu Ile Phe His Ser Pro Ala His Pro Tyr Thr Glu Asp Leu
245     250     255
Leu Ala Ser Arg Pro Ser Gln Tyr Arg Gln Gln Thr Phe Val Pro Ile
260     265     270
Ala Gly Gln Pro Pro His Tyr Thr Arg Leu Pro Lys Gly Cys Cys Tyr
275     280     285
Ser Pro Arg Cys Arg Lys Ala Gln Pro Ile Cys Phe Glu Lys Ser Pro
290     295     300
Asp Ser Leu Ser Leu Asn Asp His His Arg Val Arg Cys Trp Leu His
305     310     315     320
Glu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 731:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 266 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 721559..722356

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 731:

Gly	Ala	Gly	Tyr	Met	Asn	Asn	Pro	Leu	Leu	Leu	Gln	Ala	Ser	Arg	Leu
1				5					10					15	
Thr	Lys	His	Tyr	Tyr	Lys	Arg	Ser	Phe	Trp	Phe	Gln	Lys	Lys	Lys	Val
			20					25					30		
Ala	Thr	Thr	Pro	Leu	Asn	Gln	Val	Ser	Phe	Ser	Leu	Pro	Arg	His	Lys
		35					40					45			
Ile	Ile	Gly	Leu	Ile	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Ala
	50					55					60				
Leu	Gly	Leu	Ala	Gly	Leu	Ile	Pro	Leu	Thr	Ser	Gly	His	Leu	Ile	Leu
65					70					75					80
Asn	Asp	Lys	Ala	Ile	Pro	Leu	His	Asn	Lys	Lys	Gly	Arg	Gln	Tyr	Leu
				85					90					95	
Ser	Ser	Gln	Val	Arg	Met	Val	Phe	Gln	Asn	Pro	Arg	Ser	Ser	Leu	Asn
			100					105					110		
Pro	Arg	Lys	Thr	Ile	Phe	Asp	Thr	Leu	Ser	His	Ser	Leu	Leu	Tyr	His
		115					120					125			
Arg	Leu	Val	Ser	Lys	Glu	Glu	Leu	Gly	Ala	Thr	Val	Glu	Lys	Ala	Leu
	130					135					140				
Ser	Leu	Val	Gly	Leu	Ser	Thr	Asp	Tyr	Leu	Tyr	Ser	Tyr	Pro	His	Gln
145					150					155					160
Leu	Ser	Gly	Gly	Gln	Leu	Gln	Arg	Ile	Ser	Ile	Ala	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Ala	Pro	Gln	Leu	Ile	Ile	Cys	Asp	Glu	Ile	Val	Ser	Ala	Leu	Asp
			180					185					190		
Leu	Ser	Met	Gln	Ala	Gln	Ile	Leu	Asn	Met	Leu	Thr	Ser	Leu	Gln	Gln
		195					200					205			
Gln	Ala	Arg	Leu	Thr	Tyr	Leu	Phe	Ile	Ser	His	Asp	Leu	Ala	Val	Val
	210					215					220				
Arg	Ser	Phe	Cys	Ser	Glu	Leu	Ile	Ile	Met	Tyr	Lys	Gly	Gln	Ile	Val
225					230					235					240
Glu	Thr	Gly	Ala	Thr	Glu	Glu	Ile	Phe	Cys	Asn	Pro	Gln	His	Ser	Tyr
				245					250					255	
Thr	Arg	Met	Leu	Leu	His	Ser	Gln	Leu	Pro						
			260					265							

(2) INFORMATIONS POUR LA SEQ ID NO: 732:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(722397..723248)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 732:

Glu	Asn	Ile	Val	Ser	Arg	Leu	Pro	Ser	Glu	Asp	Thr	Leu	Leu	Glu	Val
1				5					10					15	
Asn	Ile	Glu	Asp	Ile	Arg	Val	Ser	Pro	Phe	Gln	Pro	Arg	Arg	Thr	Phe

```

      20      25      30
Leu Glu Glu Asp Leu Lys Glu Leu Val Leu Ser Ile Lys Thr Val Gly
      35      40      45
Leu Ile His Pro Pro Val Val Arg Glu Ile Arg Asn Gly Asp Lys Val
      50      55      60
Leu Tyr Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Leu Gln
      65      70      75      80
Leu Ala Gly Tyr Lys Thr Val Pro Val Val Leu Lys Gln Val Leu Ala
      85      90      95
Asp Asp Met Ala Ala Glu Ala Thr Leu Ile Glu Asn Ile Gln Arg Val
      100      105      110
Asn Leu Asn Pro Leu Glu Met Ala Glu Ala Phe Arg Arg Leu Ile Val
      115      120      125
Val Phe Gly Leu Thr Gln Asp Lys Val Ala Lys Lys Val Gly Lys Lys
      130      135      140
Arg Ser Thr Val Ala Asn Tyr Leu Arg Leu Phe Ser Leu Pro Gln Glu
      145      150      155      160
Val Gln Glu Lys Met Asn Ser Gly Glu Ile Ser Leu Gly His Ala Lys
      165      170      175
Val Ile Leu Ser Leu Glu Asp Glu Asn Leu Arg Gln Ile Leu Ser Gln
      180      185      190
Lys Ile Ile Ser Cys Lys Leu Ala Val Arg Glu Ala Glu Met Glu Ala
      195      200      205
Lys Arg Leu Val Lys Gly Lys Gly Ala Ser Leu Lys Glu Asp Ser Ser
      210      215      220
Ser Gln Pro Ser Ser Arg Leu Gly Phe Cys Gln Glu Arg Leu Ala Thr
      225      230      235      240
Thr Phe Gly Tyr Pro Val Thr Val Lys Pro Gln Gly Arg Arg Ile Cys
      245      250      255
Val Ser Phe Phe Val Glu Gly Glu Glu Ala Leu Glu Ala Leu Glu Lys
      260      265      270
Ala Leu Thr Thr Ser Ser Ser Glu Ala Ile Leu Thr
      275      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 733:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 407 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(723378..724598)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 733:

```

Arg Asn Arg Ile Phe Thr Met Tyr Asn Val Lys Lys Asp Phe Pro Ile
1      5      10      15
Phe Lys Asn Gln Gly Asp Pro Tyr Val Tyr Leu Asp Ser Ala Ala Thr
      20      25      30
Thr His Lys Pro Gln Cys Val Ile Asp Ser Ile Val Asp Tyr Tyr Ser
      35      40      45
Ser Ser Tyr Ala Thr Val Asn Arg Ala Leu Tyr Thr Ala Ser His Asp
      50      55      60
Ile Thr Phe Ala His Trp Gln Val Arg Ser Lys Val Gly Ser Trp Ile
65      70      75      80

```

Gly	Ala	Gln	Tyr	Asp	Gln	Glu	Ile	Ile	Phe	Thr	Arg	Gly	Thr	Thr	Ser
				85					90					95	
Ser	Leu	Asn	Leu	Leu	Ala	Ile	Ala	Ala	Asn	Asp	Ser	Trp	Leu	Ala	Gly
			100					105					110		
Gly	Thr	Val	Val	Ile	Ser	Glu	Ala	Glu	His	His	Ala	Asn	Leu	Val	Ser
		115					120					125			
Trp	Glu	Leu	Ala	Cys	Gln	Arg	Ser	Gly	Ala	Thr	Ile	Lys	Lys	Val	Arg
	130					135					140				
Val	Asp	Asp	Glu	Gly	Met	Val	Asp	Cys	Asn	His	Leu	Glu	Gln	Leu	Leu
	145				150					155					160
Lys	Gln	Gly	Val	Gln	Leu	Val	Ser	Leu	Ala	His	Val	Ser	Asn	Val	Ser
				165					170					175	
Gly	Ala	Val	Leu	Pro	Leu	Pro	Glu	Ile	Ala	His	Leu	Val	His	Arg	Tyr
			180					185					190		
Glu	Ala	Leu	Phe	Ala	Val	Asp	Gly	Ala	Gln	Gly	Val	Gly	Lys	Gly	Pro
		195					200					205			
Leu	Asn	Leu	Ser	Glu	Trp	Gly	Val	Asp	Phe	Tyr	Ala	Phe	Ser	Gly	His
	210					215					220				
Lys	Leu	Tyr	Ala	Pro	Thr	Gly	Ile	Gly	Val	Leu	Tyr	Gly	Lys	Lys	Glu
	225				230					235					240
Leu	Leu	Glu	Ser	Leu	Pro	Pro	Val	Glu	Gly	Gly	Gly	Asp	Met	Val	Ile
				245					250					255	
Val	Tyr	Asp	Phe	Glu	Glu	Leu	Ser	Tyr	Gln	Glu	Pro	Pro	Leu	Arg	Phe
			260					265					270		
Glu	Ala	Gly	Thr	Pro	His	Ile	Ala	Gly	Val	Leu	Gly	Leu	Gly	Ala	Ala
		275					280					285			
Ile	Asp	Tyr	Leu	Gln	Ala	Leu	Pro	Phe	Ser	Ile	Thr	Asp	Arg	Leu	Thr
	290					295					300				
Glu	Leu	Thr	His	Phe	Leu	Tyr	Glu	Gln	Leu	Leu	Thr	Val	Pro	Gly	Ile
	305				310					315					320
Gln	Ile	Ile	Gly	Pro	Lys	Gln	Gly	Ala	Ala	Arg	Gly	Ser	Leu	Cys	Ser
				325					330					335	
Ile	Ser	Ile	Pro	Gly	Val	Gln	Ala	Ser	Asp	Leu	Gly	Phe	Leu	Leu	Asp
			340					345					350		
Gly	Arg	Gly	Ile	Ser	Val	Arg	Ser	Gly	His	Gln	Cys	Ser	Gln	Pro	Ala
		355					360					365			
Met	Val	Arg	Trp	Asp	Leu	Gly	His	Val	Leu	Arg	Ala	Ser	Leu	Gly	Ile
	370					375				380					
Tyr	Asn	Asp	Gln	Gln	Asp	Ile	Leu	Leu	Phe	Val	Glu	Ala	Leu	Lys	Asp
	385				390					395					400
Ile	Leu	Arg	Ala	Tyr	Arg	Ser									
						405									

(2) INFORMATIONS POUR LA SEQ ID NO: 734:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 396 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(724576..725763)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 734:

Thr Met Trp Gly Thr His Gln Gln Arg Gln Ile His Pro Asp Ala Arg

1		5		10		15
Leu	Ala	Asp	Val	Thr	Arg	Ser
		20				25
Val	Phe	Arg	Glu	Ala	Cys	Ser
		35				40
Ser	Trp	Ile	Tyr	Cys	Val	Gly
		50				55
Glu	Glu	Arg	Ser	Ala	Thr	Cys
		65				70
Ser	Leu	Ser	Val	Leu	Pro	Ala
						85
Ala	Arg	Ala	Phe	Gln	Lys	His
						100
Leu	His	Ser	Leu	Leu	Arg	Gly
						115
Glu	Gly	Arg	Glu	Leu	Gln	Thr
						130
Cys	Ser	Glu	Glu	Glu	Asn	Lys
						145
Phe	Val	Leu	Gly	Lys	Gly	Ala
						165
Ala	Leu	Pro	Asp	Asn	Val	Tyr
						180
Gly	Glu	Glu	Ala	Glu	Leu	Val
						195
Thr	Glu	Arg	Ile	Ile	Trp	Ala
						210
Ala	Cys	Ala	Leu	Ile	Gln	Asp
						225
Arg	Asn	Ser	Phe	Phe	Leu	Lys
						245
Val	Lys	Val	Leu	Gly	Gly	Asp
						260
His	Asp	Asp	Arg	Glu	Thr	Thr
						275
Glu	Glu	Gly	Ser	Phe	Ser	Phe
						290
Gly	Thr	Leu	Ser	Asn	Ala	Tyr
						305
Asn	Arg	Ala	Ser	Ala	Ser	Thr
						325
Asp	Val	Lys	Ala	Ser	His	Gly
						340
Leu	Leu	Thr	Tyr	Leu	Arg	Ser
						355
Gln	Ala	Leu	Gln	Lys	Ser	Phe
						370
Phe	Pro	Lys	Leu	Gln	Lys	Gln
						385
						390
						395

(2) INFORMATIONS POUR LA SEQ ID NO: 735:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(725767..726516)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 735:

```

Met Tyr Met Tyr Val Val Lys Lys Lys Arg Ser Leu Glu Gly Leu Ser
1      5      10      15
Leu Ser Ile His Pro Gly Glu Leu His Ile Ile Met Gly Pro Asn Gly
      20      25      30
Ala Gly Lys Ser Thr Leu Ala Lys Val Leu Ser Gly Asp Glu Ser Val
      35      40      45
Glu Val Ser Ser Gly Thr Met Thr Leu Ala Gly Gln Asp Leu Leu Glu
      50      55      60
Leu Ser Pro Glu Glu Arg Ala His Ala Gly Met Phe Ile Ser Phe Gln
      65      70      75      80
His Pro Pro Glu Ile Pro Gly Val Asn Asn Arg Ile Phe Leu Lys Glu
      85      90      95
Ala Cys Asn Ala Cys Arg Lys Ala Arg Asn Gln Val Val Leu Asp Asp
      100     105     110
Ala Ala Phe Glu Glu Leu Leu Thr His Leu Glu Glu Val Tyr Gly Phe
      115     120     125
Pro Gly Phe His Phe Phe Ser Asn Arg Asn Val Asn Glu Gly Phe Ser
      130     135     140
Gly Gly Glu Lys Lys Lys Asn Glu Leu Trp Gln Met Leu Ala Leu Glu
      145     150     155     160
Pro Lys Met Val Val Leu Asp Glu Pro Asp Ser Gly Leu Asp Val Asp
      165     170     175
Ala Leu Lys Gly Ile Cys Ser Val Leu Gln Arg Tyr Arg Gln Gln His
      180     185     190
Pro Glu Thr Ala Phe Cys Ile Val Thr His Asn Pro Arg Leu Gly Asp
      195     200     205
Leu Leu Gln Pro Asp His Val His Ile Leu Leu Asn Gly Arg Val Val
      210     215     220
Phe Ser Gly Asp Met His Leu Met Glu Glu Leu Glu Arg Lys Ser Tyr
      225     230     235     240
Gln Glu Leu Leu Asp Val Val Thr Gln Glu
      245     250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 736:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 94 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(726538..726819)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 736:

```

Leu His Ala Gly Asp Ser Met Leu Val Gly Glu Arg Cys Gly Ala Tyr
1      5      10      15
Thr Asp Pro Gln Ile Val Val Asn Asn Gly Glu Ser Cys Val Glu His
      20      25      30
Glu Ala Ala Thr Ser Lys Leu Arg Glu Asp Gln Leu Phe Tyr Leu Arg

```





## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 172 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(727469..727984)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 738:

```

Met Asp Ala Pro Val Asp Lys Phe Leu Gln Gln Gln Glu Tyr Pro Tyr
1           5           10           15
Gly Phe Val Thr Pro Ile Gln Ser Glu Gly Leu Ala Pro Gly Ile Ser
          20           25           30
Glu Glu His Ile Glu Gln Leu Val His Leu Arg Gly Glu Pro Lys Phe
          35           40           45
Leu Leu Asp Phe Arg Leu Lys Ala Phe Arg Leu Trp Gln Lys Met Glu
          50           55           60
Glu Pro Thr Trp Ala Arg Leu Arg Tyr Pro Pro Ile Ala Tyr Asp Asp
65           70           75           80
Ile Val Tyr Phe Ser Ala Pro Lys Thr Lys Lys Pro Leu Gly Lys Leu
          85           90           95
Glu Asp Ala Asp Pro Glu Ile Leu Glu Thr Phe Lys Lys Leu Gly Ile
          100          105          110
Pro Ile Asp Glu Gln Lys Arg Leu Leu Asn Val Gln Asp Val Ala Met
          115          120          125
Asp Leu Val Phe Asp Ser Val Ser Ile Gly Thr Thr Phe Lys Lys Thr
          130          135          140
Leu Glu Asp Ala Gly Val Ile Phe Cys Ser Phe Arg Glu Ala Ile His
145          150          155          160
Asn Tyr Pro Asp Leu Val Lys Arg Tyr Leu Gly Ser
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 739:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(728329..728778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 739:

```

Val Ile Tyr Phe Leu Glu Ile Arg Phe Trp Val Val Ala Arg Glu Gly
1           5           10           15
Phe Gly Val Phe Leu Arg Leu Val Leu Val Phe Trp Val Gly His Tyr
          20           25           30
Asn Leu Gly Leu Cys Tyr Leu Thr Leu Asp Lys Thr Arg Leu Ala Leu
          35           40           45
Lys Ala Phe Gln Glu Ser Leu Leu Asn Ala Glu Asp Ala Asp Ala
          50           55           60
His Phe Tyr Ile Gly Leu Ala His Met Asp Leu Lys Gln Asn Glu Gln

```

65				70				75				80			
Ala	Tyr	Asp	Ala	Phe	Tyr	Arg	Ala	Leu	Gly	Ile	Asn	Leu	Asp	His	Glu
				85					90					95	
Arg	Ser	His	Tyr	Leu	Leu	Gly	Tyr	Leu	His	His	Met	Gln	Gly	Glu	Ser
			100					105					110		
Glu	Lys	Ala	Glu	Thr	Glu	Leu	Ser	Phe	Leu	Val	Ala	Lys	Glu	Ser	Val
		115					120					125			
Phe	Ala	Pro	Leu	Leu	Gln	Lys	Thr	Val	Ser	Ser	Ser	Val	Phe	Leu	Ser
	130					135					140				
Lys	Lys	Glu	Thr	Leu	Phe										
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 740:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 196 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(728759..729346)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 740:

Gln	Gly	Thr	Thr	Met	Glu	Glu	Ala	Glu	Lys	His	Leu	Ala	Lys	Glu	Phe
1				5					10					15	
Leu	Cys	Ser	Gly	Ile	Asn	Leu	Phe	Leu	Ser	Gly	Glu	Tyr	Glu	Gln	Ala
			20					25					30		
Glu	Glu	Arg	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Asp	Ser	Glu	Ala	Gly	Leu
		35					40					45			
Ala	Tyr	Cys	Tyr	Leu	Gly	Ile	Ile	Ala	Leu	Glu	Thr	Gly	Arg	Thr	Ala
	50					55					60				
Glu	Ala	Leu	Val	Trp	Cys	Lys	Gln	Gly	Leu	Glu	Ala	Glu	Pro	Gly	Asp
65					70				75					80	
Ser	Tyr	Leu	Arg	Tyr	Cys	Tyr	Gly	Val	Ala	Leu	Asp	Lys	Ala	Asp	Arg
			85					90					95		
Leu	Glu	Glu	Ala	Ile	Gly	His	Tyr	Gln	Val	Tyr	Ala	Glu	Leu	His	Pro
			100					105					110		
Glu	Asp	Ile	Glu	Cys	Leu	Phe	Ser	Leu	Gly	Ser	Ala	Tyr	His	Arg	Leu
		115					120					125			
Leu	Arg	Tyr	Glu	Glu	Ala	Ile	Ala	Cys	Phe	Asp	Arg	Ile	Ala	Gln	Leu
	130					135					140				
Asp	Pro	Trp	Asn	Pro	Gln	Gly	Leu	Tyr	Asn	Lys	Ala	Val	Ile	Leu	Ser
145					150				155					160	
Asp	Met	Glu	Asp	Glu	Gly	Ala	Ile	Asp	Leu	Leu	Glu	Ser	Thr	Val	
			165					170					175		
Lys	Arg	Asn	Pro	Leu	Tyr	Trp	Lys	Ala	Trp	Val	Lys	Leu	Gly	Tyr	Leu
			180					185					190		
Leu	Ser	Arg	Asn												
			195												

(2) INFORMATIONS POUR LA SEQ ID NO: 741:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 995 acides aminés

(B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(729442..732426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 741:

Thr	Leu	Ala	Glu	Asn	Val	Leu	Gln	Tyr	Asn	Val	Gly	Ile	Ser	Tyr	Arg	1	5	10	15
Ala	Ile	Arg	Asp	Ile	Pro	Thr	Arg	Val	Trp	His	Thr	Asp	Glu	Gln	Gly	20	25	30	
Asn	Lys	Arg	Leu	Val	Pro	Val	Arg	Lys	Asp	Tyr	Ile	Lys	Lys	Phe	Ala	35	40	45	
Asp	Phe	Leu	Ala	Gln	Glu	Leu	His	Met	Asp	Arg	Asp	Phe	Val	Glu	Asp	50	55	60	
Thr	Ile	His	Ala	Lys	Ala	Ser	Val	Leu	Gly	Ser	Val	Pro	Tyr	Ile	Leu	65	70	75	80
Gln	Thr	Asn	Val	Ser	Glu	Arg	Thr	Phe	Leu	Arg	Leu	Lys	Met	Leu	Glu	85	90	95	
Lys	Asp	Trp	Pro	Gly	Leu	His	Val	Glu	Ser	Ser	Val	Arg	Arg	His	Tyr	100	105	110	
Pro	Glu	Gly	Arg	Thr	Val	Ala	Asp	Leu	Leu	Gly	Tyr	Val	Gly	Pro	Ile	115	120	125	
Ser	Ala	Glu	Glu	His	Arg	Lys	Ile	Thr	Arg	Glu	Leu	Gly	Asn	Leu	Arg	130	135	140	
Glu	Cys	Ile	Arg	Ala	Tyr	Glu	Glu	Gly	Glu	Asp	Pro	Lys	Phe	Pro	Ala	145	150	155	160
Gly	Ile	Ser	Ser	Val	Asp	Gln	Val	Arg	Lys	Leu	Leu	His	Glu	Leu	Glu	165	170	175	
Met	His	Ala	Tyr	Gly	Leu	Asn	Ser	Leu	Ile	Gly	Lys	Leu	Val	Val	Glu	180	185	190	
Ala	Phe	Cys	Asp	Arg	Lys	Leu	Arg	Gly	Leu	Ile	Gly	Lys	Arg	Ser	Met	195	200	205	
Leu	Val	Asp	Arg	Arg	Gly	Asn	Phe	Ile	Gln	Glu	Met	Glu	Gly	Ser	Ser	210	215	220	
Val	Gly	Ser	Pro	Gly	Arg	Thr	Ile	Gln	Leu	Thr	Ile	Ser	Thr	Glu	Leu	225	230	235	240
Gln	Ala	Phe	Ala	His	Glu	Leu	Leu	Ala	Glu	His	Glu	Arg	Gly	Glu	Cys	245	250	255	
Phe	Thr	Ile	Ile	Asp	Ser	Gly	Val	Ser	Asn	Asn	Ile	Leu	Pro	Pro	Phe	260	265	270	
Phe	Pro	Trp	Ile	Lys	Gly	Gly	Ala	Ile	Val	Ala	Met	Asp	Pro	Lys	Asn	275	280	285	
Gly	Gln	Ile	Leu	Ala	Met	Ala	Ser	Ser	Pro	Arg	Tyr	Asp	Asn	Asn	Asp	290	295	300	
Phe	Ile	Asn	Met	Lys	Asp	Ser	Pro	Asn	Gln	Glu	Glu	Cys	Arg	Ser	Ser	305	310	315	320
Val	Leu	Arg	Trp	Leu	Glu	Asn	Leu	Glu	Tyr	Ile	Gly	Glu	Val	Phe	Asp	325	330	335	
Arg	Arg	Val	Pro	Leu	Arg	Arg	Glu	Arg	Leu	Asp	Pro	Leu	Ser	Gly	Lys	340	345	350	
Tyr	Phe	Asp	Glu	Glu	Leu	Ser	Phe	Ser	Tyr	Arg	Ala	Phe	Leu	Asp	Phe	355	360	365	
Ile	Leu	Pro	Asp	Thr	Ser	Lys	Val	Lys	Gln	Met	Leu	Cys	Glu	Lys	Gly	370	375	380	
Ser	Ile	Gly	Leu	Ser	Ile	Tyr	Leu	Gln	Gly	Thr	Ile	Glu	Gln	Leu	Leu				

385	390										395										400
Glu Met Phe Glu Cys Glu Glu Lys Glu Cys Gly Leu Val Phe Asp Val																					
	405										410										415
Leu Phe Pro Lys Glu Asp Gly His Glu Ile Ile Gly Glu Val Thr Ser																					
	420										425										430
Leu Lys Arg Gln Lys Gln Phe Lys Ala Ile Leu Ala Glu Arg Glu Glu																					
	435										440										445
Glu Val Gln Ala Phe Arg Glu Arg Leu Gly Ser Ile Phe Ala Asp Leu																					
	450										455										460
Ser Ala Asn Tyr Asp Lys Ile Leu Phe Leu Asp Leu Leu Arg Thr Ala																					
465	470										475										480
Val Asp Pro Glu Lys Val Ser Ile Ser Leu Leu Ala Glu Ile Gly His																					
	485										490										495
Met Ser Val Leu Asp Phe Val Asp Tyr Gln Gly His Phe Ile Ala Leu																					
	500										505										510
Arg Lys Ser Phe Ala Lys Leu Met Glu Asn Ala Phe Ile Asp His Asp																					
	515										520										525
Phe Thr Ala Trp Arg Glu Glu His Phe Thr Gln Phe Ile Lys Gln Lys																					
	530										535										540
Arg Asp Glu Glu Leu Glu Arg Lys Gln Arg Tyr Pro Thr Pro Tyr Val																					
545	550										555										560
Asp Tyr Leu Val Glu Glu Arg Ser Arg Gln Tyr Ala Leu Phe Cys Arg																					
	565										570										575
Glu His Met Asp Ser Phe Ile Thr Phe Leu Leu Ser Glu Ile Glu Pro																					
	580										585										590
Pro Leu Gly Asn Pro Tyr Tyr Gln Glu Ile Ala Cys Trp Arg Gln Glu																					
	595										600										605
Leu Arg Ser Gly Ala Tyr Pro Ala Leu Glu Trp Arg Glu His Tyr Asp																					
	610										615										620
Phe Leu His Lys His Leu Ser Gln Thr Ser Tyr Asp Leu Cys Glu Leu																					
625	630										635										640
Phe Ala Ala Phe Arg Glu Phe Ser Glu Leu Lys Arg Pro Leu Tyr Gly																					
	645										650										655
Gln Tyr Pro Leu Thr Leu Thr Arg Asn Ile Glu Gln Ile Glu Gln Asp																					
	660										665										670
Leu Ile Ala Ser Phe Tyr Pro Leu Tyr Gly Tyr Gly His Leu Ser Ala																					
	675										680										685
His Ala Phe Gly Gln Ala Ala Thr Leu Gly Ser Ile Phe Lys Leu Val																					
	690										695										700
Ser Ala Tyr Ser Val Leu Val Gln His Leu Ser Asp Gln Glu Asp Leu																					
705	710										715										720
Ser Lys Leu Leu Val Ile Val Asp Lys Gln Ser Leu Gly Leu Arg Ser																					
	725										730										735
Gly Lys Pro His Val Gly Phe Phe Lys Asp Gly Ser Pro Ile Ala Ser																					
	740										745										750
Phe Phe Lys Gly Gly Ile Leu Pro Gly Asn Asp Tyr Ser Gly Arg Gly																					
	755										760										765
Tyr Ile Asp Leu Ile Ala Ala Leu Glu Met Ser Ser Asn Pro Tyr Phe																					
	770										775										780
Ser Leu Leu Val Ser Glu Tyr Leu Ser Asp Pro Glu Asp Leu Cys Glu																					
785	790										795										800
Ala Ala Lys Leu Phe Gly Phe Gly Glu Lys Thr Gly Ile Gly Leu Pro																					
	805										810										815
Gly Glu Tyr Ala Gly Arg Val Pro Ile Asp Val Ala Tyr Asn Arg Ser																					
	820										825										830
Gly Leu Tyr Ala Thr Ala Ile Gly Gln His Thr Leu Val Val Thr Pro																					
	835										840										845
Leu Gln Thr Ala Val Met Met Ala Thr Leu Val Asn Gly Gly Ile Val																					
	850										855										860

Tyr Gln Pro Ser Leu Ile Gln Gly Glu Trp Tyr Gln Gly Ser Phe Ser  
 865 870 875 880  
 Pro Glu Gln Ala Lys Lys Lys Arg Glu Ile Phe Leu Pro Asp Ser Ile  
 885 890 895  
 Val Asp Leu Phe Lys Arg Gly Met His Asn Val Ile Trp Gly Gln Tyr  
 900 905 910  
 Gly Thr Thr Arg Phe Met Arg Gln Arg Phe Ala Pro Glu Arg Leu Ala  
 915 920 925  
 Arg Ile Ile Gly Lys Thr Ser Thr Ala Glu Val Ile Ala Arg Val Gly  
 930 935 940  
 Leu Asp Arg Glu Arg Gly Arg Met Lys Leu Lys Asp Val Trp Phe Ala  
 945 950 955 960  
 Ala Val Gly Tyr Glu Asp Glu Ala Leu Ser His Pro Asp Ile Val Val  
 965 970 975  
 Val Val Tyr Leu Arg Leu Gly Glu Phe Gly Arg Asp Leu Arg Leu Trp  
 980 985 990  
 Gln Cys Val  
 995

(2) INFORMATIONS POUR LA SEQ ID NO: 742:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 394 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 733246..734427

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 742:

Met Lys Lys Leu Leu Lys Ser Val Leu Val Phe Ala Ala Leu Ser Ser  
 1 5 10 15  
 Ala Ser Ser Leu Gln Ala Leu Pro Val Gly Asn Pro Ala Glu Pro Ser  
 20 25 30  
 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys  
 35 40 45  
 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr  
 50 55 60  
 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Gln Thr Asp Val Asn Lys  
 65 70 75 80  
 Glu Phe Gln Met Gly Ala Lys Pro Thr Thr Ala Thr Gly Asn Ala Ala  
 85 90 95  
 Ala Pro Ser Thr Cys Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His  
 100 105 110  
 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Tyr Met Ala Leu Asn  
 115 120 125  
 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Thr Ser Gly  
 130 135 140  
 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly  
 145 150 155 160  
 Asp Asn Glu Asn His Ala Thr Val Ser Asp Ser Lys Leu Val Pro Asn  
 165 170 175  
 Met Ser Leu Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Thr Phe  
 180 185 190  
 Ala Trp Ser Ala Gly Ala Arg Ala Ala Leu Trp Glu Tyr Gly Cys Ala

```

      195              200              205
Thr Leu Gly Xaa Ser Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu
  210              215              220
Glu Leu Asn Val Leu Cys Asn Ala Ala Glu Phe Thr Ile Asn Lys Pro
  225              230              235              240
Lys Gly Tyr Val Gly Gln Glu Phe Pro Leu Asp Leu Lys Ala Gly Thr
              245              250              255
Asp Gly Val Thr Gly Thr Lys Asp Ala Ser Ile Asp Tyr His Glu Trp
              260              265              270
Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro Tyr
  275              280              285
Ile Gly Val Lys Trp Ser Arg Ala Ser Phe Asp Ala Asp Thr Ile Arg
  290              295              300
Ile Ala Gln Pro Lys Ser Ala Thr Thr Val Phe Asp Val Thr Thr Leu
  305              310              315              320
Asn Pro Thr Ile Ala Gly Ala Gly Asp Val Lys Ala Ser Ala Glu Gly
              325              330              335
Gln Leu Gly Asp Thr Met Gln Ile Val Ser Leu Gln Leu Asn Lys Met
              340              345              350
Lys Ser Arg Lys Ser Cys Gly Ile Ala Val Gly Thr Thr Ile Val Asp
  355              360              365
Ala Asp Lys Tyr Ala Val Thr Val Glu Thr Arg Leu Ile Asp Glu Arg
  370              375              380
Ala Ala His Val Asn Ala Gln Phe Arg Phe
  385              390

```

(2) INFORMATIONS POUR LA SEQ ID NO: 743:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 734814..735659

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 743:

```

Leu Glu Leu Pro Cys Lys Leu Thr Leu Lys Glu Leu Leu Glu Ser Gly
 1              5              10              15
Ala His Phe Gly His Gln Thr Ser Arg Trp Asn Pro Lys Met Lys Pro
 20              25              30
Phe Ile Phe Glu Glu Lys Asn Gly Leu Tyr Ile Ile Asp Leu Ala Lys
 35              40              45
Thr Leu Gly Gln Leu Lys Lys Ala Val Ser Cys Ile Gln Lys Thr Ile
 50              55              60
Asp Gln Glu Arg Ser Ile Leu Phe Val Gly Thr Lys Lys Gln Ala Lys
 65              70              75              80
Gln Ile Ile Arg Glu Ala Ala Ile Glu Cys Gly Glu Phe Phe Ala Ser
 85              90              95
Glu Arg Trp Leu Gly Gly Met Leu Thr Asn Met Ala Thr Ile Arg Asn
 100             105             110
Ser Val Lys Thr Leu Asn Arg Ile Glu Leu Asp Leu Glu Ala Ser Asn
 115             120             125
Ser Gly Leu Thr Lys Lys Glu Leu Ala Leu Leu Ala Lys Arg His Arg
 130             135             140

```

```

Lys Leu Leu Asn Asn Leu Glu Gly Val Arg His Met Asn Ser Leu Pro
145                      150                      155                      160
Gly Leu Leu Ile Val Ile Asp Pro Gly Tyr Glu Arg Ile Ala Val Ala
                      165                      170                      175
Glu Ala Gly Lys Leu Gly Ile Pro Val Met Ala Leu Val Asp Thr Asn
                      180                      185                      190
Cys Asp Pro Thr Pro Ile Asn His Val Ile Pro Cys Asn Asp Asp Ser
                      195                      200                      205
Ile Lys Ser Ile Arg Leu Ile Val Asn Thr Leu Lys Asp Ala Val Ile
                      210                      215                      220
Asp Ala Lys Lys Arg Leu Gly Val Glu Ile Leu Ser Pro Val Arg Pro
225                      230                      235                      240
Ala Glu Arg Pro Ala Glu Glu Ala Val Glu Glu Leu Pro Leu Pro Thr
                      245                      250                      255
Gly Glu Ala Gln Asp Glu Ala Ser Ser Lys Glu Gly Val Leu Leu Trp
                      260                      265                      270
Ala Asp Ile Asp Asn Cys Glu Ala Leu Lys
                      275                      280

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 744:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 282 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: 735659..736504

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 744:

```

Met Ser Asp Phe Ser Met Glu Thr Leu Lys Asn Leu Arg Gln Gln Thr
1      5      10      15
Gly Val Gly Leu Thr Lys Cys Lys Glu Ala Leu Glu His Ala Lys Gly
20      25      30
Asn Leu Glu Asp Ala Val Val Tyr Leu Arg Lys Leu Gly Leu Ala Ser
35      40      45
Ala Gly Lys Lys Glu His Arg Glu Thr Lys Glu Gly Val Ile Ala Ala
50      55      60
Arg Val Asp Glu Arg Gly Ala Ala Leu Val Glu Val Asn Val Glu Thr
65      70      75      80
Asp Phe Val Ala Asn Asn Ser Val Phe Arg Ala Phe Val Thr Ser Leu
85      90      95
Leu Ser Asp Leu Leu Asp His Lys Leu Ser Asp Val Glu Ala Leu Ala
100     105     110
Arg Val Met Ser Ser Gln Glu Pro Ser Leu Ser Val Glu Glu Leu Lys
115     120     125
Ala Val Thr Met Gln Thr Val Gly Glu Asn Ile Arg Ile Ser Arg Ala
130     135     140
Phe Tyr Thr Pro Val Asn Ser Gly Gln Ser Val Gly Ile Tyr Ser His
145     150     155     160
Gly Asn Gly Lys Ala Val Ala Ile Val Phe Leu Ser Gly Ser Glu Asn
165     170     175
Gln Glu Ala Leu Ala Lys Asp Ile Ala Met His Ile Val Ala Ser Gln
180     185     190
Pro Gln Phe Leu Ser Lys Glu Ser Val Pro Gln Glu Ile Leu Glu Arg

```





(2) INFORMATIONS POUR LA SEQ ID NO: 746:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 178 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 737254..737787

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 746:

Met	Thr	Leu	Ala	Ser	Ala	Glu	Lys	Glu	Met	Ala	Gly	Val	Leu	Thr	Phe	1	5	10	15
Phe	Gln	Lys	Glu	Thr	Arg	Gly	Phe	Arg	Thr	Gly	Lys	Ala	His	Pro	Ala	20	25	30	
Leu	Val	Glu	Thr	Val	Thr	Val	Glu	Val	Tyr	Gly	Thr	Thr	Met	Arg	Leu	35	40	45	
Ser	Asp	Ile	Ala	Ser	Ile	Ser	Val	Ser	Asp	Met	Arg	Gln	Leu	Leu	Ile	50	55	60	
Ser	Pro	Tyr	Asp	Ala	Gly	Thr	Val	Ser	Ala	Ile	Ser	Lys	Gly	Ile	Leu	65	70	75	80
Ala	Ala	Asn	Leu	Asn	Leu	Gln	Pro	Ile	Val	Glu	Gly	Ala	Thr	Val	Arg	85	90	95	
Ile	Asn	Val	Pro	Ala	Tyr	Gly	Arg	Ile	Pro	Thr	Arg	Ser	Asn	Lys	Gln	100	105	110	
Leu	Lys	Arg	Lys	Ser	Glu	Glu	Ala	Lys	Val	Ala	Ile	Arg	Asn	Ile	Arg	115	120	125	
Arg	Thr	Phe	Asn	Asp	Arg	Leu	Xaa	Lys	Asp	Asp	Asn	Leu	Thr	Glu	Asp	130	135	140	
Ala	Val	Lys	Ser	Leu	Glu	Lys	Lys	Ile	Gln	Glu	Leu	Thr	Asp	Lys	Phe	145	150	155	160
Cys	Lys	Gln	Ile	Glu	Glu	Leu	Ala	Lys	Gln	Lys	Glu	Ala	Glu	Leu	Ala	165	170	175	
Thr	Val																		

(2) INFORMATIONS POUR LA SEQ ID NO: 747:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 246 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 737942..738679

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 747:

Gln	Gly	Phe	Glu	Ser	Pro	Trp	Gly	His	Tyr	Lys	Lys	Lys	Cys	Gly	Ser	1	5	10	15
Leu	Ala	Gln	Arg	Leu	Glu	His	Leu	Thr	Phe	Asn	Glu	Arg	Val	Glu	Gly				



Gly	Thr	Ala	Leu	Ile	Ala	Arg	Ala	Phe	Val	His	Val	Pro	Ala	Leu	Lys
		115					120					125			
Tyr	Gly	Asp	Ala	Leu	Ser	Glu	Leu	Leu	Val	Pro	Tyr	Gln	Arg	Glu	Phe
	130					135					140				
Ala	Ser	Ser	Ser	Leu	Leu	Pro	Leu	Ser	Gln	Glu	Ser	Leu	Gly	Asp	Ile
145					150					155					160
Leu	Cys	Leu	Ser	Asn	Ile	Cys	Ser	Leu	Gly	Leu	Ser	Glu	Glu	Gln	Ile
				165					170					175	
Leu	Ser	Ser	Leu	Arg	Leu	Val	Val	Ser	Lys	Ile	Leu	Ser	Ala	Glu	Lys
			180					185					190		
Glu	Ala	Arg	Asn	Gln	Leu	Val	Lys	Glu	Asn	Xaa	Thr	Glu	Xaa	Lys	Asn
	195						200					205			
Arg	Ile	Leu	Arg	Ser	Val	Gly	Met	Leu	Thr	His	Ser	Cys	Cys	Leu	Asp
	210					215					220				
Leu	Gln	Glu	Ala	Leu	Asp	Ala	Thr	Ser	Trp	Ile	Gln	Leu	Gly	Met	Ser
225					230					235					240
Met	Gln	Trp	Ile	Glu	Asp	Ser	Glu	Asn	His	Pro	Leu	Trp	Asn	Pro	Leu
				245					250					255	
Phe	Trp	Asp	Leu	Arg	Arg	Gly	His	Leu	Ala	Leu	Tyr	Asn	Gln	Asp	Thr
			260				265						270		
Ala	Asn	Arg	Ser	Ile	Glu	Lys	Glu	Val	Ile	Ala	Gln	Ile	Arg	Ala	Lys
	275						280					285			
Ala	Thr	Lys	Pro	Gln	Ala	Glu	Arg	Leu	Ile	Ile	Arg	Ile			
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 749:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 666 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(740060..742057)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 749:

Arg	Val	Arg	Ile	Leu	Lys	Lys	Ser	Asp	Asn	Thr	Val	Asn	Phe	Glu	Asp
1				5				10						15	
Ile	Ser	Ile	Leu	Glu	Leu	Leu	Gln	Phe	Val	Ser	Lys	Ile	Ser	Gly	Thr
			20				25						30		
Asn	Phe	Val	Phe	Asp	Ser	Asn	Asp	Leu	Gln	Phe	Asn	Val	Thr	Ile	Val
	35					40					45				
Ser	His	Asp	Pro	Thr	Ser	Val	Asp	Asp	Leu	Ala	Thr	Ile	Leu	Leu	Gln
	50					55					60				
Val	Leu	Lys	Met	His	Asp	Leu	Lys	Val	Val	Glu	Gln	Gly	Asn	Asn	Val
65				70					75					80	
Leu	Ile	Tyr	Arg	Asn	Pro	Lys	Leu	Ser	Lys	Leu	Ser	Thr	Val	Val	Thr
			85					90					95		
Asp	Gly	Ser	Ala	Lys	Asp	Thr	Cys	Glu	Ala	Val	Val	Val	Thr	Arg	Val
			100					105					110		
Phe	Arg	Leu	Tyr	Ser	Val	Ser	Pro	Ser	Ala	Ala	Val	Gly	Ile	Ile	Gln
	115					120						125			
Pro	Leu	Leu	Ser	His	Asp	Ala	Ile	Ile	Ser	Ala	Ser	Glu	Ser	Thr	Arg
	130					135					140				
His	Ile	Ile	Val	Ser	Asp	Ile	Ala	Gly	Asn	Ile	Glu	Lys	Val	Arg	Glu

145					150					155					160
Leu	Leu	Gln	Ala	Leu	Asp	Ser	Pro	Gly	Thr	Ala	Ile	Asp	Met	Ser	Glu
				165					170					175	
Tyr	Asp	Val	Gln	Phe	Ala	Asn	Pro	Ala	Ala	Leu	Val	Ser	Tyr	Cys	Gln
			180					185					190		
Asp	Val	Leu	Gly	Ala	Met	Ala	Glu	Glu	Glu	Ala	Phe	Gln	Ile	Phe	Ile
		195					200					205			
Gln	Pro	Gly	Thr	Asn	Lys	Ile	Phe	Val	Ile	Ser	Ser	Pro	Arg	Leu	Thr
	210					215					220				
Ala	Lys	Thr	Ile	Gln	Leu	Leu	Glu	Ser	Leu	Asp	Ile	Pro	Glu	Met	Ala
225					230					235					240
His	Thr	Leu	Asp	Asp	Val	Thr	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Ser	Ser
				245					250					255	
Gly	Ala	Ala	Asn	Pro	Lys	Ser	Leu	Arg	Phe	Phe	Met	Tyr	Lys	Leu	Lys
			260					265					270		
Tyr	Gln	Asn	Gly	Ala	Ala	Ile	Ala	Gln	Ala	Ile	Gln	Asp	Ile	Gly	Tyr
		275					280					285			
Asn	Leu	Tyr	Val	Thr	Thr	Ala	Met	Asp	Glu	Asp	Phe	Ile	Asn	Thr	Leu
	290					295					300				
Asn	Ser	Ile	Gln	Trp	Leu	Pro	Val	Asn	Asn	Ser	Ile	Val	Val	Ile	Gly
305					310					315					320
Asn	Gln	Ala	Asn	Val	Asp	Lys	Val	Val	Ser	Leu	Leu	Asn	Gly	Leu	Asp
				325					330					335	
Leu	Pro	Pro	Lys	Gln	Val	Tyr	Ile	Glu	Val	Leu	Ile	Leu	Glu	Thr	Ser
			340					345					350		
Leu	Glu	Lys	Ser	Trp	Asp	Phe	Gly	Val	Gln	Trp	Ala	Ala	Leu	Gly	Asp
		355					360					365			
Glu	Gln	Gly	Lys	Val	Ala	Tyr	Ala	Ser	Gly	Leu	Leu	Ser	Asn	Thr	Gly
	370					375					380				
Leu	Thr	Asp	Pro	Leu	Arg	Asn	Gln	Ser	Leu	Pro	Val	Ala	Leu	Asn	Pro
385					390					395					400
Gly	Asn	Ile	Ser	Leu	Pro	Thr	Pro	Gly	Gln	Leu	Ala	Gly	Ile	Ser	Asp
				405					410					415	
Met	Met	Tyr	Gly	Ser	Ser	Ala	Phe	Gly	Leu	Gly	Ile	Ile	Gly	Asn	Val
			420					425					430		
Leu	Ser	His	Asn	Gly	Lys	Ser	Tyr	Leu	Thr	Leu	Gly	Gly	Leu	Leu	Ser
		435					440					445			
Ala	Leu	Asp	Gln	Asp	Gly	Asp	Thr	Thr	Val	Val	Leu	Asn	Pro	Arg	Ile
	450					455					460				
Met	Ala	Gln	Asp	Thr	Gln	Gln	Ala	Ser	Phe	Phe	Val	Gly	Gln	Thr	Ile
465					470					475					480
Pro	Phe	Gln	Thr	Thr	Ser	Thr	Val	Ile	Gln	Glu	Thr	Gly	Ser	Val	Thr
				485					490					495	
Gln	Asn	Ile	Glu	Tyr	Glu	Asp	Ile	Gly	Val	Asn	Leu	Val	Val	Thr	Ser

```

Tyr Arg Tyr Asn Trp Glu Ser Glu Arg Gly Ser Leu Glu Val Ala Pro
625                      630                      635                      640
Arg His Ala Pro Glu Cys Gln His Ile Pro Lys Val Gln Ala Glu Ser
                      645                      650                      655
Asn Phe Lys Met Leu Glu Ile Glu Ala Glu
                      660                      665

```

(2) INFORMATIONS POUR LA SEQ ID NO: 750:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 275 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(742045..742869)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 750:

```

Gln Lys Ser Leu Ser Leu Asn Thr Tyr Gln Leu Lys Lys Ser Pro Val
1                      5                      10                      15
Asn Ile Val Thr Ser Asn Ile Gly Ser Lys Ile Leu Arg Ile Ile Gln
20                      25                      30
Asn Asn Lys Lys Leu Gly Leu Leu Ser Ala Leu Val Val Leu Asp Ala
35                      40                      45
Ala Leu Leu Ser Val Asn Ser Arg Ser Gly Glu Gly Leu Ile Gly Gln
50                      55                      60
Ser Ala Ser Leu Pro Asn Tyr His Glu Ala Glu Gln Gln Ile Ala Ala
65                      70                      75                      80
Cys Pro Lys Asn Ile Ala Lys Asn Leu Ala Lys Lys Ser Ser Pro Gly
85                      90                      95
Ala Lys Pro Thr Val Gly Ala Pro Ser Pro Ala Arg Pro Val Ser Val
100                      105                      110
Lys Ala Ala Pro Ala Lys Pro Gln Ala Pro Val Ala Gln Thr Arg His
115                      120                      125
Phe Lys Lys Ser His Gln Ile Phe Ser Pro Asn Phe Thr Gln Ser Ser
130                      135                      140
Gln Gln Val Asn Lys Leu Glu Glu Arg Arg Arg Pro Leu Glu Ser Arg
145                      150                      155                      160
Tyr Leu Gln Gly Ala Ala Lys Gln Ala Ala Ala Lys Glu Lys Lys
165                      170                      175
Ala Leu Glu Gln Glu Val Ser Lys Gln Glu Glu Glu Ala Ser Lys Leu
180                      185                      190
Trp Glu Glu Lys Gln Ser Tyr Ala Arg Arg Ala Val Asn Ala Ile Asn
195                      200                      205
Phe Ser Val Arg Lys Gln Ile Glu Glu Gln Gln Lys Thr Ile Ser Asn
210                      215                      220
Pro Gly Asn Asp Gln Thr Leu Pro Gly Lys Lys Asp Pro His Thr Ser
225                      230                      235                      240
Gly Glu Pro Val Ile Gln Thr Val Gln Asp Cys Ser Gln Asp Gln Glu
245                      250                      255
Ala Arg Glu Lys Ser Ser Arg Ala Ile Lys Gln Thr Phe Ser Asp Val
260                      265                      270
Ser Gly Ser
275

```

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 751:

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 752:

Val	Phe	Met	Leu	Arg	Ser	Gly	Val	Ser	Phe	Ser	Ser	Ser	Lys	Thr	Asn
1				5					10					15	
Tyr	Leu	Leu	Thr	Arg	Glu	Leu	Ser	Arg	Lys	Val	Gly	Leu	Thr	Val	Tyr
			20					25					30		

Gln Gly Val Asp Glu His Ser Ser Arg Pro Val Val Ile Lys Thr Leu  
                   35                                  40                                  45  
 Val Ser Pro Gly Ile His Asp Arg Arg Phe Leu Arg Ala Phe Glu Glu  
                   50                                  55                                  60  
 Glu Ala Arg Ile Met Gln Leu Val Thr His Pro Ala Phe Val Arg Leu  
   65                                  70                                  75                                  80  
 Glu Asp Arg Gly Glu Cys Glu Gln Gly Arg Tyr Leu Val Ser Glu Tyr  
                                   85                                  90                                  95  
 Ile Leu Gly Ser Ser Leu Arg Asp Ser Ile Leu Ser Ser Gln Ile Ser  
                                   100                                  105                                  110  
 Leu Asp Lys Ala Ile Ser Ile Val Leu Gln Val Ala Gln Val Ile Thr  
                                   115                                  120                                  125  
 Thr Leu His Arg His Gly Val Leu His Leu Asp Ile Lys Pro Glu Asn  
                                   130                                  135                                  140  
 Ile Val Leu Ser Gln Ser Gly Glu Ile Lys Leu Ile Asp Tyr Gly Leu  
   145                                  150                                  155                                  160  
 Ser Ala Trp Gln Phe Asn His Trp Gly Ser Pro Ala Tyr Met Ser Pro  
                                   165                                  170                                  175  
 Glu Gln Ser Arg Gln Glu Pro Pro Ser Pro Ala Ser Asp Val Tyr Ser  
                                   180                                  185                                  190  
 Leu Ala Leu Leu Ala Tyr Glu Leu Ile Met Gly Gln Leu Ala Leu Gly  
                                   195                                  200                                  205  
 Lys Val Tyr Val Ser Leu Leu Pro Ser Lys Ile Ser Lys Ile Leu Ile  
                                   210                                  215                                  220  
 Gln Ala Leu Gln Pro Ser Pro Ala Ala Arg Phe Ser Ser Met Gln Glu  
   225                                  230                                  235                                  240  
 Phe Ala Glu Ala Leu Gln Asp Tyr Leu Leu His Asp Val His Glu Asp  
                                   245                                  250                                  255  
 Tyr Arg Lys Lys Asp His Val Val Ala Gln Ile Glu Gln Trp His Asn  
                                   260                                  265                                  270  
 Gln Arg Ala Trp Leu Ser Pro Glu Lys Leu Ser Ala Pro Glu Glu Ile  
                                   275                                  280                                  285  
 Cys Val His Ile Tyr Ser Gln Lys Glu Pro Cys Tyr Leu His Asn Ile  
                                   290                                  295                                  300  
 Tyr Tyr Asp Met Leu Thr Ser Gly Asn Val Ala Glu Phe Trp Phe Ser  
   305                                  310                                  315                                  320  
 Thr Leu Gln Glu Thr Val Val Leu Arg Leu Ala  
                                   325                                  330

(2) INFORMATIONS POUR LA SEQ ID NO: 753:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 95 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(744430..744714)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 753:

Leu Lys Leu Gln Asp Cys Lys Arg Cys Asn Gln Lys Arg Arg Leu Lys  
   1                                  5                                  10                                  15  
 Asn Leu Val Lys Glu Val Arg Gln Leu Pro Leu Pro Ser Ala Thr Lys  
                                   20                                  25                                  30  
 Ile Val Ala Glu Val Ala Arg Tyr Ser Leu Ser Val Gly Glu Phe Leu

```

          35          40          45
Lys Leu Gly Pro Gly Ser Val Leu Gln Phe Asp Gly Val His Pro Thr
  50          55          60
Leu Gly Val Asp Ile Ile Leu Asn Gly Ala Gln Val Gly Arg Gly Asn
  65          70          75          80
Ile Ile Ala Leu Gln Asp Val Leu Gly Ile Arg Val Leu Glu Val
          85          90          95

```

(2) INFORMATIONS POUR LA SEQ ID NO: 754:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(744611..744985)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 754:

```

Asn Tyr Ser Ala Glu Pro Cys Arg Phe Leu Glu Glu Lys Asp Gln Ala
 1          5          10          15
Phe Asp Met Gln Lys Val Asp Leu Gln Thr Pro Ile Thr Leu Ala Val
 20          25          30
Glu Val Gly Phe Cys Gln Ile Ser Glu Glu Asp Trp His Gln Val Val
 35          40          45
Pro Gly Ser Phe Ile Leu Leu Asp Ala Cys Leu Tyr Asp Pro Asp Thr
 50          55          60
Gly Asp Ala Gly Ala Phe Leu Ser Ile Gln Arg Thr Arg Phe Phe Gly
 65          70          75          80
Gly Arg Phe Leu Asp Lys Gln Ser Gly Ser Phe Lys Ile Thr Gly Leu
 85          90          95
Gln Glu Met Gln Pro Glu Glu Ala Pro Glu Glu Pro Ser Glu Gly Gly
 100          105          110
Pro Ala Thr Pro Phe Ala Phe Gly Asn Lys Asn Arg Cys
 115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 755:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 200 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(744958..745557)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 755:

```

Gly Ile Pro Met Ala Val Ala Ala Glu Pro Ser Ser Asn Trp Leu Lys
 1          5          10          15
Ala Arg Asp Glu Leu Leu Ser Ser Leu Gln Glu Gln Lys Glu Gly Met
 20          25          30

```



Phe	Ser	Phe	Pro	Val	Phe	Pro	Lys	Gln	Glu	Cys	Glu	Gln	Lys	Leu	Lys
		35					40					45			
Asp	Lys	Phe	His	Met	Glu	Glu	Val	Glu	Leu	Ser	Phe	Glu	Ser	Arg	Gly
	50					55					60				
Leu	Leu	Ser	Val	Ala	Ala	Ala	Val	Gln	Glu	Tyr	Gly	Glu	Arg	Ile	Leu
65				70						75					80
Leu	Gln	Pro	Phe	Leu	Ala	Asn	Pro	Phe	Glu	Ser	Gly	Glu	Phe	Tyr	Ile
			85						90					95	
Val	Ser	Ser	Glu	Glu	Asp	Leu	Gln	Ala	Leu	Ile	Gly	Thr	Ile	Phe	Asn
			100					105					110		
Asp	Ser	Ser	Leu	Ala	Ser	Tyr	Phe	Tyr	Glu	Lys	Asp	Arg	Leu	Leu	Gly
		115					120					125			
Phe	His	Tyr	Tyr	Phe	Val	Ala	Glu	Ile	Cys	Lys	Leu	Leu	Gln	Glu	Ser
	130					135					140				
Pro	Trp	Ile	Pro	Ser	Met	Ser	Val	Lys	Val	Thr	Gly	Asp	Val	Ala	Phe
145					150					155					160
Ser	Ala	Arg	Ala	Leu	Glu	Gly	Glu	Tyr	His	Val	Ile	Gln	Val	Ser	Cys
				165					170					175	
Cys	Leu	Asp	Gly	Ser	Cys	Ile	Arg	Phe	Ser	Ile	Leu	Val	Pro	Glu	Thr
			180					185					190		
Thr	Ala	Gln	Ser	Leu	Val	Asp	Ser								
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 756:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(745561..746412)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 756:

Phe	Met	Glu	Leu	Asn	Lys	Thr	Ser	Glu	Ser	Leu	Phe	Ser	Ala	Lys	Ile
1				5					10					15	
Asp	His	Asn	His	Pro	Arg	Thr	Glu	Ala	His	Glu	Pro	Arg	Asp	Gln	Arg
		20						25					30		
Glu	Val	Arg	Val	Phe	Ser	Leu	Glu	Gly	Arg	Ser	Ser	Thr	Arg	Gln	Glu
		35					40					45			
Lys	Ala	Asp	Arg	Met	Pro	Gly	Arg	Thr	Ser	Ser	Arg	Gln	Glu	Ser	Ser
	50					55					60				
Lys	Ser	Ser	Glu	Glu	Gly	Ala	Val	His	Glu	Ser	Thr	Ala	Gly	Val	Ser
65				70					75					80	
Ser	Lys	Glu	Glu	Glu	Ser	Lys	Gly	Asp	Gly	Phe	Phe	Thr	Gly	Gly	
			85					90					95		
Asn	Pro	Thr	Ser	Gly	Met	Ala	Leu	Val	Glu	Thr	Pro	Met	Ala	Val	Val
			100					105					110		
Ser	Glu	Ala	Met	Met	Glu	Thr	Ser	Thr	Met	Thr	Val	Ser	Gln	Val	Asp
		115					120					125			
Leu	Gln	Trp	Val	Glu	Gln	Leu	Val	Thr	Ser	Thr	Val	Glu	Ser	Leu	Leu
	130					135					140				
Val	Ala	Asp	Ile	Asp	Gly	Lys	Gln	Leu	Val	Glu	Ile	Val	Leu	Asp	Asn
145					150					155					160
Ser	Asn	Thr	Val	Pro	Ala	Ala	Phe	Cys	Gly	Ala	Asn	Leu	Thr	Leu	Val

				165					170					175					
Gln	Thr	Gly	Glu	Glu	Ile	Ser	Val	Ser	Phe	Ser	Asn	Phe	Val	Asp	Gln				
			180					185						190					
Ala	Gln	Leu	Thr	Glu	Ala	Thr	Gln	Leu	Val	Gln	Gln	Asn	Pro	Lys	Gln				
		195					200					205							
Leu	Val	Ser	Leu	Val	Glu	Ser	Leu	Lys	Ala	Arg	Gln	Leu	Asn	Leu	Thr				
		210				215					220								
Glu	Leu	Val	Val	Gly	Asn	Val	Ala	Val	Ser	Leu	Pro	Met	Ile	Glu	Lys				
225					230					235					240				
Ile	Glu	Thr	Pro	Leu	His	Met	Ile	Ala	Ala	Thr	Ile	Arg	His	His	Asp				
				245					250					255					
Gln	Glu	Gly	Asp	Gln	Glu	Gly	Glu	Gly	Arg	Gln	Asp	Gln	His	Gln	Gly				
			260				265							270					
Gln	His	Gln	Glu	Lys	Lys	Val	Glu	Glu	Ala	His	Ile								
		275					280												

(2) INFORMATIONS POUR LA SEQ ID NO: 757:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(746416..746772)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 757:

Glu	Ser	Leu	Tyr	Ala	Glu	Asn	Ser	Pro	Leu	Arg	Glu	Gln	Leu	Asp	Asp				
1				5				10					15						
Gly	Thr	Thr	Ser	Asp	Ala	Ile	Leu	Lys	Met	Lys	Ala	Tyr	Ile	Lys	Val				
			20				25					30							
Val	Ala	Ile	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Val	Asn	Lys	Gln	Lys					
		35				40				45									
Glu	Asn	Val	Leu	Ala	Ala	Xaa	Lys	Glu	Leu	Glu	Arg	Ala	Glu	Val	Glu				
	50					55				60									
Leu	Thr	Lys	Arg	Arg	Lys	Glu	Glu	Glu	Lys	Thr	Arg	Leu	His	Lys	Glu				
65				70				75					80						
Glu	Trp	Met	Lys	Glu	Ala	Leu	Lys	Glu	Glu	Ala	Arg	Gln	Glu	Glu	Lys				
			85				90						95						
Glu	Gln	Asp	Glu	Met	Gly	Gln	Leu	Leu	His	Gln	Leu	Leu	Lys	Gln	Lys				
		100					105						110						
Gln	Arg	Glu	Ser	Gly	Glu	Asn													
		115																	

(2) INFORMATIONS POUR LA SEQ ID NO: 758:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 442 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEO ID NO: 758:

Met 1	Glu	Glu	Ile	Thr 5	Thr	Glu	Phe	Asn	Thr 10	Leu	Met	Thr	Glu	Leu 15	Pro
Asp	Val	Gln	Leu 20	Thr	Ala	Val	Val	Gly 25	Arg	Ile	Ile	Glu 30	Val	Val	Gly
Met	Leu	Ile 35	Lys	Ala	Val	Val	Pro 40	Asp	Val	Arg	Val	Gly 45	Glu	Val	Cys
Leu	Val 50	Lys	Arg	His	Gly	Met 55	Glu	Pro	Leu	Val	Thr 60	Glu	Val	Val	Gly
Phe 65	Thr	Gln	Asn	Phe 70	Val	Phe	Leu	Ser	Pro	Leu	Gly 75	Glu	Leu	Thr	Gly 80
Val	Ser	Pro	Ser 85	Ser	Glu	Val	Met	Ala	Thr 90	Gly	Leu	Pro	Leu	His 95	Ile
Arg	Ala	Gly 100	Glu	Gly	Leu	Leu	Gly	Arg 105	Val	Leu	Asn	Gly 110	Leu	Gly	Asn
Pro	Ile 115	Asp	Thr	Glu	Thr	Lys	Gly 120	Pro	Leu	Glu	Asn 125	Val	Asp	Ala	Ile
Tyr	Pro 130	Ile	Phe	Lys	Ala	Pro 135	Pro	Asp	Pro	Leu	His 140	Arg	Ala	Lys	Leu
Arg 145	Thr	Ile	Leu	Ser 150	Thr	Gly	Val	Arg	Cys	Ile	Asp 155	Gly	Met	Leu	Thr 160
Val	Ala	Lys 165	Gly	Gln	Arg	Ile	Gly	Ile	Xaa 170	Ala	Gly	Ala	Gly	Val 175	Gly
Lys	Ser	Ser 180	Leu	Leu	Gly	Met	Ile	Ala 185	Arg	Asn	Ala	Glu 190	Glu	Ala	Asp
Ile	Asn 195	Val	Ile	Ala	Leu	Ile	Gly 200	Glu	Arg	Gly	Arg 205	Glu	Val	Arg	Glu
Phe 210	Ile	Glu	Asn	Asp	Leu	Gly 215	Glu	Glu	Gly	Met 220	Lys	Arg	Ser	Ile	Ile
Val 225	Val	Ser	Thr	Ser 230	Asp	Gln	Ser	Ser	Gln	Leu 235	Arg	Leu	Asn	Ala	Ala 240
Tyr	Val	Gly 245	Thr	Ala	Ile	Ala	Glu	Tyr	Phe 250	Arg	Asp	Gln	Gly	Lys 255	Thr
Val	Val	Leu 260	Met	Met	Asp	Ser	Val	Thr 265	Arg	Phe	Ala	Arg 270	Ala	Leu	Arg
Glu	Val	Gly 275	Leu	Ala	Ala	Gly	Glu 280	Pro	Pro	Ala	Arg 285	Ala	Gly	Tyr	Thr
Pro	Ser 290	Val	Phe	Ser	Thr	Leu 295	Pro	Lys	Leu	Leu	Glu 300	Arg	Ala	Gly	Ala
Ser 305	Asp	Lys	Gly	Thr 310	Ile	Thr	Ala	Phe	Tyr	Thr 315	Val	Leu	Val	Ala	Gly 320
Asp	Asp	Met	Asn 325	Glu	Pro	Val	Ala	Asp	Glu 330	Val	Lys	Ser	Ile	Leu 335	Asp
Gly	His	Ile 340	Val	Leu	Ser	Asn	Ala	Leu 345	Ala	Gln	Ala	Tyr 350	His	Tyr	Pro
Ala	Ile 355	Asp	Val	Leu	Ala	Ser	Ile 360	Ser	Arg	Leu	Leu 365	Thr	Ala	Ile	Val
Pro	Glu 370	Glu	Gln	Arg	Arg	Ile 375	Ile	Gly	Arg	Ala	Arg 380	Glu	Val	Leu	Ala
Lys 385	Tyr	Lys	Ala	Asn 390	Glu	Met	Leu	Ile	Arg	Ile 395	Gly	Glu	Tyr	Arg	Arg 400
Gly	Ser	Asp	Arg 405	Glu	Val	Asp	Phe	Ala	Ile 410	Asp	His	Ile	Asp	Lys 415	Leu
Asn	Arg	Phe 420	Leu	Lys	Gln	Asp	Ile	His 425	Glu	Lys	Thr 430	Asn	Tyr	Glu	Glu
Ala	Ala	Gln	Gln	Leu	Arg	Ala	Ile	Phe	Arg						

435

440

(2) INFORMATIONS POUR LA SEQ ID NO: 759:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 231 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(748274..748966)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 759:

```

Ile Arg Glu Arg Val Gly Tyr Ser Met Ile Asp Pro Leu Lys Leu Phe
1           5           10           15
Pro Asn Phe Asp Gly Asp Lys Glu Ser Ala Ala Val Asn Lys Pro Ser
          20           25           30
Ala Ser Pro Met Pro Ser Glu Leu Ser Lys Asn Val Ala Ser Phe Ser
          35           40           45
Leu Gly Gly Gly Gly Ala Ala Leu Asp Ser Thr Val Ser Thr Glu Lys
          50           55           60
Leu Ser Leu Met Ala Met Met Gln Asp Lys Asn Ser Gln Leu Ile Asp
65           70           75           80
Pro Glu Leu Glu Glu Ala Leu Asn Ser Glu Glu Leu Gln Glu Gln Ile
          85           90           95
His Leu Leu Lys Ser Arg Leu Trp Asp Ala Gln Thr Gln Met Gln Met
          100          105          110
Gln Asp Pro Asp Lys Leu Ala Ser Glu His Val Asp Ala Leu Gly Val
          115          120          125
Ile Val Asp Leu Ile Asn Gly Asp Phe Gln Ala Ile Ala Glu His Thr
          130          135          140
Gln Gln Thr Val Lys Gln Gly Asn Gly Asp Glu Glu Lys Ser Val Thr
          145          150          155          160
Arg Lys Ile Val Asp Trp Val Ser Ser Gly Glu Glu Ile Leu Asn Arg
          165          170          175
Ala Leu Leu Tyr Phe Ser Asp Arg Asn Gly Glu Arg Glu Thr Leu Ala
          180          185          190
Asp Phe Leu Lys Val Gln Tyr Ala Val Gln Arg Ala Thr Gln Arg Ala
          195          200          205
Glu Leu Phe Ala Ser Ile Leu Gly Ala Thr Val Ser Ser Val Lys Thr
          210          215          220
Ile Met Thr Thr Gln Leu Gly
225          230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 760:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(748965..749426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 760:

Asn	Lys	Arg	Trp	Val	Met	Ala	Asp	Leu	Asp	Val	Phe	Lys	Glu	Asp	Phe
1				5					10					15	
Ala	Leu	Leu	Phe	Glu	Ala	Gly	Met	Val	Ala	Ile	Lys	Gln	Gly	Asp	Glu
			20					25					30		
Ala	Ser	Ala	Lys	Ala	Leu	Phe	Gln	Ala	Leu	Gln	Val	Leu	Asp	Pro	Glu
		35					40					45			
His	Thr	Ala	His	Glu	Leu	Gly	Ser	Gly	Leu	Leu	His	Leu	His	Lys	Met
	50					55					60				
Glu	Leu	Thr	Lys	Ala	Glu	Val	Leu	Phe	Arg	Ala	Ile	Val	Glu	Lys	Asp
65					70				75						80
Pro	Glu	Asn	Trp	Ser	Ala	Lys	Ala	Phe	Leu	Ser	Leu	Thr	Leu	Met	Met
				85					90					95	
Ile	Val	Leu	Gln	Gln	Gly	Ser	Ser	Phe	Glu	Val	Arg	Arg	Ser	Ser	Leu
			100					105					110		
Glu	Arg	Cys	Leu	Gln	Leu	Ala	Asp	Gln	Val	Leu	Glu	Ser	Cys	Glu	Val
		115					120					125			
Glu	Ser	Thr	Arg	Ala	Leu	Ala	Lys	Ser	Val	Leu	Asp	Trp	His	Asp	Gly
	130					135					140				
Leu	Val	Ala	Lys	Ser	Gly	Gly	Pro	Leu	Asn						
145						150									

(2) INFORMATIONS POUR LA SEQ ID NO: 761:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 90 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(749433..749702)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 761:

Thr	Val	Lys	Glu	Arg	Val	Ser	Met	Ala	Ser	Gly	Ser	Cys	Ser	Ala	Phe
1				5					10					15	
Asn	Phe	Asn	Gln	Met	Leu	Asp	Gly	Val	Cys	Lys	Tyr	Val	Gln	Gly	Val
			20					25					30		
Gln	Gln	Tyr	Leu	Thr	Glu	Leu	Glu	Thr	Ser	Thr	Gln	Gly	Thr	Val	Asp
		35					40					45			
Leu	Gly	Thr	Met	Phe	Asn	Leu	Gln	Phe	Arg	Met	Gln	Ile	Leu	Ser	Gln
	50					55					60				
Tyr	Met	Glu	Ser	Val	Ser	Asn	Ile	Leu	Thr	Ala	Val	Asn	Thr	Glu	Met
65					70					75					80
Ile	Thr	Met	Ala	Arg	Ala	Val	Lys	Gly	Ser						
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 762:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 103 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(749721..750029)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 762:

```

Asn Ile Lys Leu Ser Thr Ile Asn Arg Gln Phe Glu Val Tyr Leu Ile
1           5           10           15
Leu Pro Gly Arg Asn Lys Ser Met Phe Asn Met Glu Asn Ser Ala Ala
20           25           30
Lys Gly Glu Lys Ala Ala Arg Gln Leu Phe Asp Leu Glu Gln Asp Met
35           40           45
His Asp Val Ala Lys Ala His Glu Val Asn Ala Asn Val Gln Ser Lys
50           55           60
Val Gln Thr Leu Thr Ser Ser Leu Arg Glu Gly Ala Phe Lys Glu Ser
65           70           75           80
Phe Glu Lys Gln Gln Thr Leu Leu Ala Gly Ile Cys Ser Ser Ser Lys
85           90           95
Gly Ala Arg Thr Tyr Gln Pro
100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 763:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 767 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(750007..752307)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 763:

```

Met Leu Pro Arg Pro Val Ser Val Asp Gly Thr Val Ile Thr Ala Pro
1           5           10           15
Val Leu Leu Lys Asp Gly Val Ser Phe Val Met Gly Ser Cys Gln Val
20           25           30
Ser Phe Phe Lys Gly Glu Glu Val Glu Gly Asp Ile Glu Leu Ser Phe
35           40           45
Gln Thr Glu Gly Gly Asn Glu Gly Glu Pro Ala Ala Gln Gly Ser Ser
50           55           60
Ser Val Ser Ser Glu Gly Pro Lys Lys Glu Thr Gly Asn Pro Ser Leu
65           70           75           80
Pro Ser Glu Thr Lys Val Ser Gly Glu Val Ser Ser Ser Ala Ile Ala
85           90           95
Lys Glu Gln Glu Leu Ala Val Phe Phe Leu Ala Ser Val Glu Lys Glu
100          105          110
Pro Gly Thr Pro Lys Glu Val Ser Glu Pro Lys Val Ser Ser Gln Glu
115          120          125
Gly Gln Thr Pro Ser Val Thr Gly Glu Lys Lys Asp Leu Glu Leu Pro
130          135          140
Leu Ala Ser Gln Glu Gln Pro Lys Gln Thr Thr Pro Ser Gly Ser Gly
145          150          155          160

```

Glu	Pro	Thr	Gln	Ser	Gln	Asn	Ala	Ser	Met	Glu	Glu	Asn	Arg	Thr	Ser
				165					170					175	
Pro	Asp	Gln	Asn	Gln	Gln	Pro	Gln	Leu	Ser	Ser	Ala	Ser	Glu	Ser	Gly
			180					185					190		
Ser	Gln	Ser	Pro	Glu	Asn	Gln	Glu	Gln	Gln	Pro	Ser	Gln	Thr	Pro	Pro
			195				200					205			
Pro	Ser	Pro	Glu	Thr	Pro	Glu	Pro	Ser	Gly	Glu	Pro	Asn	Ser	Ala	Thr
	210					215					220				
Glu	Glu	Asn	Ser	Pro	Ser	Pro	Met	Glu	Lys	Ala	Ser	Val	Thr	Glu	Glu
225						230					235				240
Gly	Ser	Ser	Gly	Thr	Ser	Glu	Glu	Glu	Lys	Glu	Gly	Glu	Glu	Asp	Thr
				245					250					255	
Ala	Glu	Ser	Ala	Ala	Asn	Glu	Glu	Leu	Lys	Ala	Glu	Ala	Ser	Gln	Glu
			260					265						270	
Glu	Glu	Lys	Lys	Glu	Glu	Asp	Lys	Xaa	Glu	Val	Leu	Ala	Pro	Phe	Asn
		275					280					285			
Val	Gln	Asp	Leu	Phe	Arg	Phe	Asp	Gln	Gly	Ile	Phe	Pro	Ala	Glu	Ile
	290					295					300				
Glu	Asp	Leu	Ala	Gln	Lys	Gln	Val	Ala	Val	Asp	Leu	Thr	Gln	Pro	Ser
305					310					315					320
Arg	Phe	Leu	Leu	Lys	Val	Leu	Ala	Gly	Ala	Asn	Ile	Gly	Ala	Glu	Phe
				325					330					335	
His	Leu	Asp	Ser	Gly	Lys	Thr	Tyr	Ile	Val	Gly	Ser	Asp	Pro	Gln	Val
			340					345					350		
Ala	Asp	Ile	Val	Leu	Ser	Asp	Met	Ser	Ile	Ser	Arg	Gln	His	Ala	Lys
		355					360					365			
Ile	Ile	Ile	Gly	Asn	Asp	Asn	Ser	Val	Leu	Ile	Glu	Asp	Leu	Gly	Ser
	370					375					380				
Lys	Asn	Gly	Val	Ile	Val	Glu	Gly	Arg	Lys	Ile	Glu	His	Gln	Ser	Thr
385					390					395					400
Leu	Ser	Ala	Asn	Gln	Val	Val	Ala	Leu	Gly	Thr	Thr	Leu	Phe	Leu	Leu
			405						410					415	
Val	Asp	Tyr	Thr	Ala	Pro	Ser	Asp	Thr	Val	Met	Ala	Thr	Ile	Ser	Ser
			420					425					430		
Glu	Asp	Tyr	Gly	Leu	Phe	Gly	Arg	Pro	Gln	Ser	Pro	Glu	Glu	Ile	Ala
		435					440					445			
Ala	Arg	Ala	Ala	Glu	Glu	Glu	Glu	Glu	Lys	Arg	Lys	Arg	Ala	Thr	Leu
	450					455					460				
Pro	Thr	Gly	Ala	Phe	Ile	Leu	Thr	Leu	Phe	Ile	Gly	Gly	Leu	Ala	Leu
465					470					475					480
Leu	Phe	Gly	Ile	Gly	Thr	Thr	Ser	Leu	Phe	His	Thr	Lys	Glu	Val	Val
				485					490					495	
Ser	Ile	Asp	Gln	Ile	Asp	Leu	Ile	His	Asp	Ile	Glu	His	Val	Ile	Gln
			500					505					510		
Gln	Phe	Pro	Thr	Val	Arg	Phe	Thr	Phe	Asn	Lys	Asn	Asn	Gly	Gln	Leu
		515					520						525		
Phe	Leu	Ile	Gly	His	Val	Arg	Asn	Ser	Ile	Asp	Lys	Ser	Glu	Leu	Leu
	530					535					540				
Tyr	Lys	Val	Asp	Ala	Leu	Ser	Phe	Val	Lys	Ser	Val	Asp	Asp	Asn	Val
545					550					555					560
Ile	Asp	Asp	Glu	Ala	Val	Trp	Gln	Glu	Met	Asn	Ile	Leu	Leu	Ser	Lys
				565					570					575	
Asn	Pro	Glu	Phe	Lys	Gly	Ile	Ser	Met	Gln	Ser	Pro	Glu	Pro	Gly	Ile
			580					585					590		
Phe	Val	Ile	Ser	Gly	Tyr	Leu	Lys	Thr	Glu	Glu	Gln	Ala	Ala	Cys	Leu
		595					600					605			
Ala	Asp	Tyr	Leu	Asn	Leu	His	Phe	Asn	Tyr	Leu	Ser	Leu	Leu	Asp	Asn
	610					615					620				
Lys	Val	Ile	Ile	Glu	Ser	Gln	Val	Met	Lys	Ala	Leu	Ala	Gly	His	Leu

```

625                      630                      635                      640
Val Gln Ser Gly Phe Ala Asn Val His Val Ser Phe Thr Asn Gly Glu
                      645                      650                      655
Ala Val Leu Thr Gly Tyr Ile Asn Asn Lys Asp Ala Asp Lys Phe Arg
                      660                      665                      670
Thr Val Val Gln Glu Leu Gln Asp Ile Ala Gly Ile Arg Ala Val Lys
                      675                      680                      685
Asn Phe Val Val Leu Leu Xaa Ala Glu Glu Gly Val Ile Asp Leu Asn
                      690                      695                      700
Met Arg Tyr Pro Gly Arg Tyr Arg Val Thr Gly Phe Ser Lys Cys Gly
705                      710                      715                      720
Asp Ile Ser Ile Asn Val Val Val Asn Gly Arg Ile Leu Thr Arg Gly
                      725                      730                      735
Asp Ile Leu Asp Gly Met Thr Val Thr Ser Ile Gln Pro His Cys Ile
                      740                      745                      750
Phe Leu Glu Arg Glu Gly Leu Lys Tyr Lys Ile Glu Tyr Asn Lys
                      755                      760                      765

```

(2) INFORMATIONS POUR LA SEQ ID NO: 764:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(752503..752913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 764:

```

Ala Arg Glu His Met Leu Glu Lys Leu Ile Lys Asn Phe Val Ala Tyr
1                      5                      10                      15
Met Gly Val Ala Ser Glu Leu Glu Phe Asp Ala Asp Gly Ser Tyr Val
                      20                      25                      30
Leu Pro Ile Ser Ser Leu Val Arg Met Arg Val Arg Gln Asn Ala Asp
                      35                      40                      45
Glu Glu Ile Ile Ile Ser Ala Phe Leu Gly Glu Ile Pro Ala Phe Met
50                      55                      60
Asp Ile Glu Lys Ala Tyr Ala Arg Met Met Glu Gly Asn Leu Phe Gly
65                      70                      75                      80
Gln Glu Thr Gly Gly Ala Ala Leu Gly Leu Asp Ser Asp Gly His Ala
                      85                      90                      95
Val Leu Val Arg Arg Val Pro Gly Glu Val Ser Gln Glu Asp Phe Ala
100                      105                      110
Ser Phe Ile Gly Gly Val Leu Asn Tyr Ala Glu Ala Trp Leu Glu Asp
115                      120                      125
Leu Gly Leu Ser Lys Thr Glu Gln Xaa
130                      135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 765:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 324 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire



(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(753616..754587)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 765:

Arg	Val	Leu	Leu	Gly	Val	Ile	Gly	Val	Ser	Tyr	Arg	Glu	Thr	Thr	Leu
1			5					10					15		
Gln	Gln	Arg	Glu	Gln	Val	Leu	His	Ile	Leu	Gln	Gln	Ala	Gln	Gly	Ser
		20					25					30			
Phe	Arg	Pro	Glu	Val	Phe	Gln	Glu	Glu	Arg	Asp	Tyr	Val	Leu	Leu	Ala
	35					40					45				
Thr	Cys	His	Arg	Val	Glu	Leu	Tyr	Ser	Val	Ala	Pro	Ala	Glu	Leu	Phe
	50				55				60						
Asp	Ser	Leu	Ala	Gln	Glu	Ile	Lys	Leu	Leu	Gly	Val	Ser	Pro	Tyr	Phe
65				70				75						80	
Tyr	Arg	Asn	Gln	Asp	Cys	Phe	Ala	His	Leu	Phe	Cys	Val	Ala	Gly	Gly
		85					90					95			
Leu	Asp	Ser	Leu	Val	Leu	Gly	Glu	Thr	Glu	Ile	Gln	Gly	Gln	Val	Lys
		100					105					110			
Arg	Ala	Tyr	Leu	Gln	Ala	Ala	Arg	Glu	Gln	Lys	Leu	Ser	Phe	Ala	Leu
	115					120					125				
His	Phe	Leu	Phe	Gln	Lys	Ala	Leu	Lys	Glu	Gly	Lys	Val	Phe	Arg	Ala
	130				135					140					
Lys	Gly	Gly	Ala	Pro	Tyr	Ala	Ala	Ile	Thr	Ile	Pro	Ile	Leu	Val	Asp
145				150				155						160	
Gln	Glu	Leu	Arg	Arg	Gln	Ile	Asp	Lys	Lys	Ala	Ser	Leu	Leu	Phe	
		165					170					175			
Ile	Gly	Tyr	Ser	Glu	Ile	Asn	Arg	Ser	Val	Ala	Tyr	His	Leu	Arg	Arg
		180				185						190			
Gln	Gly	Phe	Ser	Cys	Ile	Thr	Phe	Cys	Ser	Arg	Gln	Gln	Leu	Pro	Thr
	195					200					205				
Leu	Ser	Met	Arg	Gln	Val	Val	Arg	Glu	Glu	Leu	Cys	Phe	Gln	Asp	Pro
	210				215					220					
Tyr	Arg	Val	Val	Phe	Leu	Gly	Ser	Leu	Glu	Leu	Gln	Tyr	Ala	Leu	Pro
225			230					235						240	
His	Ser	Leu	Trp	Glu	Ser	Ile	Trp	Asp	Ile	Pro	Asp	Arg	Ile	Val	Phe
		245					250					255			
Asp	Phe	Ala	Val	Pro	Arg	Ala	Leu	Pro	Ser	His	Thr	Val	Phe	Pro	His
	260					265						270			
Arg	Tyr	Met	Asp	Met	Asp	Gln	Ile	Ser	Asp	Trp	Leu	Arg	Glu	His	Arg
	275					280					285				
Lys	Glu	Val	Asn	Ser	Ala	His	Leu	Asp	Ser	Leu	Arg	Glu	Val	Ala	Tyr
	290				295					300					
Arg	Tyr	Trp	Asn	Ser	Leu	Asn	Gln	Arg	Leu	Glu	Arg	His	Asp	Cys	Val
305				310				315					320		
Gly	Ala	Asn	Ala												

(2) INFORMATIONS POUR LA SEQ ID NO: 766:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 605 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 755000..756814

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 766:

```

Met Arg Lys Lys Thr Ala Tyr Ser Glu Ser Ser Ile Ile Ser Leu Ala
1      5      10      15
Ser Leu Asp His Ile Arg Leu Arg Ala Gly Met Tyr Ile Gly Arg Leu
20     25     30
Gly Asp Gly Ser Gln Ala Glu Asp Gly Ile Tyr Thr Leu Phe Lys Glu
35     40     45
Val Val Asp Asn Ala Ile Asp Glu Phe Val Met Gly Tyr Gly His Thr
50     55     60
Ile His Ile Thr Gly Asp Ala His Glu Leu Ser Ile Arg Asp Glu Gly
65     70     75     80
Arg Gly Ile Pro Leu Gly Lys Val Ile Asp Cys Val Ser Lys Ile Asn
85     90     95
Thr Gly Ala Lys Tyr Thr Gln Asp Val Phe His Phe Ser Val Gly Leu
100    105    110
Asn Gly Val Gly Leu Lys Ala Val Asn Ala Leu Ser Gln His Phe Ser
115    120    125
Val Arg Ser Val Arg Asn Lys Lys Phe Leu Lys Ala Ser Phe Ser Lys
130    135    140
Gly Ile Leu Leu His Thr Glu Gln Gly Ala Thr Gln Asp Pro Asp Gly
145    150    155    160
Thr Glu Val Val Phe Ser Pro Asp His Glu Leu Phe Glu Asn Phe Ser
165    170    175
Phe Gln Val Glu Phe Leu Lys Lys Lys Ile Arg Gln Tyr Thr Tyr Leu
180    185    190
His Pro Gly Leu Thr Ile Ile Tyr Asn Gly Glu Arg Ile Val Ser Thr
195    200    205
Arg Gly Leu Leu Asp Leu Phe Glu Glu Glu Val Gln Thr Pro Leu Leu
210    215    220
Tyr Ser Pro Ile Thr Phe Gln Tyr Ser Asp Leu Ala Phe Leu Phe Ser
225    230    235    240
His Thr Glu Thr Ser Ser Glu Gln Tyr Phe Ser Phe Val Asn Gly Gln
245    250    255
Glu Thr Thr Asp Gly Gly Thr His Leu Val Ala Phe Lys Glu Gly Ile
260    265    270
Val Lys Gly Val Asn Glu Phe Phe Gly Lys Asn Phe Ser Ser Gln Asp
275    280    285
Ile Arg Glu Gly Leu Ala Gly Cys Ile Ala Ile Lys Ile Ala Ser Pro
290    295    300
Ile Phe Glu Ser Gln Thr Lys Asn Lys Leu Gly Asn Thr Asn Ile Arg
305    310    315    320
Ala Glu Leu Ala Lys Arg Val Lys Glu Ala Val Leu Ser Ser Leu Lys
325    330    335
Lys Asn Pro Ser Ser Ala Glu Arg Ile Gln Glu Lys Ile Lys Leu Asn
340    345    350
Glu Lys Thr Arg Lys Asn Ala Gln Phe Leu Lys Gln Glu Leu Lys Asp
355    360    365
Lys Gln Lys Lys Leu His Tyr Lys Ile Pro Lys Leu Arg Asp Cys Lys
370    375    380
Phe His Leu Thr Asp Asn Ser Leu Tyr Gly Lys Asn Ser Ser Ile Phe
385    390    395    400
Ile Thr Glu Gly Glu Ser Ala Ser Ala Ser Ile Leu Ala Ser Arg Asn
405    410    415

```

```

Pro Leu Thr Gln Ala Val Phe Ser Leu Arg Gly Lys Pro Met Asn Val
      420      425      430
Phe Ser Ser Lys Glu Glu Thr Ile Tyr Lys Asn Asp Glu Leu Phe Tyr
      435      440      445
Leu Ala Thr Ala Leu Gly Leu His Lys Asp Ser Leu Gln Asn Leu Arg
      450      455      460
Tyr Asn Gln Val Ile Leu Ala Thr Asp Ala Asp Val Asp Gly Met His
465      470      475      480
Ile Arg Asn Leu Met Ile Thr Phe Phe Leu Lys Thr Phe Leu Pro Leu
      485      490      495
Val Ala Ser Asn His Leu Phe Ile Leu Glu Thr Pro Leu Phe Lys Val
      500      505      510
Arg His Lys Asp Ala Thr Phe Tyr Cys Tyr Ser Glu Glu Lys Leu
      515      520      525
Ser Thr Ile Glu His Ile Gly Lys Lys Glu Ser Ser Leu Glu Ile Thr
      530      535      540
Arg Phe Lys Gly Leu Gly Glu Ile Ser Pro Lys Glu Phe Lys Ser Phe
545      550      555      560
Ile Gly Ala Asp Met Arg Leu Thr Pro Val Ser Leu Pro Asp Thr Glu
      565      570      575
Thr Leu Asp Thr Leu Leu Gln Phe Tyr Met Gly Lys Asn Thr Lys Glu
      580      585      590
Arg Lys Leu Phe Ile Ile Glu Asn Leu Val Thr Asn Leu
      595      600      605

```

(2) INFORMATIONS POUR LA SEQ ID NO: 767:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 502 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 756796..758301

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 767:

```

Glu Ser Cys Tyr Gln Pro Leu Ala Ile Asn Glu Leu Met Ser Asp Leu
1      5      10      15
Ser Asp Leu Phe Lys Thr His Phe Thr Gln Tyr Ala Ser Tyr Val Ile
      20      25      30
Leu Glu Arg Ala Ile Pro His Val Leu Asp Gly Leu Lys Pro Val Gln
      35      40      45
Arg Arg Leu Leu Trp Thr Leu Phe Arg Met Asp Asp Gly Lys Met His
      50      55      60
Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala Leu His Pro His Gly
65      70      75      80
Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu Ala Asn Lys Gly Phe
      85      90      95
Leu Ile Glu Thr Gln Gly Asn Phe Gly Asn Pro Leu Thr Gly Asp Pro
      100      105      110
His Ala Ala Ala Arg Tyr Ile Glu Ala Arg Leu Ser Pro Leu Ala Lys
      115      120      125
Glu Val Leu Phe Asn Thr Asp Leu Met Thr Phe His Asp Ser Tyr Asp
      130      135      140
Gly Arg Glu Gln Glu Pro Asp Ile Leu Ala Ala Lys Ile Pro Leu Leu

```

```

145          150          155          160
Leu Leu His Gly Val Asp Gly Ile Ala Val Gly Met Thr Thr Lys Ile
          165          170          175
Phe Pro His Asn Phe Cys Asp Leu Leu Glu Ala Gln Ile Ala Ile Leu
          180          185          190
Asn Asp Gln Pro Phe Ser Leu Leu Pro Asp Phe Pro Ser Gly Gly Thr
          195          200          205
Met Asp Ala Ser Asp Tyr Gln Asp Gly Leu Gly Ser Ile Val Leu Arg
          210          215          220
Ala Thr Ile Asp Ile Ile Asn Asp Lys Thr Leu Leu Ile Lys Glu Ile
          225          230          235          240
Cys Pro Ser Thr Thr Thr Glu Thr Leu Ile Arg Ser Ile Glu Asn Ala
          245          250          255
Ala Lys Arg Gly Ile Ile Lys Ile Asp Ser Ile Gln Asp Phe Ser Thr
          260          265          270
Asp Leu Pro His Ile Glu Ile Lys Leu Pro Lys Gly Ile His Ala Lys
          275          280          285
Asp Leu Leu Arg Pro Leu Tyr Thr His Thr Glu Cys Gln Val Ile Leu
          290          295          300
Thr Ser Arg Pro Thr Ala Ile Tyr Gln Gly Lys Pro Trp Glu Thr Thr
          305          310          315          320
Ile Ser Glu Ile Leu Arg Leu Gln Thr Glu Thr Leu Gln Asn Tyr Leu
          325          330          335
Lys Lys Glu Leu Leu Ile Leu Glu Asp Ser Leu Ser Arg Glu Leu Tyr
          340          345          350
His Lys Thr Leu Glu Tyr Leu Phe Ile Lys His Lys Leu Tyr Asp Thr
          355          360          365
Val Arg Ser Met Leu Ser Lys Arg Lys Thr Ser Pro Ser Ser Ser Ala
          370          375          380
Ile His Asn Ala Val Leu Glu Ala Leu Thr Pro Phe Leu Asp Thr Leu
          385          390          395          400
Pro Ala Pro Asp Lys Gln Ala Thr Ala Gln Leu Ala Ala Leu Thr Ile
          405          410          415
Lys Lys Ile Leu Cys Phe Asp Glu Asn Ser Tyr Glu Lys Glu Leu Ala
          420          425          430
Cys Leu Glu Lys Lys Arg Ser Ser Val Gln Lys Asp Leu Ser Gln Leu
          435          440          445
Lys Lys Tyr Thr Val Leu Tyr Ile Lys Lys Leu Leu Glu Thr Tyr Arg
          450          455          460
Gln Leu Gly His Arg Lys Thr Lys Ile Ala Lys Phe Asp Asp Leu Pro
          465          470          475          480
Thr Glu Arg Val Ser Ala His Lys Lys Ala Lys Glu Pro Ala Ala Leu
          485          490          495
Asp Gln Glu Glu Asn Phe -
          500

```

(2) INFORMATIONS POUR LA SEQ ID NO: 768:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 82 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(758446..758691)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 768:

```

Asp Leu Leu Arg Met Lys Glu Phe Leu Ala Tyr Ile Val Lys Asn Leu
1           5           10           15
Val Asp Lys Pro Glu Glu Val His Leu Lys Glu Val Gln Gly Thr Asn
          20           25           30
Thr Ile Ile Tyr Glu Leu Thr Val Ala Lys Gly Asp Ile Gly Lys Ile
          35           40           45
Ile Gly Lys Glu Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val
          50           55           60
Ser Val Ala Ser Arg Asp Asn Val Lys Val Ser Leu Glu Ile Met Glu
65           70           75           80
Glu Arg

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 769:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(759338..759775)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 769:

```

Ile Pro Ala Pro Thr Ala Val Phe Ser Phe Val Ile Asp Glu Gln Leu
1           5           10           15
Thr Gly Arg Leu Asp Lys Gly Leu Val Ser Tyr Asn Gly Ala Tyr Ser
          20           25           30
Arg Ala Phe Tyr Gln Gln Gln Ile Glu Leu Gly Arg Val Arg Val Asn
          35           40           45
Gly Arg Val Tyr Thr Arg Val Ser His Pro Leu Ser Leu Gly Asp Val
          50           55           60
Val Glu Val Glu Leu Ile Glu Glu Glu Glu Pro Ser Ser Leu Ile Pro
65           70           75           80
Glu Asp Ile Pro Leu Asp Lys Val Tyr Glu Asp Asp Met Ile Leu Val
          85           90           95
Ile Asn Lys Pro Arg Asp Met Val Val His Pro Ala Pro Gly His Thr
          100          105          110
Gln Gly Thr Val Val His Ala Leu Leu His Glu Ile Gly Glu Arg Leu
          115          120          125
Lys Gln Glu Leu Pro Arg Gly Ala Met Ala Pro Arg Asp Cys Thr Ser
          130          135          140
Leu Arg
145

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 770:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 124 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(759871..760242)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 770:

```

Arg Asn Gly Ser Ser Thr Thr Arg Phe Lys Glu Asn Ala Phe Gly Ile
1      5      10      15
Gln Arg Leu Met Glu Ile Arg Tyr Phe Leu Ala Arg Pro Leu Leu Glu
      20      25      30
Glu Glu Val Cys Arg Leu Ala Asn Arg Lys Asn Phe Leu Phe Asp
      35      40      45
Ala Glu Lys Tyr Leu Ile Pro Ile Cys Tyr Lys Gln Thr Ile Tyr Leu
      50      55      60
Ala Lys Pro Leu Ser Arg Phe Pro Met Thr Gln Glu Val Trp Glu Leu
65      70      75      80
His Val Gln His Val Ile Ser Leu Leu Lys Gln Gln Phe Gly Ile Leu
      85      90      95
Thr Asp His Ala Pro Ile Leu Leu Ala Cys Glu Ala Arg Gln Val Val
      100      105      110
Leu Leu Glu Ser Leu Asp Ser Phe Val Asn Ile Ser
      115      120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 771:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 117 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(760188..760538)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 771:

```

Lys Ile Leu Leu Thr Gln Val Lys Tyr Arg Lys Ile Phe Val Leu Gly
1      5      10      15
Glu Ser Leu Val Met Asp Thr Gln Phe Ile Ala Ser Arg Ser Val Arg
      20      25      30
Asn Gln Gly Val Thr Ser Val Ser Gly Gln Val Lys Glu Glu Leu Met
      35      40      45
Ser Pro Ser Asn Met Thr Phe Glu Gly Pro Val Arg Ser Leu Asp Gln
      50      55      60
Leu Arg Gln Ala Leu Ile Ala Lys Met Gly Glu Gln Lys Gly Gln Glu
65      70      75      80
Met Tyr Asp Arg Phe Ile Gln Ser Leu Leu Ile Ser Thr Phe Thr Thr
      85      90      95
Val His Lys Glu Met Asp Arg Ala Gln Arg Ala Ser Lys Lys Met Arg
      100      105      110
Ser Val Tyr Arg Asp
      115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 772:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 269 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 760966..761772

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 772:

Met	Phe	Pro	Glu	Asn	Lys	Met	Leu	Leu	Ile	Ala	Gly	Pro	Cys	Val	Ile	1	5	10	15
Glu	Asp	Asn	Ser	Val	Phe	Glu	Thr	Ala	Arg	Arg	Leu	Lys	Glu	Ile	Val	20	25	30	
Ala	Pro	Tyr	Ala	Ser	Ser	Val	His	Trp	Ile	Phe	Lys	Ser	Ser	Tyr	Asp	35	40	45	
Lys	Ala	Asn	Arg	Ser	Ser	Val	His	Asn	Tyr	Arg	Gly	Pro	Gly	Leu	Arg	50	55	60	
Leu	Gly	Leu	Gln	Thr	Leu	Ala	Lys	Ile	Lys	Glu	Glu	Leu	Asp	Val	Glu	65	70	75	80
Ile	Leu	Thr	Asp	Val	His	Ser	Pro	Asp	Glu	Ala	Arg	Glu	Ala	Ala	Lys	85	90	95	
Val	Cys	Asp	Ile	Ile	Gln	Val	Pro	Ala	Phe	Leu	Cys	Arg	Gln	Thr	Asp	100	105	110	
Leu	Leu	Val	Thr	Ala	Gly	Glu	Thr	Gln	Ala	Ile	Val	Asn	Ile	Lys	Lys	115	120	125	
Gly	Gln	Phe	Leu	Ser	Pro	Trp	Glu	Met	Gln	Gly	Pro	Ile	Asp	Lys	Val	130	135	140	
Leu	Ser	Thr	Gly	Asn	Asn	Lys	Ile	Ile	Leu	Thr	Glu	Arg	Gly	Cys	Ser	145	150	155	160
Phe	Gly	Tyr	Asn	Asn	Leu	Val	Ser	Asp	Met	Arg	Ser	Ile	Glu	Val	Leu	165	170	175	
Arg	Arg	Phe	Gly	Phe	Pro	Val	Val	Phe	Asp	Gly	Thr	His	Ser	Val	Gln	180	185	190	
Leu	Pro	Gly	Ala	Leu	His	Ser	Gln	Ser	Gly	Gly	Gln	Thr	Glu	Phe	Ile	195	200	205	
Pro	Val	Leu	Thr	Arg	Ser	Ala	Ile	Ala	Ala	Gly	Val	Gln	Gly	Leu	Phe	210	215	220	
Ile	Glu	Thr	His	Pro	Asn	Pro	Ser	Ser	Ala	Leu	Ser	Asp	Ala	Ala	Ser	225	230	235	240
Thr	Leu	Ser	Leu	Lys	Asp	Leu	Glu	Arg	Leu	Leu	Pro	Ala	Trp	Val	Gln	245	-	250	255
Leu	Phe	Thr	Tyr	Ile	Gln	Glu	Met	Asp	Ala	Val	Ser	Val				260	265		

## (2) INFORMATIONS POUR LA SEQ ID NO: 773:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 761759..762142

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 773:

Met	Leu	Phe	Leu	Tyr	Asp	Xaa	Xaa	Leu	Phe	His	Gly	Ile	Trp	Cys	Val
1			5						10					15	
Val	Val	Leu	Ile	Leu	Cys	Ala	Cys	Val	Thr	Ala	Leu	Ala	Val	Val	Lys
		20						25					30		
Met	Gly	Asp	Phe	Thr	Asn	Pro	Thr	Leu	Val	His	Gln	Asp	Ser	Val	Thr
	35					40						45			
Pro	Ala	Pro	Pro	Phe	Leu	Lys	Ile	Lys	Lys	Leu	Gly	Val	Arg	Lys	Arg
	50					55					60				
Ile	Ile	Ser	Pro	Glu	Lys	Gln	Leu	Phe	Tyr	Cys	Thr	Ile	Asp	Lys	Ser
65					70					75				80	
Cys	Met	Glu	Leu	His	Phe	Ser	Asn	Thr	Ser	Leu	His	Cys	Arg	Glu	Leu
			85						90					95	
Leu	Ser	His	Leu	Thr	Gly	Cys	Leu	Gln	Thr	Glu	Xaa	Ala	Asp	Pro	Leu
			100					105					110		
Cys	Phe	Leu	Glu	Val	Leu	Glu	Asp	Phe	Leu	Ile	Thr	Lys	Ile	Ile	Leu
		115					120						125		

(2) INFORMATIONS POUR LA SEQ ID NO: 774:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 239 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 762267..762983

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 774:

Met	Ser	Val	Leu	Ser	Val	Cys	Asn	Leu	Ile	Lys	Lys	Tyr	Asn	Lys	Lys
1			5						10					15	
Pro	Val	Thr	Asn	Asp	Val	Ser	Phe	Gln	Val	Asn	Ala	Gly	Glu	Ile	Val
		20						25					30		
Gly	Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Ala	Phe	Tyr	Gln
	35					40						45			
Thr	Val	Gly	Leu	Ile	Arg	Pro	Asp	Ser	Gly	Lys	Ile	Leu	Phe	Lys	Asn
	50					55					60				
Thr	Asp	Ile	Thr	Lys	Lys	Pro	Met	Asp	Tyr	Arg	Ala	Arg	Leu	Gly	Ile
65					70					75				80	
Gly	Tyr	Leu	Ala	Gln	Glu	Pro	Thr	Ile	Phe	Lys	Glu	Leu	Thr	Val	Lys
			85						90					95	
Glu	Asn	Leu	Ile	Cys	Val	Leu	Glu	Ile	Ile	Tyr	Lys	Thr	Arg	Lys	Glu
		100						105					110		
Gln	Thr	His	Leu	Leu	Asn	Ala	Leu	Ile	Asp	Asp	Leu	Gln	Leu	Thr	Thr
		115				120						125			
Ser	Leu	His	Lys	Lys	Ala	Gly	Ser	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg
	130					135					140				
Leu	Glu	Ile	Ala	Cys	Val	Leu	Ala	Leu	Asn	Pro	Ser	Val	Leu	Leu	Leu
145				150					155					160	
Asp	Glu	Pro	Phe	Ala	Asn	Val	Asp	Pro	Leu	Val	Ile	Gln	Asn	Val	Lys
			165					170					175		
Tyr	Leu	Ile	Lys	Ile	Leu	Ala	Ser	Arg	Gly	Ile	Gly	Ile	Leu	Ile	Thr
		180						185					190		



```

Asp His Asn Ala Lys Glu Leu Leu Ser Ile Ala Asp Arg Cys Tyr Leu
      195                200                205
Ile Ile Asp Gly Lys Ile Phe Phe Glu Gly Ser Ser Ala Gln Met Ile
      210                215                220
Ala Asn Pro Met Val Arg Gln His Tyr Leu Gly Asp Ser Phe Ser
225                230                235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 775:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 377 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(763335..764465)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 775:

```

Ile Gly Gly Thr Phe Pro Arg Thr Pro Leu Ile Phe Glu Glu Ile Ala
1      5      10      15
Leu Leu Ser Glu Glu Gln Asn Gln Val Leu Lys Thr Val Leu Asn Ser
      20      25      30
Cys Phe Ser Leu Val Cys Gly Gly Pro Gly Thr Gly Lys Thr Phe Leu
      35      40      45
Ala Val Gln Met Ile Xaa Leu Ile Leu Ala Gln Ile Pro Ser Ala Gln
      50      55      60
Ile Met Val Ala Ser Pro Thr Gly Lys Ala Ser Ala His Leu His Ser
65      70      75      80
Val Leu Thr Ser Gln Gly Ile Val Gly Asp Ser Val Glu Val Val Thr
      85      90      95
Ile His Lys Phe Leu Lys Asp Met Arg Arg Gly Arg Ser Pro Val Asp
      100     105     110
Leu Leu Leu Val Asp Glu Gly Ser Met Val Thr Met Asn Leu Leu His
      115     120     125
Gly Leu Ile Lys Thr Ile Arg Gly Glu Ser Arg Gly Glu Thr Ile Tyr
      130     135     140
Ala Asp Arg Met Val Ile Phe Gly Asp Ala Asn Gln Leu Ser Pro Ile
145     150     155     160
Gly Ile Gly Val Gly Asn Pro Phe His Glu Val Val Ser Glu Phe Ser
      165     170     175
Lys Gln Ala Cys Phe Leu Ser Thr Ser His Arg Ala Lys His Lys Glu
      180     185     190
Leu Gln Glu Leu Ala Ser Ala Val Leu Arg Lys Glu Leu Ile Pro Phe
      195     200     205
Gln Pro Leu Pro Ser Arg Gln Glu Ala Ile Arg Arg Leu Ser Phe Ala
      210     215     220
Phe Thr Gln Ala Ala Lys Glu Gly Val Ser Leu Cys Ala Leu Thr Pro
225     230     235     240
Met Arg Gln Gly Leu Trp Gly Phe Leu Gln Leu Asn Arg Leu Leu Phe
      245     250     255
Asn Glu Met Gln Glu Lys His Pro Arg Ala Pro Ile Pro Ile Ile Val
      260     265     270
Thr Glu Arg Tyr Glu Thr Trp Gly Leu Thr Asn Gly Asp Thr Gly Val
      275     280     285
Leu Asp Pro Val Thr Glu Gln Leu Arg Phe Met Asn Gly Glu Ile Leu

```

290		295		300											
His	Gln	Ala	Asp	Phe	Pro	Tyr	Tyr	Ser	Tyr	Asn	Tyr	Val	Met	Ser	Val
305					310					315					320
His	Lys	Ser	Gln	Gly	Ser	Glu	Tyr	Asp	Arg	Val	Ile	Val	Ile	Leu	Pro
			325							330				335	
Lys	Gly	Ser	Glu	Val	Phe	Asp	Ser	Ala	Ile	Leu	Tyr	Thr	Ala	Ile	Thr
			340					345					350		
Arg	Thr	Lys	Gln	His	Val	Glu	Ile	Trp	Ala	Asp	Arg	Glu	Ala	Leu	Glu
		355					360					365			
Ala	Ile	Ile	Leu	Lys	Arg	Gly	Arg	Tyr							
	370					375									

(2) INFORMATIONS POUR LA SEQ ID NO: 776:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(764438..764857)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 776:

Ile	His	Ser	Thr	Thr	Ala	Lys	Arg	Lys	Ile	Phe	Pro	Val	Asn	Val	Asn
1				5					10					15	
Gln	His	Val	Gln	Asp	Ile	Val	Pro	Ser	Leu	Leu	Ala	Gln	His	Ile	Leu
			20					25					30		
Leu	Pro	Phe	Asp	Ile	Ala	Phe	Ala	Gln	Lys	His	Leu	Ser	Gln	Glu	Glu
		35				40						45			
Phe	Ser	Gln	Glu	Ala	Glu	Ala	Phe	Leu	Ala	Thr	Ala	Ser	Ala	Leu	Leu
	50				55					60					
Arg	Cys	Gly	Tyr	Pro	Tyr	Phe	Ser	Ile	Cys	Asp	Glu	Thr	Ile	His	Pro
65				70					75					80	
Thr	Leu	Pro	Gly	Ile	Ser	Asn	Lys	Gln	Leu	Phe	Gln	Trp	Phe	Gln	Leu
			85					90					95		
Leu	Ser	Ser	Arg	Ile	Lys	Glu	Glu	Leu	Phe	Glu	Val	Val	Asn	His	Lys
			100					105					110		
Ile	Tyr	Leu	Arg	Ser	Leu	Phe	Leu	Leu	Arg	Glu	Lys	Val	Phe	His	Lys
	115					120						125			
Leu	His	Arg	Leu	Ala	Gly	Arg	Phe	His	Val	His	Leu				
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 777:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 416 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(764821..766068)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 777:

Lys	Leu	Ile	Gly	Ala	Arg	Arg	Tyr	Ala	Glu	Gly	Arg	Ile	Val	Ile	Asn	1	5	10	15
Ser	Ile	Phe	Asn	Lys	Ile	Phe	Ser	Arg	Glu	Tyr	Ala	Trp	Ser	Val	Asp	20	25	30	
Met	Tyr	Asn	Arg	Leu	Val	Leu	Met	Leu	Gly	Gln	Ser	Tyr	Leu	Leu	Glu	35	40	45	
Leu	Gln	Glu	Gly	Val	Arg	Ser	Asp	Leu	Leu	Pro	Glu	Tyr	Tyr	Glu	Thr	50	55	60	
Ile	Leu	Phe	Tyr	Gln	Lys	Gln	Met	Lys	Gly	Phe	Asp	Ala	Gly	Ala	Tyr	65	70	75	80
Lys	Thr	Phe	Phe	Pro	Glu	Ser	Met	Leu	Val	Pro	Thr	Ile	Met	Gln	His	85	90	95	
Ile	Phe	Val	Ile	Pro	Glu	Thr	Gln	Leu	Pro	Leu	Phe	Met	Asp	Ala	Leu	100	105	110	
Leu	Met	Trp	Glu	Asn	Ser	Tyr	Val	His	Pro	Asp	Tyr	Ser	Leu	Val	Leu	115	120	125	
Glu	Arg	Met	Lys	Pro	Ala	Val	Leu	Gln	Asp	Gly	Ile	His	Thr	Gln	Lys	130	135	140	
Ile	Cys	Gln	Ala	Ile	Ala	Asp	Ser	Lys	Ile	Lys	Lys	Leu	Lys	Glu	Lys	145	150	155	160
Leu	Ile	Glu	Leu	Phe	Ser	Asp	Glu	Leu	Val	Phe	Cys	Val	Ser	Gln	Gly	165	170	175	
Asn	Thr	Val	Cys	Ala	Asp	Gln	Tyr	Leu	Ala	Leu	Leu	Lys	Thr	Leu	Asp	180	185	190	
Pro	Arg	Ser	Ser	Trp	Gly	His	Lys	Leu	Leu	Leu	Ser	Glu	Lys	Glu	Ile	195	200	205	
Val	Asn	Met	Val	Cys	Glu	Asp	Asp	Ala	Gln	Tyr	Ser	Arg	Leu	Lys	Asp	210	215	220	
Tyr	Leu	Leu	Leu	Trp	Glu	Gln	Asp	Ile	Ala	Asp	Val	Asp	Arg	Gln		225	230	235	240
Gln	Leu	Val	His	Tyr	Leu	Phe	Phe	Ser	Ala	Lys	His	Leu	Trp	Arg	Gly	245	250	255	
Gly	Gln	Glu	Glu	Ala	Cys	Leu	Arg	Leu	Leu	Lys	Glu	Ile	Leu	Leu	Phe	260	265	270	
Ser	Gln	Asn	Glu	Lys	Ala	Cys	Leu	Asn	Arg	Thr	Leu	Arg	Leu	Val	Lys	275	280	285	
Asp	Phe	Tyr	Thr	Gln	Ala	Leu	Ala	Met	Arg	Asn	Phe	Thr	His	Leu	Val	290	295	300	
Trp	Ile	Glu	Asn	Phe	Leu	Asp	Glu	Val	Gly	Leu	Pro	Lys	Thr	Leu	Ala	305	310	315	320
Ser	Asp	Ala	Glu	Ile	Ala	Asn	Cys	Leu	Ala	Asp	Ala	Gln	Tyr	Leu	Phe	325	330	335	
Ser	Lys	Gly	Asp	Tyr	Arg	Leu	Cys	Ile	Val	Tyr	Ser	Ser	Trp	Leu	Ala	340	345	350	
Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Leu	Gln	Leu	Leu	Gly	Leu	Ser	Leu	355	360	365	
Val	Glu	Gln	Lys	Glu	Tyr	Thr	Glu	Ala	Leu	Glu	Val	Phe	Gln	Lys	Leu	370	375	380	
Pro	Leu	Gly	Glu	Asp	Ala	Trp	Asn	Ser	Gln	Val	His	Lys	Ala	Ser	Leu	385	390	395	400
Leu	Cys	Tyr	Lys	Tyr	Ile	Ala	Arg	Gln	Gln	Lys	Glu	Lys	Ser	Phe	Pro	405	410	415	

## (2) INFORMATIONS POUR LA SEQ ID NO: 778:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(766065..766475)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 778:

```

Met Glu Gln Glu Gln Met Tyr Leu Leu Cys Cys Gln Gly Phe Ser Leu
1           5           10           15
Gln Ile Gln Arg Lys Phe Gln Glu Ser Lys Glu Ile Phe Ser Arg Ile
          20           25           30
Asp Lys Arg Lys Thr Ser Ala Pro Phe Val Leu Gln Arg Glu Leu Leu
          35           40           45
Glu Gly Arg Ile Leu Asn Ala Tyr Phe Leu Asn Asn Leu Ser Leu Met
50          55          60
Ala Glu Cys Ile Ala Glu Leu Glu Arg Val Ser Gly Ser Glu Ala His
65          70          75          80
Leu Leu Phe Phe Lys Ala Leu His Ala His Arg Thr Lys Gln Tyr Asn
          85          90          95
Leu Ala Val Asp Val Leu Ser Arg Trp Phe Gly His Val Asp Gln Thr
          100         105         110
Lys Pro Leu Cys Leu Asp Thr Asn Val Tyr Glu Leu Phe Ser Pro Tyr
          115         120         125
Val Leu Glu Glu Ile Ala Ala Glu Ser
          130         135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 779:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(766934..767989)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 779:

```

Met Ser Val Pro Asp Arg Lys Arg Ala Leu Glu Ala Ala Ile Ala Tyr
1           5           10           15
Ile Glu Lys Gln Phe Gly Ala Gly Ser Ile Met Ser Leu Gly Lys His
          20           25           30
Ser Ser Ala His Glu Ile Ser Thr Ile Lys Thr Gly Ala Leu Ser Leu
          35           40           45
Asp Leu Ala Leu Gly Ile Gly Gly Val Pro Lys Gly Arg Ile Val Glu
50          55          60
Ile Phe Gly Pro Glu Ser Ser Gly Lys Thr Thr Leu Ala Thr His Ile
65          70          75          80
Val Ala Asn Ala Gln Lys Met Gly Gly Val Ala Ala Tyr Ile Asp Ala
          85          90          95
Glu His Ala Leu Asp Pro Asn Tyr Ala Ala Leu Ile Gly Ala Asn Ile
          100         105         110

```

```

Asn Asp Leu Met Ile Ser Gln Pro Asp Cys Gly Glu Asp Ala Leu Ser
  115                      120                      125
Ile Ala Glu Leu Leu Ala Arg Ser Gly Ala Val Asp Val Ile Val Ile
  130                      135                      140
Asp Ser Val Ala Ala Leu Val Pro Lys Ser Glu Leu Glu Gly Glu Ile
  145                      150                      155                      160
Gly Asp Val His Val Gly Leu Gln Ala Arg Met Met Ser Gln Ala Leu
                      165                      170                      175
Arg Lys Leu Thr Ala Thr Leu Ala Arg Thr Asn Thr Cys Ala Ile Phe
                      180                      185                      190
Ile Asn Gln Ile Arg Glu Lys Ile Gly Val Ser Phe Gly Asn Pro Glu
                      195                      200                      205
Thr Thr Thr Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Ile Arg Ile
  210                      215                      220
Asp Ile Arg Arg Ile Gly Ser Ile Lys Gly Gly Glu Asn Phe Asp Ile
  225                      230                      235                      240
Gly Asn Arg Ile Lys Val Lys Val Ala Lys Asn Lys Leu Ala Pro Pro
                      245                      250                      255
Phe Arg Thr Ala Glu Phe Asp Ile Leu Phe Asn Glu Gly Ile Ser Ser
                      260                      265                      270
Ala Gly Cys Ile Ile Asp Leu Ala Val Glu Lys Asn Ile Ile Asp Lys
  275                      280                      285
Lys Gly Ser Trp Phe Asn Tyr Gln Asp Arg Lys Leu Gly Gln Gly Arg
  290                      295                      300
Glu Ala Val Arg Glu Glu Leu Lys Arg Asn Lys Glu Leu Phe His Glu
  305                      310                      315                      320
Leu Glu Arg Arg Ile Tyr Glu Ser Val Gln Ala Ser Gln Ala Pro Ala
                      325                      330                      335
Ala Ala Cys Val Asp Ser Glu Ser Arg Glu Val Ala Glu Ala Ala Lys
  340                      345                      350

```

(2) INFORMATIONS POUR LA SEQ ID NO: 780:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 178 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(768252..768785)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 780:

```

Met Lys Asn Ile Val Glu Gln Lys Arg Cys Leu Arg Arg Glu Gly Leu
  1                      5                      10                      15
Ala Lys Arg Glu Gln Leu Ser Val Gln Arg Arg Asp Glu Ala Ala Arg
  20                      25                      30
Glu Leu Met His Phe Val Met Gln Thr Ile Xaa Gln Gly Phe Val Leu
  35                      40                      45
Ser Tyr Ile Pro Phe Arg Ser Glu Leu Asp Val Arg Gly Ile Asn Ala
  50                      55                      60
Trp Leu Ala Gln Glu Asn Arg Leu Leu Leu Pro Lys Met Gln Gly Met
  65                      70                      75                      80
Asp Ile Val Pro Ile Ala Leu Pro Phe Thr Met Ile Glu Ser Leu Tyr
                      85                      90                      95
Ser Pro Lys Asp Leu Asn Gln Ile Glu Gly Glu Glu Ile Glu Ala Gln

```



Lys Gly Lys Gln Val Ile Tyr Gly Lys Tyr Ala Ile Ile Glu Thr Arg  
                   260                  265                  270  
 Gln Ile Val His Gly Val Pro His Gly Glu Val Leu Leu Phe Asp Glu  
                   275                  280                  285  
 His Gly Lys Ser Leu Leu Gln Ala Tyr Ser Leu Ile Asn Gly Gln Lys  
                   290                  295                  300  
 Glu Gly Glu Glu Val Phe Phe Tyr Pro Gly Gly Glu Gly Arg Lys Met  
 305                  310                  315                  320  
 Leu Leu Thr Trp Ser Gln Gly Ile Leu Gln Gly Ala Val Lys Thr Trp  
                   325                  330                  335  
 Tyr Pro Asn Gly Ala Leu Glu Ser Ser Lys Glu Leu Val Gln Asn Lys  
                   340                  345                  350  
 Lys Thr Gly Ile Leu Met Leu Tyr Tyr Pro Glu Gly Gln Val Met Ala  
                   355                  360                  365  
 Thr Glu Glu Tyr Val Asp Asp Leu Leu Ile Lys Gly Glu Tyr Phe Arg  
                   370                  375                  380  
 Pro Asn Asp Arg Tyr Pro Tyr Ala Lys Val Glu Lys Gly Ser Gly Thr  
 385                  390                  395                  400  
 Ala Val Phe Phe Ser Ala Thr Gly Gly Leu Lys Lys Val Leu Tyr  
                   405                  410                  415  
 Glu Asp Gly Lys Pro Val Ile His  
                   420

## (2) INFORMATIONS POUR LA SEQ ID NO: 782:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 770138..770470

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 782:

Glu Arg Lys Thr Met Gly Ile Trp Val Tyr Leu Gly Ser Asn Asn His  
 1                  5                  10                  15  
 Asn Asn Thr Gly Met Ser Ser Ser Ser Ile Trp Ser Ser Phe Trp Lys  
                   20                  25                  30  
 Glu Asn Asn Val Leu Phe Ser Pro Lys Val Cys Ser Cys His Asp Lys  
                   35                  40                  45  
 Arg Leu Ser Ser Lys Lys Ala Phe Arg Ser Leu Thr Ala Arg Leu Leu  
                   50                  55                  60  
 Thr Thr Gln Ala Val Ala Gly Ser Leu Ala Arg Ala Ser Arg Ser Leu  
 65                  70                  75                  80  
 Phe Lys Lys Thr Arg Phe Ser Pro Trp Ala Ile Gln Leu Gly Lys Leu  
                   85                  90                  95  
 Ala Cys Leu Cys Ala Ala Phe Ser Arg Ala Phe Leu Ile Ala Thr  
                   100                  105                  110

## (2) INFORMATIONS POUR LA SEQ ID NO: 783:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 159 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(770185..770661)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 783:

```

Cys Thr Asn Arg Ser Ala Arg Glu Gly Ile Met Arg Arg Leu Gly Val
1      5      10      15
Trp Val Leu Leu Leu Ala Ser Gly Ala Ala Ser Leu Pro Ala Ile
      20      25      30
Gly Ala Trp Cys Trp Arg Gln Arg Thr Ala Glu Ala Trp Glu Asn Leu
      35      40      45
Leu Ile Asp Met Arg Asp Phe Gln Ser Lys Arg Glu Arg Ser Ser Gln
      50      55      60
Val Ala Ile Lys Asn Ala Arg Leu Lys Ala Ala His Lys Gln Ala Ser
65      70      75      80
Phe Pro Asn Trp Ile Ala Gln Gly Glu Asn Leu Val Phe Leu Asn Lys
      85      90      95
Glu Arg Asp Ala Leu Ala Lys Leu Pro Ala Thr Ala Trp Val Val Arg
      100     105     110
Ser Arg Ala Val Lys Asp Arg Lys Ala Phe Leu Glu Asp Asn Arg Leu
      115     120     125
Ser Trp Gln Glu Gln Thr Leu Gly Glu Lys Ser Thr Leu Phe Ser Phe
      130     135     140
Gln Lys Glu Leu Gln Ile Asp Asp Glu Asp Ile Pro Val Leu Leu
145      150      155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 784:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(770634..770924)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 784:

```

Ile Pro Pro Thr Val Pro Thr Asn Gln Glu Val Met Glu Val Leu Gly
1      5      10      15
Arg Met Thr Ala Asn Leu Pro Ser Val Ser Phe Ser His Tyr Leu Tyr
      20      25      30
Lys Leu Glu Asp Ile Pro Ser Glu Arg Pro Leu Gly Tyr Arg
      35      40      45
Ala Tyr Ile Ser Leu Gln Gly Ala Ala Asn Asp Glu Asp Phe Ala Ser
      50      55      60
Phe Ile Asp Gln Leu Ser Ala Trp Ile Gly Ala Arg Val Leu Ser Lys
65      70      75      80
Lys Leu Ala Asp Arg Gln Phe Asp Val Arg Ile Ala Leu Gln Gly Arg
      85      90      95
Gly

```



## (2) INFORMATIONS POUR LA SEQ ID NO: 785:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 227 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(771330..772010)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 785:

```

Met Asp Phe Lys Leu Pro Ile Tyr Cys Ile Gly Val Thr Gln Ser Ala
1      5      10      15
Glu Asn Val Thr Arg Ile Ala Ile Leu Gln Lys Thr Cys Lys Gly Trp
20      25      30
Ser Leu Cys Arg Cys Glu Lys Leu Thr Glu Thr Gly Ala Leu Ser Trp
35      40      45
Pro Lys Arg Phe Leu Ser Ser Lys Val Val Leu Ser Leu Gln Gly Gln
50      55      60
Glu Thr Leu Val Lys Ser Val Ser Ser Ser Leu Lys Ser Lys Lys Asn
65      70      75      80
Phe Leu Lys Met Val Tyr Ala Glu Gln Glu Ala Thr Ala Ala Phe Pro
85      90      95
Leu Lys Asp Leu Val Ile Ala His Asp Leu Gly Glu Trp Asn Ser Ala
100     105     110
Gln Glu Arg Val Val Thr Leu Trp Met Leu Gln Arg Gln Ser Val Ala
115     120     125
Leu Ala Thr Ala Leu Leu Glu Glu Lys Gly Gly Phe Ala Thr His Ile
130     135     140
Ser Cys Arg Ala Lys Asp Leu Phe Ser Ala Leu Gln Gln Ser Leu Leu
145     150     155     160
Arg Asn Leu Glu Thr Tyr Phe Phe Val Tyr Glu Gly Leu Asp Glu Thr
165     170     175
Val Cys Leu Phe Val Gln Glu Gly Ser Val Leu Leu Ser Arg Ser Phe
180     185     190
Lys Asn Asp Ser Glu Ser Leu Leu Asp Asp Leu Leu Ala Ser Phe Ala
195     200     205
Tyr Val Gln Glu Val Tyr Thr Ala Ser Phe Ile Arg Asp Pro Arg Arg
210     215     220
Leu Ser Ile
225

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 786:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 334 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 772390..773391

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 786:

```

Met Ala Pro Ser Ile Phe Ile Lys Asn Leu Pro Leu Lys Ser Pro Val
1      5      10      15
Val Tyr Ala Pro Leu Ala Gly Phe Ser Asp Phe Pro Tyr Arg Arg Met
20      25      30
Ser Ala Glu Tyr Arg Pro Ala Leu Met Phe Cys Glu Met Val Lys Met
35      40      45
Glu Gly Leu His Tyr Cys Pro Gln Arg Thr Leu Arg Leu Leu Asp Phe
50      55      60
Ala Glu Ser Met Arg Pro Ile Gly Gly Gln Leu Cys Gly Ser Arg Pro
65      70      75      80
Asp Leu Ala Gly Glu Ser Ala Lys Ile Leu Glu Gly Leu Gly Phe Asp
85      90      95
Leu Ile Asp Leu Asn Cys Gly Cys Pro Thr Asp Arg Ile Thr Lys Asp
100     105     110
Gly Ser Gly Ser Gly Met Leu Lys Thr Pro Glu Leu Ile Gly Lys Val
115     120     125
Val Glu Lys Met Val Glu Val Val Ser Val Pro Val Thr Val Lys Ile
130     135     140
Arg Ser Gly Trp Asp Phe Asp His Ile Asn Val Glu Glu Thr Val Arg
145     150     155     160
Ile Ile Lys Glu Ser Gly Ala Ser Ala Val Phe Val His Gly Arg Thr
165     170     175
Arg Ser Gln Gly Tyr Gln Gly Pro Ser Asn Leu Glu Phe Ile Ser Arg
180     185     190
Ala Lys Gln Ala Ala Gly Asp Asp Phe Pro Val Phe Gly Asn Gly Asp
195     200     205
Val Phe Ser Pro Glu Ala Ala Lys Thr Met Leu Glu Thr Thr His Cys
210     215     220
Asp Gly Val Leu Val Ala Arg Gly Thr Met Gly Ala Pro Trp Ile Gly
225     230     235     240
Lys Gln Ile Glu Asp Tyr Leu Thr Thr Gly Thr Tyr Ser Ser Pro Ser
245     250     255
Phe Ser Thr Arg Lys Gln Ala Phe Val Gln His Leu Gln Trp Ile Glu
260     265     270
Glu Tyr Tyr Gln Ser Glu Glu Lys Leu Leu Thr Asp Thr Arg Lys Leu
275     280     285
Cys Gly His Tyr Leu Ile Leu Ser Pro Lys Val Arg Ser Leu Arg Ala
290     295     300
Asn Leu Ala Lys Ala Ser Ser Ser Gln Glu Val Tyr Gln Leu Ile Asp
305     310     315     320
Gly Phe Glu Glu Leu Thr Glu Glu Glu Glu Leu Leu Ser Glu
325     330

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 787:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 265 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: complement(773427..774221)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 787:

Asn	Arg	Leu	Ser	Lys	Cys	His	Lys	Gly	Lys	Leu	Val	Lys	Ile	Trp	Ala	1	5	10	15
Lys	Asn	Arg	Tyr	Phe	Phe	Gly	Cys	Ser	Glu	Tyr	Pro	Thr	Cys	Asp	Tyr	20	25	30	
Lys	Thr	Ser	Glu	Glu	Glu	Leu	Thr	Phe	Asp	Lys	Asn	Glu	Tyr	Ala	Glu	35	40	45	
Asp	Thr	Pro	Trp	Asp	Ala	Pro	Cys	Ala	Leu	Cys	Gly	Gly	Glu	Met	Lys	50	55	60	
Val	Arg	His	Gly	Lys	Phe	Gly	Ser	Phe	Leu	Gly	Cys	Glu	Asn	Tyr	Pro	65	70	75	80
Lys	Cys	His	Tyr	Ile	Val	Asn	Leu	Phe	Lys	Lys	Gly	Glu	Ala	Gly	Ala	85	90	95	
Glu	Pro	Glu	Ala	Thr	Val	His	Cys	Pro	Ala	Glu	Gly	Cys	Thr	Gly	His	100	105	110	
Leu	Val	Lys	Arg	Arg	Ser	Arg	Phe	Asn	Lys	Met	Phe	Tyr	Ser	Cys	Ser	115	120	125	
Glu	Tyr	Pro	Ala	Cys	Ser	Val	Ile	Gly	Asn	Ser	Val	Asp	Ala	Val	Ile	130	135	140	
Glu	Lys	Tyr	Ala	Gly	Thr	Pro	Lys	Thr	Pro	Tyr	Glu	Lys	Lys	Pro	Lys	145	150	155	160
Ala	Lys	Lys	Ser	Ile	Ala	Ser	Thr	Lys	Gly	Lys	Ala	Ala	Lys	Thr	Val	165	170	175	
Lys	Lys	Ser	Ser	Ala	Thr	Thr	Lys	Lys	Arg	Ala	Thr	Lys	Ala	Tyr	Thr	180	185	190	
Pro	Ser	Ala	Ala	Leu	Ala	Gly	Val	Ile	Gly	Ala	Asp	Pro	Val	Gly	Arg	195	200	205	
Pro	Glu	Ala	Thr	Lys	Lys	Leu	Trp	Glu	Tyr	Ile	Lys	Glu	Lys	Gly	Leu	210	215	220	
Gln	Ser	Pro	Gln	Asn	Lys	Lys	Ile	Ile	Ile	Pro	Asp	Ser	Lys	Leu	Gln	225	230	235	240
Gly	Val	Ile	Gly	Ala	Asp	Pro	Ile	Asp	Met	Phe	Ala	Leu	Ser	Lys	Lys	245	250	255	
Leu	Ser	Ala	His	Leu	Ile	Lys	Glu	Glu								260	265		

## (2) INFORMATIONS POUR LA SEQ ID NO: 788:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 602 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(774191..775996)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 788:

Met	Lys	Lys	Ser	Leu	Ile	Ile	Val	Glu	Ser	Pro	Ala	Lys	Ile	Lys	Thr	1	5	10	15
Leu	Arg	Lys	Leu	Leu	Gly	Glu	Gly	Phe	Ile	Phe	Asp	Ser	Ser	Leu	Gly	20	25	30	
His	Ile	Val	Asp	Leu	Pro	Ala	Lys	Gly	Phe	Gly	Ile	Asp	Ile	Glu	Asn	35	40	45	
Gly	Phe	Val	Pro	Asp	Tyr	Gln	Ile	Leu	Glu	Gly	Lys	Glu	Glu	Val	Ile				

50	55	60
Arg Lys Ile Cys Ala Glu	Ala Lys Lys Cys Asp	Val Val Tyr Leu Ala
65	70	75
Pro Asp Pro Asp Arg Glu	Gly Glu Ala Ile Ala	Trp His Ile Ala Asn
85	90	95
Gln Leu Pro Lys Asp Thr	Lys Ile Gln Arg Ile Ser	Phe Asn Ala Ile
100	105	110
Thr Lys Gly Ala Val Thr	Glu Ala Leu Lys His Pro	Arg Glu Ile Asp
115	120	125
Met Ala Leu Val Asn Ala	Gln Gln Ala Arg Arg	Phe Leu Asp Arg Ile
130	135	140
Val Gly Tyr Lys Ile Ser	Pro Ile Leu Gly Arg	Lys Leu Gln Arg Trp
145	150	155
Ser Gly Val Ser Ala Gly	Arg Val Gln Ser Val	Ala Leu Lys Leu Val
165	170	175
Val Asp Arg Glu Tyr Ala	Ile Glu Arg Phe Val	Pro Val Glu Phe Trp
180	185	190
Asn Ile Arg Val His Leu	Lys Asp Pro Gln Thr	Gln Lys Thr Phe Trp
195	200	205
Ala His Leu His Ser Val	Asn Gly Lys Lys Trp	Glu Lys Glu Ile Pro
210	215	220
Glu Gly Lys Thr Ser Asp	Glu Val Ile Leu Ile	Asp Ser Lys Glu Lys
225	230	235
Ala Asp Glu Ile Val Ala	Leu Leu Glu Ser Ala	Thr Tyr Val Val Asp
245	250	255
Arg Val Glu Ser Lys Glu	Lys Lys Arg His Ala	Tyr Pro Pro Phe Ile
260	265	270
Thr Ser Thr Leu Gln Gln	Glu Ala Ser Arg His	Tyr Arg Phe Ser Ser
275	280	285
Ser Arg Thr Met Asn Ile	Ala Gln Thr Leu Tyr	Glu Gly Val Asp Leu
290	295	300
Asp Ser Gln Gly Ala Val	Gly Leu Ile Thr Tyr	Met Arg Thr Asp Ser
305	310	315
Val Arg Thr Asp Pro Glu	Ala Val Lys Gln Val	Arg Lys Tyr Ile Glu
325	330	335
Gly His Phe Gly Lys Glu	Phe Val Pro Ser Ser	Pro Asn Val Tyr Ala
340	345	350
Thr Lys Lys Met Ala Gln	Asp Ala His Glu Ala	Ile Arg Pro Thr Asp
355	360	365
Val Thr Ile Thr Pro Glu	Ser Ile Arg Ser Lys	Leu Thr Glu Asp Gln
370	375	380
Tyr Lys Leu Tyr Ser Leu	Ile Trp Lys Arg Phe	Val Ala Ser Gln Met
385	390	395
Ile Ser Ala Ile Tyr Asp	Thr Leu Ala Ile Arg	Ile Thr Thr Asn Lys
405	410	415
Gly Ile Asp Leu Arg Ala	Thr Gly Ser Cys Leu	Lys Phe Lys Gly Phe
420	425	430
Leu Ala Val Tyr Glu Glu	Lys Arg Asp Glu Glu	Gly Asp Glu Glu Glu
435	440	445
Asn Ile His Leu Pro Lys	Leu Asn Glu Arg Asp	Val Leu Thr Lys Glu
450	455	460
Glu Leu Glu Ala Glu Gln	Ser His Thr Lys Pro	Leu Pro Arg Phe Thr
465	470	475
Glu Ala Ser Leu Val Lys	Glu Leu Glu Lys Ser	Gly Ile Gly Arg Pro
485	490	495
Ser Thr Tyr Ala Thr Ile	Met Asn Lys Ile Gln	Ser Arg Glu Tyr Thr
500	505	510
Leu Lys Glu Gly Gln Arg	Leu Arg Pro Thr Glu	Leu Gly Lys Val Val
515	520	525

Cys Gln Phe Leu Glu Thr Asn Phe Pro Arg Ile Met Asp Ile Gly Phe  
 530 535 540  
 Thr Ala Gly Met Glu Asp Glu Leu Glu Leu Ile Ala Asp Asn Lys Lys  
 545 550 555 560  
 Pro Trp Lys Gln Leu Leu Gln Glu Phe Cys Glu Leu Phe Leu Pro Phe  
 565 570 575  
 Val Val Thr Ala Glu Lys Glu Ala Phe Ile Pro Arg Ile Val Thr Glu  
 580 585 590  
 Ile Asp Cys Pro Asn Val Ile Lys Gly Asn  
 595 600

(2) INFORMATIONS POUR LA SEQ ID NO: 789:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 348 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 776663..777706

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 789:

Val Phe Pro Gly Pro Asn Asp Ile Gly Ser Gln Glu Asn Val Lys Asp  
 1 5 10 15  
 Ile Cys Ser Leu Asp Pro Thr Asn Tyr Val Asn Ser Ser Cys Tyr Ser  
 20 25 30  
 Arg Ser Phe Pro His Gln Pro Ile Gly Thr Pro Leu Phe Gly Lys  
 35 40 45  
 Lys Pro Val Leu Thr Tyr Gly Glu Val Ser Lys Leu Ile Ser Ser Lys  
 50 55 60  
 Thr Asp Pro Glu Pro Phe Ser Tyr Cys Arg Pro Thr Phe Leu Arg Ala  
 65 70 75 80  
 Ala Leu Asn Thr Leu Glu Phe Leu Ser Ser Pro Pro Ser Ser Asp Pro  
 85 90 95  
 Tyr Asp Asp Leu Leu Gln Leu Asn Lys Glu Gly Phe Leu Ala Gly Pro  
 100 105 110  
 Glu Glu Glu Lys Gln Ala Phe Phe Leu Arg Val Glu Arg Thr Leu Ala  
 115 120 125  
 Glu Ala Pro Val His Pro Thr Pro Phe Pro Ile Glu Phe Gln Lys Leu  
 130 135 140  
 Phe Asp Val Asn Pro Ser Phe Leu Glu Val Val Tyr Ser Asn Glu Ser  
 145 150 155 160  
 Leu Asp Ala Trp Glu Ala Gly Cys Thr Trp Ile Thr Asp Asn Arg Val  
 165 170 175  
 Ser Ile Gln Leu Arg Lys Gly Phe Gln Lys Ala Ser Phe Trp Phe Gly  
 180 185 190  
 Phe Phe Ser Lys Glu Glu Val Leu Ser His Glu Ala Val His Ala Val  
 195 200 205  
 Arg Met Lys Phe Tyr Glu Pro Ile Phe Glu Glu Val Leu Ala Tyr Ser  
 210 215 220  
 Thr Ser Lys His Phe Trp Arg Arg Phe Phe Gly Pro Leu Phe Arg Ser  
 225 230 235 240  
 Ala Gly Glu Thr His Phe Phe Leu Phe Phe Val Leu Phe Gly Ala Phe  
 245 250 255  
 Leu Phe Pro Trp Phe Pro Trp Ile Gly Leu Ser Cys Ile Leu Ala Pro



Tyr Phe Phe His Ile His Ser Val Val Gly Gly Tyr Phe Val Leu Val  
 35 40 45  
 Leu Met Ala Cys His Ser Ala Ile Phe Gly Pro Ala Lys Met Gly Ile  
 50 55 60  
 Leu Pro Glu Met Leu Pro Ile Glu Glu Leu Ser Lys Ala Asn Gly Ala  
 65 70 75 80  
 Met Thr Ala Ala Thr Tyr Ser Gly Ser Ile Leu Gly Ser Cys Leu Ala  
 85 90 95  
 Pro Leu Met Val Asp Leu Thr Lys Asp Phe Val Thr Asn Ser Tyr Glu  
 100 105 110  
 Leu Ser Ala Cys Phe Cys Val Val Ser Ser Val Leu Ser Leu Phe Ile  
 115 120 125  
 Ala Leu Gly Ile Arg Ala Ser Asn Val Lys Asn Lys Gly Gln Lys Ile  
 130 135 140  
 Ala Tyr Val Ser Phe Arg Asn Leu Trp Gln Val Phe Gln Glu Thr Arg  
 145 150 155 160  
 Asn Ile Ala Tyr Leu Met Ile Ser Val Phe Leu Val Ala Phe Phe Leu  
 165 170 175  
 Phe Val Gly Ala Tyr Val Gln Leu Gln Ile Ile Pro Phe Val Glu Phe  
 180 185 190  
 Thr Leu Gly Tyr Ser Lys His Tyr Gly Ala Tyr Leu Phe Pro Ile Val  
 195 200 205  
 Ala Val Gly Met Gly Val Gly Ser Tyr Met Ala Gly Trp Ile Ser Gly  
 210 215 220  
 Lys Asp Ile Lys Leu Gly Phe Ser Pro Leu Ala Ala Ile Gly Val Gly  
 225 230 235 240  
 Leu Ser Met Met Val Leu Cys Leu Leu Ser Phe Ser Ile Thr Ala Val  
 245 250 255  
 Leu Ile Leu Leu Phe Cys Leu Gly Leu Val Gly Gly Ile Tyr Gln Val  
 260 265 270  
 Pro Leu His Ala Tyr Ile Gln Phe Val Ser Pro Glu His Lys Arg Gly  
 275 280 285  
 Gln Val Leu Ala Leu Asn Asn Phe Leu Asp Phe Ser Gly Val Leu Leu  
 290 295 300  
 Ala Ala Gly Phe Val Arg Leu Leu Gly Ala Gly Leu Arg Leu Thr Pro  
 305 310 315 320  
 Asp Gln Ser Phe Leu Tyr Met Gly Ser Leu Val Val Cys Phe Ala Ile  
 325 330 335  
 Leu Ser Leu Trp Met Leu Lys Glu His Val Tyr Arg Leu Leu Leu Thr  
 340 345 350  
 Arg Val Leu Lys Arg Gln Leu Gly Thr Ser Phe Ser Ser Pro Lys Ala  
 355 360 365  
 Glu Glu Val Trp Cys Phe Phe Val Pro Ala Thr Ser Tyr Lys Glu Thr  
 370 375 380  
 Arg Arg Ile Leu Ala Leu Phe Pro Lys Thr Val Arg Ser Cys Val Phe  
 385 390 395 400  
 Ile Leu Asp Lys Ala Leu Gln Pro Gly Trp Thr Ser Tyr Leu Ile Pro  
 405 410 415  
 His Cys Val Pro Thr Ile Phe Ser Tyr Gly Val Glu Gly Gln Ala Phe  
 420 425 430  
 Ala Gln Trp Ile Asp Arg Gln Val Val Glu Val Lys Ala Leu Leu Lys  
 435 440 445  
 Arg Gln Pro Ser Leu Gly Val Val Cys Leu Gly Asn Gln Ala Gln Ser  
 450 455 460  
 Gln Phe Phe Phe Ser Gln Leu Gln Ala Ser Gly Leu Ala Val Gln Ser  
 465 470 475 480  
 Gly Thr Leu Val Gln Asp Ser Glu Leu Lys Tyr Ser Leu His Leu Ala  
 485 490 495  
 Asn

(2) INFORMATIONS POUR LA SEQ ID NO: 792:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 744 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 779321..781552

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 792:

Lys	Lys	Leu	Ile	Glu	Ile	Val	Ile	Tyr	Asn	Cys	Lys	Lys	Met	Cys	Asn
1				5					10					15	
Asp	Gln	Cys	Thr	Glu	Arg	Ser	Phe	Pro	Arg	Asn	Asn	Thr	His	Glu	Cys
			20					25					30		
Lys	Pro	Met	Asn	Glu	Leu	Ser	His	Ser	Gln	Ser	Thr	Phe	Ser	Asn	Tyr
		35					40					45			
Pro	Glu	Val	Leu	Leu	Ala	Lys	Leu	Ala	Gln	Asp	Leu	Phe	Ser	Ile	Asn
	50					55					60				
Gln	Thr	Pro	Met	Thr	Lys	Arg	Trp	Ile	Leu	Val	Pro	Ser	Ser	Asp	Thr
65				70						75				80	
Asp	His	Trp	Leu	Arg	Arg	Glu	Leu	Val	Lys	Ala	Ser	Ser	Asn	His	Ile
			85						90					95	
Phe	Met	Gly	Thr	His	Ile	Phe	Ala	Ser	Phe	Asp	Ala	Phe	Val	Lys	Tyr
		100						105					110		
Leu	Phe	Thr	Gly	Thr	Arg	Leu	Val	Asp	Leu	Ser	Thr	Pro	Asp	His	Ile
		115					120					125			
Thr	Leu	Pro	Leu	Thr	Ile	Tyr	Asn	Leu	Leu	Lys	Glu	Ser	Ser	Phe	Asn
	130					135					140				
Ser	Ser	Ser	Glu	Val	Ser	Tyr	Ser	His	Leu	Gln	Lys	Leu	Ser	Ser	Ile
145				150						155					160
Phe	Lys	Lys	Phe	Tyr	Thr	Phe	Ser	Gln	Glu	Pro	Ser	Thr	Asn	Asn	Pro
			165						170					175	
Tyr	Tyr	Lys	Asn	Leu	Phe	Ala	Gln	Leu	Lys	Asp	Ser	Tyr	Thr	Pro	Leu
		180						185					190		
Glu	Thr	Ile	Phe	Ser	Ser	Ile	Leu	Asp	His	Pro	Pro	Glu	Tyr	Pro	Cys
		195					200					205			
Ser	Leu	His	Ile	Phe	Gly	Tyr	Pro	Gln	Leu	Pro	Gln	His	Val	Ala	Ser
	210				215						220				
Phe	Phe	Val	Ala	Leu	Gly	Lys	Tyr	Phe	Pro	Val	His	Phe	Tyr	Cys	Phe
225				230						235					240
Ser	Pro	Ser	Ala	Ala	Tyr	Phe	Gly	Asp	Leu	Leu	Ser	Asp	Lys	Ala	Met
			245						250					255	
Ala	Ala	Leu	Ser	Pro	Arg	Ile	Pro	Glu	Pro	His	Gln	Glu	Thr	Trp	Glu
		260						265					270		
Lys	Tyr	Val	Leu	Thr	Asp	Arg	Leu	Ala	Leu	Leu	Ala	Asn	Leu	Ala	His
		275					280					285			
Lys	Ser	Gln	Ser	Leu	Gln	Asn	Phe	Phe	Leu	Asp	Tyr	Ser	Val	Pro	Tyr
	290				295						300				
Glu	Glu	Leu	Phe	Gln	Pro	Tyr	Glu	Lys	Leu	Ser	Ser	Leu	His	Ile	Val
305				310						315				320	
Lys	Asp	Ser	Phe	Phe	His	Leu	Gln	Pro	Ile	Asp	Gln	Lys	Leu	Phe	Ser
			325						330					335	



(2) INFORMATIONS POUR LA SEQ ID NO: 793:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 382 acides aminés

(B) TYPE: acide aminé

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 382 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 781297..782442

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 793:

Leu	Ser	Leu	Phe	Ile	Gln	Glu	Ser	Ser	Ile	Thr	Glu	Leu	Cys	Phe	Ala	1	5	10	15
Lys	His	Leu	Leu	Asp	Ala	Val	Pro	Ile	Gln	Glu	Glu	His	Leu	Ser	Gly	20	25	30	
Lys	Leu	Tyr	Ala	Lys	Glu	Asn	Phe	Ser	Ser	Glu	Pro	Leu	His	Gln	Ser	35	40	45	
Tyr	Gln	Val	Tyr	Tyr	Arg	Met	Ala	Gln	Val	Ser	Pro	Leu	Gln	Asn	Lys	50	55	60	
Ala	Pro	Ser	Leu	Phe	Lys	Ser	Asp	Thr	Thr	Lys	Thr	Leu	Pro	Ser	His	65	70	75	80
Leu	Ser	Leu	Gln	His	Leu	Ile	Lys	Ala	Phe	Lys	Asp	Pro	Leu	Asn	Phe	85	90	95	
Phe	Leu	Ser	Thr	Gln	His	Gly	Phe	Ser	Phe	His	Pro	Lys	Ala	Leu	Phe	100	105	110	
Ser	Lys	Ser	Glu	Lys	Val	Phe	Pro	Ser	Pro	His	Asp	Ala	Lys	Ala	Phe	115	120	125	
Trp	Asn	His	Leu	Leu	Ser	Ser	Lys	Thr	Pro	Leu	Pro	Thr	Thr	Asn	Tyr	130	135	140	
Leu	Ser	Ala	Phe	Thr	Glu	Ser	Leu	Tyr	Thr	Asp	Val	Gln	Asp	Ser	Val	145	150	155	160
Ser	Lys	Arg	Leu	Glu	Thr	Leu	Gln	Lys	Asp	Pro	Ala	Thr	Thr	Pro	Phe	165	170	175	
Ser	Val	Val	Phe	Ser	Asp	Gln	Leu	Phe	His	Asp	Pro	Leu	His	Pro	Asn	180	185	190	
Asp	Gln	Gln	Val	Pro	Pro	Leu	Leu	Leu	Ser	Leu	Pro	Leu	Lys	Asn	Ile	195	200	205	
His	Leu	Gln	Gly	Thr	Ile	His	Gly	Val	Cys	Ser	Lys	Gly	Val	Tyr	Leu	210	215	220	
Phe	Ser	Met	His	Pro	Gly	Glu	Ala	Phe	Lys	Lys	Thr	Gln	Lys	Thr	His	225	230	235	240
Gly	Phe	Pro	Lys	Asp	Ala	Phe	Glu	Leu	Glu	Ser	Tyr	Leu	Glu	Ser	Tyr	245	250	255	
Leu	Ser	Leu	Ala	Leu	Leu	Gln	Ala	Ser	His	Leu	Leu	Pro	Lys	Glu	Ala	260	265	270	
Thr	Ile	Leu	Arg	Val	Thr	Pro	His	Asp	Ile	Glu	Pro	Ile	Leu	Pro	Pro	275	280	285	
Phe	Ser	Ser	Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Ala	Ile	His	Leu	Tyr	Asp	290	295	300	
Leu	Leu	Gln	Asn	Gln	Ala	Val	Pro	Leu	Pro	Ser	Ala	Gln	Ala	Trp	Glu	305	310	315	320
Tyr	Ile	Lys	Lys	Thr	Asp	Ser	Ala	Ser	Gln	Cys	Ile	Lys	Lys	Leu	Leu	325	330	335	
Asp	Ser	Glu	Glu	Asp	Pro	Leu	Thr	Ser	Ser	Phe	Trp	Trp	Phe	His	Asn	340	345	350	
Arg	Asp	Thr	Glu	Glu	Ile	Cys	Ser	Glu	Leu	Ser	Asn	Asp	Val	Leu	Ser	355	360	365	
Gln	Leu	Leu	Ser	Leu	Phe	Ile	Asn	Gln	Asp	Ser	Gln	Gln	Asn			370	375	380	

(2) INFORMATION POUR LA SEQ ID NO: 794:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1026 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 782447..785524

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 794:

Met	Ser	Ser	Phe	Asp	Ile	Phe	Ser	Pro	Thr	Ala	Ser	Val	Ser	Gly	Lys
1				5					10					15	
Phe	Phe	Leu	Glu	Ala	Ser	Ala	Gly	Thr	Gly	Lys	Thr	Phe	Thr	Ile	Glu
			20					25					30		
Gln	Val	Ile	Leu	Arg	Ser	Leu	Leu	Glu	Gly	Ser	Ile	Glu	Gln	Thr	Lys
		35					40					45			
Asn	Ile	Leu	Val	Val	Thr	Phe	Thr	Asn	Ala	Ala	Thr	Asn	Glu	Leu	Lys
	50					55					60				
Leu	Arg	Ile	Gln	Ala	Ser	Leu	Lys	Gln	Ala	Leu	Ser	Leu	Phe	Ser	Gln
65					70					75					80
Ala	Leu	Ser	His	Pro	Gly	Thr	Pro	Leu	Pro	Pro	Tyr	Ile	Ser	Ser	Ser
				85					90					95	
Glu	Thr	Lys	Val	Lys	Gln	Leu	Tyr	Met	Lys	Ile	Arg	Asn	Ser	Leu	Ala
			100					105					110		
Thr	Leu	Asp	Glu	Met	Asn	Ile	Phe	Thr	Ile	His	Gly	Phe	Cys	Arg	Phe
		115					120					125			
Thr	Leu	Glu	Gln	His	Phe	Pro	Trp	Ile	Gln	Pro	Ile	Gln	Pro	Ser	Ser
		130				135					140				
Ile	Phe	Ser	Glu	Pro	Gln	Thr	Ile	Gln	Gln	Tyr	Ile	Leu	Asp	Tyr	Leu
145					150					155					160
Arg	Lys	Asn	Leu	Trp	Asp	Thr	Val	Leu	Ser	Pro	Lys	Gln	Tyr	Ala	Phe
				165					170					175	
Leu	Ser	Tyr	His	His	Arg	Ala	Thr	Thr	Gln	Gln	Thr	Arg	His	Leu	Ile
			180					185					190		
Glu	Arg	Leu	Leu	Gln	Asp	Tyr	Thr	Ser	Thr	Pro	Asn	Leu	Ala	Leu	Ser
		195					200					205			
Pro	Leu	Ser	Ile	Thr	Leu	Gln	Lys	Leu	Lys	Ala	Trp	Val	Ser	Cys	Tyr
		210				215					220				
Gln	His	Leu	Ala	Pro	Leu	Ser	Leu	Glu	Glu	Met	Gln	Ala	Phe	Ser	Leu
225					230					235					240
Arg	Phe	Lys	Gln	Ser	Asp	Leu	Ser	Ile	Glu	Arg	Glu	Leu	Pro	Ala	Phe
				245					250					255	
Val	Gln	Gln	Phe	Glu	Thr	Asn	Pro	Tyr	Ser	Leu	Asp	Met	Leu	Phe	Phe
			260					265					270		
Pro	Gly	Met	Val	Gln	Lys	Phe	Gln	Glu	Glu	Asn	Arg	Asn	Lys	Lys	Lys
		275					280					285			
Leu	Ser	Ala	Pro	Ala	Ser	Pro	Leu	Asp	Pro	Phe	Phe	Gln	Asp	Trp	Ile
		290				295					300				
Gln	Leu	Ala	His	Pro	Phe	Cys	Gln	Lys	Glu	Pro	Ile	Phe	His	Thr	Leu
305					310					315					320
Leu	Lys	Ser	Val	Gln	Gln	His	Leu	Lys	Thr	His	Cys	Ala	Gln	Ser	Tyr
				325					330					335	
Ser	His	Asp	Glu	Ser	Ile	Ala	Thr	Leu	Glu	Ser	Leu	Leu	Asp	His	Asn
			340					345					350		
Asp	Thr	Val	Val	Ser	Gln	Leu									

355					360					365					
Asp	Glu	Phe	Gln	Asp	Thr	Asp	Lys	Arg	Gln	Xaa	Gln	Ile	Phe	Ser	Lys
370					375					380					
Leu	Phe	Ala	Ser	Pro	Asp	Tyr	Ser	Gly	Ser	Leu	Phe	Leu	Ile	Gly	Asp
385					390					395					
Pro	Lys	Gln	Ser	Ile	Tyr	Glu	Trp	Arg	Asn	Ala	Asp	Leu	Pro	Thr	Tyr
405					410					415					
Leu	Gln	Ala	Lys	His	Ser	Phe	Pro	Lys	Glu	Ala	Xaa	Leu	Ile	Leu	Asp
420					425					430					
Thr	Asn	Tyr	Arg	Ser	Thr	Pro	Xaa	Leu	Met	Gln	Gly	Leu	Asn	His	Leu
435					440					445					
Phe	Ser	Leu	Pro	Thr	Pro	Phe	Leu	Glu	Thr	Pro	Gln	Asn	Ile	Leu	Tyr
450					455					460					
His	Pro	Leu	His	Ser	Lys	Gly	Ser	Ser	Glu	Ile	Ser	Tyr	Ser	Glu	Phe
465					470					475					
Ser	Pro	Ile	His	Phe	Ser	Ser	Ser	Glu	Asp	Ile	Gln	Glu	Glu	Thr	Leu
485					490					495					
Trp	Ile	Ser	Lys	Thr	Ala	Ser	Tyr	Leu	Arg	Ser	Ala	Tyr	Ser	Ile	Pro
500					505					510					
Phe	Gly	Asn	Met	Ala	Val	Leu	Val	Gln	Asp	Tyr	Pro	Gln	Ala	Leu	Lys
515					520					525					
Leu	Ile	Thr	His	Ser	Thr	Ile	Pro	Met	Ala	Tyr	Cys	Lys	Glu	Lys	Arg
530					535					540					
Ile	Phe	Asp	Arg	Thr	Glu	Ser	Pro	Tyr	Leu	Leu	Ile	Leu	Leu	Leu	Glu
545					550					555					
Ala	Leu	Leu	Tyr	Pro	Glu	Asn	Gln	Gln	Lys	Ile	Gln	Ala	Ile	Leu	Met
565					570					575					
Ser	Arg	Leu	Phe	Gln	Leu	Ser	Ser	Thr	Glu	Ile	His	Gln	His	Leu	Lys
580					585					590					
Thr	Phe	Ser	Ser	Leu	Phe	Phe	Thr	Leu	Asn	Arg	His	Leu	Tyr	His	Tyr
595					600					605					
Ser	Leu	Leu	Ala	Thr	Phe	Tyr	Lys	Leu	Met	Gly	Glu	Asn	Val	Leu	Ser
610					615					620					
Gln	Thr	Ile	Gly	Glu	Thr	Leu	Leu	Gln	Thr	Pro	Leu	Gly	Asp	Ile	Ile
625					630					635					
Phe	Gln	Glu	Leu	Glu	Ala	Leu	Cys	Leu	Tyr	Leu	Asp	Lys	Thr	Thr	Glu
645					650					655					
Asn	Pro	His	His	Lys	Leu	Leu	His	Leu	Ile	Asn	Ile	Leu	Ile	Thr	Gly
660					665					670					
Lys	Tyr	Asp	Glu	Glu	Leu	Ser	Phe	Ser	Ser	Gln	Ser	Asn	Asp	Glu	Asn
675					680					685					
Met	Ile	Lys	Ile	Thr	Thr	Val	His	Ser	Ser	Lys	Gly	Leu	Glu	Tyr	Asp
690					695					700					
Val	Val	Phe	Cys	Ser	Cys	Leu	Asn	Lys	Ala	Lys	Glu	Lys	Thr	Pro	Ser
705					710					715					
Val	His	Met	Arg	Glu	Met	Tyr	Val	Ala	Cys	Thr	Arg	Ala	Lys	Lys	Phe
725					730					735					
Leu	Phe	Ile	Pro	Phe	Ser	Pro	Ile	Glu	Lys	Arg	Ser	Leu	Ser	Thr	Lys
740					745					750					
Lys	Leu	Ser	Ala	Leu	Ala	Asn	Tyr	Ala	Asn	Val	Thr	Lys	His	His	Ser
755					760					765					
Val	Pro	His	Leu	Val	Glu	Thr	Leu	Thr	Ser	Ser	Ser	Pro	Glu	Leu	Phe
770					775					780					
Ser	Ser	Ser	Phe	Gln	Pro	Pro	Glu	Ser	Ser	Leu	Thr	Pro	Asp	Arg	Glu
785					790					795					
Arg	Leu	Pro	Gln	Gln	Thr	Tyr	Phe	Ser	Leu	Pro	His	Leu	Pro	Ser	Arg
805					810					815					
Thr	Ile	His	Ser	Phe	Ser	Ser	Thr	Val	Glu	Asn	Leu	His	Phe	Ser	Glu

```

Pro Ile Gln Glu Leu Ser Pro Ser Leu Leu Phe Pro Gly Gly Ser Leu
      835                      840                      845
Thr Gly Thr Leu Ile His Lys Leu Leu Glu Ser Leu Ala Gly Asn Phe
      850                      855                      860
Ala Ala Cys Phe Glu Glu Ile Phe Asn Lys Ala Gln Thr Leu Leu Lys
865                      870                      875                      880
Asn Thr Pro Leu Glu Gly Tyr Glu Ser Ile Ile Ala Glu Lys Ile Tyr
      885                      890                      895
Thr Val Phe Ser Thr Thr Leu Pro Phe Ser Ser Gly Ser Phe Ala Leu
      900                      905                      910
Arg Asn Ile His Pro His Asn Ile Arg Val Glu Glu Thr Phe Leu Leu
      915                      920                      925
Gln Glu Glu Gly Glu Leu Trp Gln Gly Ile Val Asp Leu Phe Phe Glu
      930                      935                      940
His Lys Gly Arg Phe Phe Ile Ile Asp Trp Lys Thr Ser Phe Leu Gly
945                      950                      955                      960
Asp Glu Thr Ser Cys Tyr Ser Pro Asp Gln Leu His Leu Tyr Ile Gln
      965                      970                      975
Arg Gln Gly Leu Asp Arg Gln Glu Arg Leu Tyr Arg Lys Ala Ala Lys
      980                      985                      990
Arg Phe Leu His Gln Phe Asn Ser Ser Leu Gln Val Glu Met Ala Phe
      995                      1000                      1005
Val Phe Ile Arg Gly Leu Asp Asp Lys Gly Asn Gly Phe Leu Gln Pro
      1010                      1015                      1020
Gly Arg
1025

```

(2) INFORMATIONS POUR LA SEQ ID NO: 795:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 785532..786002

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 795:

```

Thr Pro Ser Asn Tyr Ser Gln Ile Lys Pro Lys Ile Ser Gly Arg Ser
1      5      -      10      15
Leu Gly Leu Lys Ser Ile Gly Gly Asn Thr Lys Lys Ser Thr Val Glu
      20      25      30
Gln Ser Gly Ala Lys Asp Cys Ala Phe Ile Phe Lys Glu Gln Asp Pro
      35      40      45
Ser Leu Leu Gly Arg Thr Ser Leu Thr Val Ala Thr Arg Ser Pro Gly
      50      55      60
Gly Lys Thr Pro Ser Asn Pro Val Val Thr Arg Thr Ser Pro Thr Ser
65      70      75      80
Ile Val Phe Pro Ser Thr Lys Pro Lys Ser Leu Pro Leu Ser Ile Glu
      85      90      95
Ala Ser Gly Phe Gln Ile Gly Ser Pro Arg Pro Gln Thr Ile Pro Arg
      100      105      110
Arg Ala Lys Ser Phe Cys Ser Asp Arg Asp Lys Glu Ser Ser Arg Ala
      115      120      125
Cys Lys Arg Cys Lys Ala Ser Cys Leu Ser Leu Ser Ala Lys Ala Asp

```

(2) INFORMATION POUR LA SEQ ID NO: 796:

(A) LONGUEUR: 289 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(785546..786412)

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(786611..787741)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 797:

Arg 1	Gly	Phe	Ile	Val 5	Ser	Leu	Phe	Glu	Gln 10	Leu	Pro	Ser	Phe	Ser 15	Pro
Asp	Ser	Ile	Leu	Gly 20	Leu	Ala	Gln	Ala	Phe 25	Gln	Glu	Asp	Pro 30	Arg	Glu
Asp	Lys 35	Ile	Asn	Leu	Leu	Leu	Gly 40	Thr	Tyr	Glu	Arg	Glu 45	Lys	Lys	Arg
Tyr	Gly 50	Gly	Phe	Ser	Ser	Val 55	Arg	Lys	Ala	Gln	Ser 60	Val	Phe	Phe	Asp
Asp 65	Glu	Lys	Asp	Lys	Asn 70	Tyr	Leu	Pro	Ile	Lys 75	Gly	Ser	Ser	Thr	Phe 80
Leu	Glu	Glu	Met	Ala 85	Ala	Leu	Cys	Phe	Gly 90	Glu	Leu	Asp	Ala	Asn 95	Arg
Trp	Val	Gly	Val	Gln 100	Ala	Ile	Gly	Gly 105	Thr	Gly	Ala	Leu	His 110	Leu	Gly
Ala	Ser	Val 115	Tyr	Ala	Asn	Ala	Ser 120	Leu	Ala	Gly	Lys	Val 125	Tyr	Ile	Pro
Ser	Gln 130	Thr	Trp	Gly	Asn 135	His	Ser	Arg	Ile	Phe	Ser 140	His	Gln	Gly	Leu
Ala 145	Leu	Glu	Tyr	Tyr	Pro 150	Tyr	Tyr	Asp	Gln	Glu	Thr	Lys	Glu	Leu	Asp 160
Leu	Gln	Gly	Leu	Lys 165	Ala	Val	Leu	Arg	Ser	Ala	Pro	Glu	Thr	Ser 175	Leu
Val	Leu	Leu	His 180	Cys	Cys	Cys	His 185	Asn	Pro	Thr	Gly	Lys	Asp 190	Ile	Pro
Leu	Ser 195	Glu	Trp	Pro	Glu	Ile	Ile 200	Thr	Ile	Ile	Lys	Glu 205	Arg	Asp	Leu
Ile	Pro 210	Phe	Phe	Asp	Met	Ala 215	Tyr	Leu	Gly	Phe	Ala 220	Ser	Gly	Ile	Glu
Glu 225	Asp	Arg	Arg	Pro	Val 230	Gln	Leu	Cys	Ile	Glu	Ala	Gly	Val	Thr	Thr 240
Phe	Val	Ala	Gly	Ser 245	Ala	Ser	Lys	Asn	Phe 250	Ser	Leu	Tyr	Gly	Ser 255	Arg
Val	Gly	Phe	Phe 260	Gly	Ala	Ile	His 265	Gln	Asp	Lys	Gln	Asp	Leu 270	Asn	Arg
Ile	Leu 275	Ser	Phe	Leu	Glu	Glu	Gln 280	Ile	Arg	Gly	Glu	Tyr 285	Ser	Ser	Pro
Ala	Arg 290	Glu	Gly	Val	Ala	Ile 295	Val	Thr	Ser	Ile	Leu 300	Ser	Asn	Pro	Tyr
Leu 305	Arg	Gln	Glu	Trp	Glu 310	Leu	Glu	Leu	Asn	Gly 315	Ile	Arg	Gln	Ser	Leu 320
Glu	Glu	Ile	Arg	Ser 325	Ser	Phe	Val	Ile	Ala 330	Met	Arg	Asn	Val	Ala 335	Gly
His	Ser	Phe	Asp 340	Phe	Ile	Ala	Ser 345	Gln	Lys	Gly	Phe	Phe	Gly 350	Tyr	Pro
Gly	Phe	Ser	Lys	Glu	Gln	Val	Leu	Phe	Leu	Arg	Glu	Glu	Leu	Gly	Ile

(2) INFORMATIONN POUR LA SEQ ID NO: 798:

(A) LONGUEUR: 134 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 787620..788021

[illegible]

(D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 799;

Cys	Asn	Ile	Ala	Leu	Phe	Cys	Tyr	Ser	Ala	Tyr	Ile	Ser	Gly	Leu	Lys
1				5					10					15	
Arg	Gly	Ala	Ile	Val	Asp	Tyr	Leu	Glu	Asn	Leu	Gln	Ser	Leu	Ile	Glu
		20						25					30		
Asn	His	Pro	Ser	Asp	Phe	Phe	Ser	Leu	Trp	Glu	Glu	Tyr	Cys	Phe	Asn
		35					40					45			



Asp	Val	Val	Lys	Gly	Asp	Glu	Leu	Val	Val	Leu	Leu	Glu	Lys	Ile	Lys	50	55	60
Gly	Ser	Thr	Ile	Ala	Pro	Ala	Phe	Gly	Lys	Ile	Ala	Glu	Ser	Val	Ile	65	70	75
Pro	Leu	Trp	Glu	Gln	Leu	Pro	Glu	Gly	Glu	Glu	Lys	Asp	Lys	Val	Leu	85	90	95
Ser	Leu	Val	Phe	Asp	Val	Gln	Thr	Thr	Asn	Ser	Lys	Asn	Leu	Leu	Glu	100	105	110
Ile	Ala	Leu	Gln	Gln	Val	Lys	Lys	Tyr	Glu	Asp	Ser	Ala	Asn	Tyr	Lys	115	120	125
Glu	Ala	Leu	Arg	Ile	Val	Gly	Leu	Arg	Asp	Gly	Ile	Thr	Phe	Ser	His	130	135	140
Cys	Leu	Gly	Arg	Phe	Ala	Leu	Leu	Met	His	Leu	Ser	Glu	Gly	Asn	Phe	145	150	155
Val	Phe	His	Gln	Gly	Gly	Trp	Gly	Val	Gly	Glu	Ile	Met	Gly	Val	Ser	165	170	175
Phe	Leu	Gln	Gln	Lys	Val	Leu	Val	Glu	Phe	Glu	Gly	Val	Leu	Thr	Ala	180	185	190
Lys	Asp	Ile	Ser	Phe	Glu	Thr	Ala	Phe	Arg	Met	Leu	Val	Pro	Leu	Arg	195	200	205
Lys	Asp	His	Phe	Leu	Ala	Arg	Arg	Phe	Gly	Asp	Pro	Asp	Ala	Phe	Glu	210	215	220
Ala	Phe	Ala	Arg	Lys	Glu	Pro	Val	Ala	Ala	Ile	Glu	Cys	Leu	Leu	Lys	225	230	235
Asp	Leu	Gly	Pro	Lys	Asn	Ala	Lys	Glu	Ile	Arg	Asn	Glu	Leu	Val	Glu	245	250	255
Leu	Val	Ile	Pro	Glu	Glu	Asp	Trp	Ser	Arg	Trp	Trp	Gln	Ser	Ala	Lys	260	265	270
Ile	Lys	Met	Lys	Lys	Asp	Ala	Arg	Ile	Leu	Ala	Pro	Ala	Ser	Ser	Lys	275	280	285
Asp	Pro	Tyr	Val	Phe	Asp	Pro	Lys	Gly	Phe	Ser	Phe	Val	Ser	Gln	Leu	290	295	300
Gln	Ala	Ser	Leu	Ser	Gly	Ser	Asn	Asp	Ala	Asn	Lys	Lys	Ile	Thr	Ser	305	310	315
Cys	Tyr	Ala	Phe	Val	Arg	Asp	Leu	Gly	Ser	Glu	Leu	Lys	Asp	Glu	Ser	325	330	335
Asn	Arg	Gln	Ser	Val	Ile	Lys	Glu	Leu	Lys	Ala	Leu	Asp	Leu	Pro	Ala	340	345	350
Asp	Ser	Ala	Leu	Leu	Ile	Gln	Arg	Ala	Met	Leu	Leu	Ser	Glu	Phe	Leu	355	360	365
Gly	Glu	Lys	Ala	Pro	Glu	Leu	Glu	Tyr	Glu	Asn	Ile	Ala	Lys	Leu	Ser	370	375	380
Glu	Asp	Gln	Leu	Phe	Asp	Ile	Val	Asn	Asn	Ile	Glu	Ile	Leu	Ser	Leu	385	390	395
Gln	Lys	Ser	Phe	Leu	Ala	Leu	Ile	His	Ser	Cys	Ser	Pro	Val	Trp	Val	405	410	415
Pro	Val	Tyr	Thr	Lys	Leu	Phe	Leu	Thr	Thr	Ser	Thr	Ser	Met	Leu	Arg	420	425	430
Glu	Gln	Val	Phe	Lys	Val	Leu	Asn	Ala	Asp	Lys	Glu	Ala	Arg	Glu	Asn	435	440	445
Ile	Leu	Lys	Lys	Val	Phe	Ala	Met	Ile	Glu	Gln	Pro	Leu	Leu	Tyr	Pro	450	455	460
Glu	Leu	Phe	Val	Trp	Leu	Phe	Ala	Arg	Val	Val	Asp	Gly	Glu	Asp	Gly	465	470	475
Leu	Phe	Ala	Glu	Ser	Asp	Lys	Lys	Glu	Ile	Glu	Arg	Gln	Met	Leu	Ala	485	490	495
Ser	Ala	Leu	Glu	Leu	Met	His	Lys	Val	Ala	Thr	Thr	Pro	Gln	Lys	Asp	500	505	510
Leu	Gly	Lys	Lys	Leu	Tyr	Ser	Phe	Leu	Val	Gly	Gln	Arg	Phe	Leu	Val			

	515		520		525										
Ile	Arg	Gln	Ile	Ile	Asp	Gln	Ala	Ser	Ile	Glu	Tyr	Leu	Lys	Glu	Phe
	530					535					540				
Val	Leu	Leu	Ser	Ser	Lys	Cys	Pro	Gln	Phe	Thr	Gln	Gly	Asp	Leu	Gly
545					550						555				560
Val	Leu	Arg	Ser	Leu	Ala	Glu	Val	Val	Gln	Pro	Ala	Leu	Lys	Arg	Gly
				565						570					575
Thr	Leu	Glu	Glu	Glu	Glu	Asn	Ile	Leu	Trp	Thr	Thr	Ser	Asp	Ser	Phe
			580					585					590		
Thr	Arg	Met	Lys	Asn	Lys	Leu	Gln	Ser	Leu	Val	Gly	Lys	Glu	Met	Val
	595					600					605				
Glu	Asn	Ala	Lys	Glu	Ile	Glu	Asp	Ala	Arg	Ala	Leu	Gly	Asp	Leu	Arg
	610					615					620				
Glu	Asn	Ser	Glu	Tyr	Lys	Phe	Ala	Ser	Glu	Arg	Arg	Ala	Arg	Leu	Gln
625					630					635					640
Glu	Glu	Ile	Arg	Val	Leu	Ser	Glu	Glu	Ile	Asn	Arg	Ala	Lys	Ile	Leu
				645						650					655
Thr	Lys	Asp	Ala	Val	Phe	Thr	Asp	Ser	Val	Gly	Val	Gly	Cys	Lys	Val
			660					665					670		
Val	Leu	Glu	Ser	Asp	Gln	Gly	Asp	Lys	Val	Cys	Tyr	Thr	Ile	Leu	Gly
	675					680					685				
Pro	Trp	Asp	Ala	Asn	Pro	Asp	Glu	Lys	Ile	Leu	Ser	Leu	Lys	Ser	Lys
	690					695					700				
Leu	Ala	Gln	Glu	Met	Val	Gly	Lys	Ala	Val	Gly	Glu	Thr	Val	Leu	Phe
705					710					715					720
Gln	Gly	Lys	Lys	His	Lys	Ile	Lys	Glu	Ile	Ser	Ser	Ile	Trp	Asp	
				725					730					735	

(2) INFORMATIONS POUR LA SEQ ID NO: 800:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 790160..790609

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 800:

Asn	Ile	Glu	Ile	Phe	Val	Met	Lys	Asn	Asn	Ser	Ala	Gln	Lys	Ile	Ile
1				5					10					15	
Asp	Ser	Ile	Lys	Gln	Ile	Leu	Ser	Ile	Tyr	Lys	Ile	Asp	Phe	Asp	Pro
			20					25				30			
Ser	Phe	Gly	Ala	Thr	Leu	Thr	Asp	Asp	Asn	Asp	Leu	Asp	Tyr	Gln	Met
		35					40					45			
Leu	Ile	Glu	Lys	Thr	Gln	Glu	Lys	Ile	Gln	Glu	Leu	Asp	Lys	Arg	Ser
	50					55					60				
Gln	Glu	Ile	Leu	Gln	Gln	Thr	Gly	Met	Thr	Arg	Glu	Gln	Met	Glu	Val
65				70					75						80
Phe	Ala	Asn	Asn	Pro	Asp	Asn	Phe	Ser	Pro	Glu	Glu	Trp	Arg	Ala	Leu
			85					90					95		
Glu	Asn	Ile	Arg	Ser	Ser	Cys	Asn	Glu	Tyr	Lys	Lys	Glu	Thr	Glu	Glu
		100					105					110			
Leu	Ile	Lys	Glu	Val	Thr	Asn	Asp	Ile	Gly	His	Ser	Ser	His	Lys	Ser
		115					120					125			

Pro Thr Pro Lys Lys Thr Lys Ser Ser Ser Gln Lys Lys Ser Lys Lys  
 130 135 140  
 Lys Asn Trp Ile Pro Leu  
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 801:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 461 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 790634..792016

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 801:

Met Lys Ile Val Val Ser Arg Gly Leu Asp Leu Ser Leu Lys Gly Ala  
 1 5 10 15  
 Pro Lys Glu Ser Gly Phe Cys Gly Lys Val Asp Pro Thr Tyr Val Ser  
 20 25 30  
 Val Asp Leu Arg Pro Phe Ala Pro Leu Pro Leu Glu Val Lys Val Thr  
 35 40 45  
 Pro Gly Asp Gln Val Thr Ala Gly Ser Pro Leu Ala Glu Tyr Lys Leu  
 50 55 60  
 Phe Ser Gly Val Phe Ile Thr Ser Pro Val Asp Gly Glu Val Val Glu  
 65 70 75 80  
 Ile Arg Arg Gly Asn Lys Arg Ala Leu Leu Glu Ile Val Ile Lys Lys  
 85 90 95  
 Lys Pro Gly Ile Ser Gln Thr Lys Phe Ser Tyr Asp Leu Gln Ser Leu  
 100 105 110  
 Thr Gln Lys Asp Leu Leu Glu Val Phe Lys Lys Glu Gly Leu Phe Ala  
 115 120 125  
 Leu Phe Lys Gln Arg Pro Phe Asp Ile Pro Ala Leu Pro Thr Gln Ser  
 130 135 140  
 Pro Arg Asp Val Phe Ile Asn Leu Ala Asp Asn Arg Pro Phe Thr Pro  
 145 150 155 160  
 Ser Val Glu Lys His Leu Ser Leu Phe Ser Ser Lys Glu Asp Gly Tyr  
 165 170 175  
 Tyr Ile Phe Val Val Gly Val Gln Ala Ile Ala Lys Leu Phe Gly Leu  
 180 185 190  
 Lys Pro His Ile Ile Ser Thr Asp Arg Leu Thr Leu Pro Thr Gln Asp  
 195 200 205  
 Leu Val Ser Ile Ala His Leu His Thr Ile Asp Gly Pro Phe Pro Ser  
 210 215 220  
 Gly Ser Pro Ser Thr His Ile His His Ile Ala Arg Ile Arg Asn Glu  
 225 230 235 240  
 Arg Asp Val Val Phe Thr Ile Ser Phe Gln Glu Val Leu Ser Ile Gly  
 245 250 255  
 His Leu Phe Leu Lys Gly Phe Val Leu Gly Gln Gln Ile Val Ala Leu  
 260 265 270  
 Ala Gly Ser Ala Leu Pro Pro Ser Gln Arg Lys Tyr Leu Ile Thr Ala  
 275 280 285  
 Lys Gly Ala Ser Phe Ser Asp Leu Leu Pro Lys Asp Ile Phe Ser Ser  
 290 295 300  
 Asp Glu Ile Thr Leu Ile Ser Gly Asp Pro Leu Thr Gly Arg Leu Cys

```

305          310          315          320
Lys Lys Glu Glu Asn Pro Cys Leu Gly Met Arg Asp His Thr Ile Thr
          325          330          335
Leu Leu Pro Asn Pro Lys Thr Arg Glu Ser Phe Ser Phe Leu Arg Leu
          340          345          350
Gly Trp Asn Lys Leu Thr Val Thr Arg Thr Tyr Leu Ser Gly Phe Phe
          355          360          365
Lys Arg Lys Arg Val Phe Met Asp Met Asp Thr Asn Met His Gly Glu
          370          375          380
Lys Arg Pro Ile Ile Asp Ala Glu Ile Tyr Glu Arg Val Ser Ala Ile
385          390          395          400
Pro Val Pro Val Ala Leu Ile Ile Lys Ala Leu Glu Thr Gln Asn Phe
          405          410          415
Glu Glu Ala Cys Arg Leu Gly Leu Leu Glu Val Ala Pro Glu Asp Phe
          420          425          430
Ala Leu Pro Thr Phe Ile Asp Pro Ser Lys Thr Glu Met Phe Ser Ile
          435          440          445
Val Lys Glu Ser Leu Leu Arg Thr Gln Lys Arg Met Trp
          450          455          460

```

(2) INFORMATIONS POUR LA SEQ ID NO: 802:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 342 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(792059..793084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 802:

```

Val Tyr Asn Phe Met Thr Arg Leu Pro Leu Leu Lys Arg Pro Arg Arg
1          5          10          15
Asn Arg Lys Ser Ala Ala Val Arg Ser Ile Ile Gln Glu Thr Gln Leu
          20          25          30
Cys Ser Ser Asp Leu Ile Trp Pro Ile Phe Leu Lys Asp Gly Ser Gly
          35          40          45
Ile Arg Glu Glu Ile Glu Ser Met Pro Gly Val Tyr Arg Trp Ser Leu
50          55          60
Asp Met Val Ser Lys Glu Leu Glu Arg Leu Cys Thr Ile Gly Leu Lys
65          70          75          80
Ala Val Ile Leu Phe Pro Val Ile Asp Ala Asn Lys Lys Glu Gln Phe
          85          90          95
Gly Ser Tyr Ala Ser His Pro Tyr Asn Ile Val Cys Lys Gly Ile Gln
          100          105          110
Ala Ile Lys Lys Ser Phe Pro Glu Leu Cys Val Ile Ser Asp Ile Ala
          115          120          125
Leu Asp Pro Phe Thr Thr Ser Gly His Asp Gly Ile Phe His Asn Asn
130          135          140
Tyr Val Ile Asn Asp Glu Ser Val Arg Val Tyr Gly Gly Ile Ala Val
145          150          155          160
Met His Ala Glu Met Gly Ala Asp Ile Val Ala Pro Ser Asp Met Met
          165          170          175
Asp Gly Arg Val Lys His Ile Arg Glu Gln Met Asp Gln Met Gly Phe
          180          185          190

```

```

Val Asn Thr Gly Ile Leu Ser Tyr Ser Ala Lys Tyr Ala Ser Ala Leu
      195                      200                      205
Tyr Gly Pro Phe Arg Asp Ala Leu Ser Ser His Leu Gln Ser Gly Asp
      210                      215                      220
Lys Arg Thr Tyr Gln Met Asp Pro Ala Asn Val Gln Glu Ala Leu Leu
225                      230                      235                      240
Glu Cys Gln Leu Asp Glu Glu Glu Gly Ala Asp Met Val Met Ile Lys
      245                      250                      255
Pro Ala Gly Phe Tyr Leu Asp Val Ile Val Lys Ala Arg Glu Asn Thr
      260                      265                      270
His Leu Pro Val Val Ala Tyr Gln Val Ser Gly Glu Phe Ser Met Ile
      275                      280                      285
Met Ala Ala Cys Leu His Gly Trp Leu Asn Lys Glu Ser Val Ile Lys
      290                      295                      300
Glu Ser Leu Leu Ala Ile Lys Arg Ala Gly Ala Thr Ala Ile Ile Ser
305                      310                      315                      320
Tyr Ala Thr Pro Trp Val Leu Glu Trp Leu Ala Lys Asp Ala Leu Pro
      325                      330                      335
Phe Glu Arg Ser Val Leu
      340

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 803:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 238 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 793343..794056

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 803:

```

Ala Asn Leu Leu Tyr Arg Ser Phe Leu Met Leu Ser Lys Glu Gly Gly
1      5      10      15
Phe Ser Glu Glu Gln Arg Ala Arg Leu Ser His Phe Val Thr Asn Leu
      20      25      30
Asp Ser Pro Ile Phe Ala Leu Lys Asn Leu Pro Glu Val Val Lys Gly
      35      40      45
Ala Leu Phe Ser Lys Tyr Ser Arg Ser Thr Leu Gly Leu Arg Thr Leu
      50      55      60
Leu Leu Lys Glu Phe Leu Asp Gly Glu Gly Gly Asn Phe Leu Asp Asp
65      70      75      80
Asp Gln Gln Asp Cys Glu Leu Gly Ile Gln Lys Ala Val Asp Phe Tyr
      85      90      95
Arg Arg Val Leu Asp Asn Phe Gly Asp Asp Ser Val Gly Glu Leu Gly
      100     105     110
Gly Ala His Leu Ala Leu Glu Gln Val Ser Met Leu Ala Ala Lys Ile
      115     120     125
Leu Glu Asp Ala Arg Ile Gly Gly Ser Pro Leu Glu Lys Ser Ser Arg
      130     135     140
Tyr Val Tyr Phe Asp Gln Lys Val Asn Gly Glu Tyr Leu Tyr Tyr Arg
145     150     155     160
Asp Pro Ile Leu Met Thr Ser Ala Phe Lys Asp Val Phe Leu Asp Thr
      165     170     175
Cys Asp Phe Leu Phe Asn Thr Tyr Ser Asp Leu Ile Pro Gln Val Arg

```

```

          180          185          190
Ser His Phe Glu Lys Leu Tyr Pro Lys Asp Pro Glu Val Ser Gln Ser
          195          200          205
Ala Tyr Thr Val Ser Leu Arg Ala Lys Val Leu Asp Cys Leu Arg Gly
          210          215          220
Leu Leu Pro Ala Ala Thr Leu Thr Asn Leu Gly Phe Phe Trp
          225          230          235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 804:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 304 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 794046..794957

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 804:

```

Gly Phe Phe Gly Asn Gly Arg Phe Trp Gln Asn Leu Leu His Arg Leu
1          5          10          15
Gln Asp Asn Ser Leu Val Glu Val Arg Asn Ile Gly Glu Gln Ser Leu
          20          25          30
Thr Glu Leu Met Lys Ile Ile Pro Ser Phe Val Ser Arg Ala Glu Ser
          35          40          45
His His Tyr His His Gln Ala Met Val Asp Tyr Arg Arg Ala Leu Lys
          50          55          60
Glu Gln Leu Lys Ser Phe Ala His Arg Tyr Gly Glu Glu Arg Glu Ile
65          70          75          80
Ser Lys Glu Ala Gly Val Lys Leu Val Tyr Gly Asp Pro Asp Gly Leu
          85          90          95
Tyr Lys Ile Ala Ala Ala Tyr Met Phe Pro Tyr Ser Glu His Thr Tyr
          100          105          110
Ala Glu Leu Leu Asp Ile Cys Arg Asn Ile Pro Asn Glu Asp Leu Met
          115          120          125
Arg Ile Leu Glu Ser Gly Ala Ser Phe Arg Glu Asn Arg Arg His Lys
          130          135          140
Ser Pro Arg Gly Leu Glu Cys Ala Glu Phe Ala Phe Asp Ile Thr Ala
145          150          155          160
Asp Phe Gly Ala Tyr Arg Asp Leu Gln Arg His Arg Ile Leu Thr Gln
          165          170          175
Glu Arg Gln Leu Leu Thr Lys Lys Leu Gly Tyr Thr Met Pro Ser Gln
          180          185          190
Leu Ile Asp Thr Pro Met Glu Ala Pro Phe Arg Gly Ala Met Glu Lys
          195          200          205
Ala Asp Gln Ala Tyr Arg Leu Ile Ala Glu Glu Phe Pro Glu Glu Ala
          210          215          220
Gln Tyr Val Val Pro Leu Ala Tyr Asn Ile Arg Trp Leu Phe His Ile
225          230          235          240
Asn Ala Arg Gly Leu Gln Trp Leu Cys Glu Leu Arg Ser Gln Pro Gln
          245          250          255
Gly His Glu Ser Tyr Arg Lys Ile Ala Ile Asp Met Ala Arg Glu Val
          260          265          270
Ile Gln Phe His Pro Ala Tyr Glu Leu Phe Leu Lys Phe Val Asp Tyr
          275          280          285

```

Ser Glu Thr Asp Leu Gly Arg Leu Gln Gln Glu Ser Arg Lys Lys Ser  
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 805:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 86 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(795144..795401)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 805:

Glu Lys Met Lys Thr Leu Ile Asp Asn Asn Ile Val Arg Phe Lys Asn  
 1 5 10 15  
 Ile Ser Lys Thr Lys Gln Gly Ile Phe Val Asn Phe Gln Val Lys Gly  
 20 25 30  
 Glu Arg Gly Gly Ala Ser Phe Thr Ala Ser Ile Ala Val Asp Ile Asp  
 35 40 45  
 Ala Ala Asp Val Ser Ala Gly Asp Ser Leu Glu Thr Ile Ile Glu Arg  
 50 55 60  
 Cys Ala Leu Ile Gly Ile Arg Glu Phe Gln Lys Cys Glu Phe Gln Phe  
 65 70 75 80  
 Asp Gly Ile Ile Cys Leu  
 85

(2) INFORMATIONS POUR LA SEQ ID NO: 806:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 227 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 795575..796255

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 806:

Met Ala Gly Pro Lys His Val Leu Leu Val Ser Glu His Trp Asp Leu  
 1 5 10 15  
 Phe Phe Gln Thr Lys Glu Leu Leu Asn Pro Glu Glu Tyr Arg Cys Thr  
 20 25 30  
 Ile Gly Gln Gln Tyr Lys Gln Glu Leu Ser Ala Asp Leu Val Val Cys  
 35 40 45  
 Glu Tyr Ser Leu Leu Pro Arg Glu Ile Arg Ser Pro Lys Ser Leu Glu  
 50 55 60  
 Gly Ser Phe Val Leu Val Leu Leu Asp Phe Phe Asp Glu Glu Thr Ser  
 65 70 75 80  
 Val Asp Leu Leu Asp Arg Gly Phe Trp Tyr Leu Ile Arg Pro Ile Thr  
 85 90 95  
 Pro Arg Ile Leu Lys Ser Ala Ile Ser Leu Phe Leu Ser Gln His Ser

```

          100          105          110
Leu His Ser Val Pro Glu Ser Ile Arg Phe Gly Pro Asn Val Phe Tyr
          115          120          125
Val Leu Lys Leu Thr Val Glu Thr Pro Glu Gly Ser Val His Leu Thr
          130          135          140
Pro Ser Glu Ser Gly Ile Leu Lys Arg Leu Leu Ile Asn Lys Gly Gln
          145          150          155          160
Leu Cys Leu Arg Lys His Leu Leu Glu Glu Ile Lys Asn His Ala Lys
          165          170          175
Ala Ile Val Ala Arg Asn Val Asp Val His Ile Ala Ser Leu Arg Lys
          180          185          190
Lys Leu Gly Ala Tyr Gly Ser Arg Ile Val Thr Leu Arg Gly Val Gly
          195          200          205
Tyr Leu Phe Ser Asp Asp Gly Asp Lys Lys Phe Ser Gln Gln Asp Thr
          210          215          220
Lys Leu Ser
          225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 807:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 246 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 796278..797015

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 807:

```

Ile Pro Ser Tyr Ala Cys Ile Arg Ser Leu Val Met Val Leu Ser Ala
1          5          10          15
Ser Leu Phe Ser Pro Glu Glu Phe Leu Tyr Pro Glu Ile Val Ser Gln
          20          25          30
Ala Glu Phe Val Trp Ser Ile Leu Thr Leu Leu Glu Glu Lys Leu Ala
          35          40          45
Ser His Thr Phe Ser Gly Ile His Gly His Leu Glu Glu Gly Val Tyr
          50          55          60
Leu Lys Asn Lys Glu Thr Ile Glu Ile Gln Glu Gly Ala Tyr Val Glu
65          70          75          80
Ser Gly Ala Tyr Ile Cys Gly Pro Cys Ile Ile Gly Pro Tyr Thr Gln
          85          90          95
Val Arg His Gly Ala Tyr Ile Arg Gly Gly Val Ile Thr Ser Ser His
          100          105          110
Cys Val Ile Gly His Cys Ser Glu Ile Lys Asn Ser Tyr Leu Gly His
          115          120          125
His Ala Lys Ala Ala His Phe Ala Tyr Val Gly Asp Ser Val Phe Gly
          130          135          140
Ser Arg Val Asn Leu Gly Ala Gly Val Arg Cys Ala Asn Phe Arg Leu
145          150          155          160
Asp Gly Lys Thr Ile Phe Phe His His Ser Gly Glu Arg Tyr Asp Thr
          165          170          175
Lys Arg Lys Lys Leu Gly Ala Phe Leu Gly Arg Gly Val Ser Val Gly
          180          185          190
Cys Asn Thr Val Leu Asn Pro Gly Cys Tyr Val Ala Ser Ala Thr Lys
          195          200          205

```



```

Ile Leu Pro Lys Ser Asn His Leu Leu Arg Asn Asn Leu Cys Gln Thr
  210                      215                      220
Lys Val Asp Glu Lys Lys Lys Ala Val Ala Trp Ile Trp Ile Ile Ser
225                      230                      235                      240
Ala Phe Ile Asp Arg Lys
                      245

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 808:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 796985..797365

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 808:

```

Met Asp Tyr Phe Ser Val Tyr Arg Ser Lys Val Glu Lys Lys Leu Arg
1                      5                      10                      15
Asp Ser Leu Gly Asp Phe Gly Asn Thr Gln Gly Gly Leu Arg Asp Pro
                      20                      25                      30
Ile Glu Tyr Ala Leu Leu Gly Gly Gly Lys Arg Val Arg Pro Leu Leu
                      35                      40                      45
Val Gly Leu Phe Ala Glu Gly Ile His Lys Glu Arg Asp Val Leu Asp
50                      55                      60
Thr Ala Ile Ala Ile Glu Tyr Ile His Thr Ser Thr Leu Ile Ala Asp
65                      70                      75                      80
Asp Leu Pro Cys Met Asp Asp Asp Asp Met Arg Arg Gly Lys Leu Arg
                      85                      90                      95
Phe Thr Lys Leu Leu Met Lys Leu Arg Leu Ser Trp Leu Arg Met Leu
                      100                      105                      110
Leu Phe Gln Leu Leu Met His Glu Phe Val Arg Met Gln Lys Arg
                      115                      120                      125

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 809:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 199 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 797260..797856

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 809:

```

Arg Gln Ala Ser Val His Lys Ala Phe Asp Glu Ala Ser Ala Leu Leu
1                      5                      10                      15
Ala Ser Tyr Ala Leu Ile Pro Ala Ala Tyr Ala Arg Ile Arg Lys Asn
                      20                      25                      30
Ala Lys Ala Leu Lys Ala Val Val Ser Cys Glu Gln Asp Val Glu Glu

```

```

      35      40      45
Ala Tyr Glu Asp Ile Leu Glu Leu Ile Glu Leu Arg Phe Gly Val Gly
  50      55      60
Gly Ile Leu Gly Gly Gln Tyr Glu Asp Val Phe Phe His Asp Phe Ser
  65      70      75      80
Lys Glu Asn Val Leu Gly Ile Ile Lys Lys Lys Thr Gly Ala Leu Phe
      85      90      95
Glu Ile Ala Cys Val Ser Gly Trp Leu Phe Gly Gly Gly Glu Arg Glu
      100      105      110
Ser Ser Thr Leu Val Ala Glu Phe Ala Glu His Phe Gly Leu Leu Phe
      115      120      125
Gln Ile Arg Asp Asp Leu Ala Asp Leu Ser Gln Asp Asp Gln Glu Glu
      130      135      140
Lys His Met Asn Tyr Ala Leu Leu Phe Gly Glu Val Ala Ala Lys Glu
      145      150      155      160
Leu Leu Asp His Ser Phe Glu Ser Cys Ile Lys Asn Leu His Leu Leu
      165      170      175
Gln Glu Arg Gly Leu Glu Cys Ser Glu Pro Leu Glu Met Leu Cys Lys
      180      185      190
Asn Val Phe Cys Gly Trp Lys
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 810:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 797772..798086

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 810:

```

Lys Ser Pro Pro Ile Ala Gly Glu Gly Ile Arg Val Phe Gly Ala Ala
  1      5      10      15
Arg Asp Val Val Gln Lys Cys Val Leu Trp Met Glu Ile Asn Thr Phe
      20      25      30
Tyr Ala Asn Leu Ala Ala Glu Asp Phe Gly Arg Gly Ala His Arg Thr
      35      40      45
Trp Ala Ser Leu Phe Phe Met Leu Val Gly Phe Leu Val Leu Leu Gly
      50      55      60
Asn Ser Ser Val Gln Leu Leu Asp Lys Gly Val Phe Tyr Gly Lys Ala
      65      70      75      80
Cys Phe Leu Ser Leu Gln Arg Lys Leu Glu Tyr Glu Glu Leu Glu Ser
      85      90      95
Ile Leu Leu Asn Ile Leu Tyr Gly
      100      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 811:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 164 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(797935..798426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 811:

Pro	Lys	Ser	Ile	Asp	Pro	Ala	Lys	Thr	Pro	Val	Met	Met	Tyr	Cys	Thr
1				5					10					15	
Gly	Gly	Ile	Arg	Cys	Glu	Leu	Tyr	Ser	Ala	Leu	Leu	Leu	Glu	Lys	Gly
			20					25					30		
Phe	Lys	Glu	Val	Tyr	Gln	Leu	Asp	Gly	Gly	Val	Ile	Ala	Tyr	Gly	Leu
		35					40					45			
Lys	Met	Gly	Thr	Gly	Lys	Trp	Arg	Gly	Lys	Leu	Phe	Val	Phe	Asp	Asp
	50					55					60				
Arg	Met	Ala	Met	Pro	Ile	Asp	Glu	Ala	Asp	Pro	Asn	Val	Ser	Pro	Ile
65					70					75					80
Ala	Arg	Cys	Ser	Leu	Cys	Asn	Thr	Asp	Ser	Asp	Thr	Tyr	Tyr	Asn	Cys
			85						90					95	
Ala	Asn	Thr	Asp	Cys	Asn	Asn	Leu	Phe	Ile	Cys	Cys	Glu	Ser	Cys	Ile
			100					105					110		
Ala	Thr	His	Lys	Gly	Cys	Cys	Ser	Glu	Glu	Cys	Ser	Gln	Ala	Pro	Arg
		115					120					125			
Ile	Arg	Ala	Phe	Ser	Ala	Glu	Arg	Gly	Asn	Lys	Pro	Phe	Arg	Arg	Lys
	130					135					140				
His	Leu	Cys	Pro	Thr	Ile	Glu	Gln	Ser	Cys	Cys	Leu	Lys	Glu	Gln	Glu
145					150					155					160
Asn	Gln	Pro	Ala												

(2) INFORMATIONS POUR LA SEQ ID NO: 812:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(798416..798925)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 812:

Asp	Val	Phe	Met	Glu	Lys	Asn	Tyr	Tyr	Ala	Leu	Ala	Tyr	Tyr	Tyr	Phe
1				5					10					15	
Gly	Pro	Val	Ser	Asn	Pro	Tyr	Glu	Glu	Ile	Ala	Leu	His	Lys	Gln	Leu
			20					25					30		
Phe	Lys	Thr	Met	Asp	Val	Ser	Cys	Arg	Ile	Tyr	Ile	Ser	Glu	Glu	Gly
		35					40					45			
Ile	Asn	Gly	Gln	Phe	Ser	Gly	Tyr	Gln	Pro	Asp	Ala	Glu	Arg	Tyr	Met
	50					55					60				
Ala	Trp	Leu	Lys	Gln	Arg	Pro	Asp	Phe	Ala	Ser	Ile	Lys	Phe	Lys	Ile
65					70					75					80
His	His	Ile	Glu	Glu	Asn	Ile	Phe	Pro	Arg	Val	Thr	Val	Lys	Tyr	Arg
			85						90				95		
Lys	Glu	Leu	Val	Ala	Leu	Gly	Cys	Ser	Val	Asp	Thr	Thr	Lys	Gln	Gly

```

          100          105          110
Lys His Ile Ser Pro Glu Glu Trp His Glu Lys Leu Gln Glu Asn Arg
      115          120          125
Cys Leu Val Leu Asp Val Arg Asn Asn Tyr Glu Trp Lys Ile Gly His
      130          135          140
Phe Glu Asn Ala Val Leu Pro Asp Ile Glu Thr Phe Arg Glu Phe Pro
145          150          155          160
Asp Tyr Ala Asp Arg Leu Ala Lys Glu His
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 813:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 209 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 799301..799927

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 813:

```

Met Ala Arg Tyr Cys Gly Pro Lys Asn Arg Ile Ala Arg Arg Phe Gly
1      5      10      15
Ala Asn Ile Phe Gly Arg Gly Arg Asn Pro Leu Leu Arg Lys Pro Asn
      20      25      30
Pro Pro Gly Gln His Gly Met Gln Arg Lys Lys Lys Ser Asp Tyr Gly
      35      40      45
Leu Gln Leu Glu Glu Lys Gln Lys Leu Lys Ala Cys Tyr Gly Met Ile
      50      55      60
Leu Glu Lys Gln Leu Val Lys Ala Tyr Lys Glu Val Val Asn Lys Gln
65      70      75      80
Gly Asn Val Ala Gln Met Phe Leu Glu Lys Phe Glu Cys Arg Leu Asp
      85      90      95
Ser Ile Val Tyr Arg Leu Gly Phe Ala Lys Thr Ile Phe Ala Ala Gln
      100      105      110
Gln Leu Val Ser His Gly His Val Leu Val Asn Gly Lys Lys Val Asp
      115      120      125
Arg Arg Ser Phe Phe Val Arg Pro Gly Met Gln Ile Ser Leu Lys Glu
      130      135      140
Lys Ser Lys Arg Leu Ala Ile Val Thr Glu Ser Leu Glu Asn Lys Asp
145      150      155      160
Gln Ser Ser Leu Pro Ala Tyr Leu Ser Leu Asp Lys Ala Ala Phe Lys
      165      170      175
Gly Glu Leu Val Val Ala Pro Glu Leu Asp Gln Ile Ala Ser Gln Leu
      180      185      190
Pro Leu Pro Val Asn Val Ser Val Ile Cys Glu Phe Leu Ser His Arg
      195      200      205
Thr

```

(2) INFORMATIONS POUR LA SEQ ID NO: 814:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(800029..800862)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 814:

```

Leu Leu Gly Ala His Thr Ser Ala Ala Gly Gly Leu His Asn Ala Leu
1           5           10           15
Tyr Glu Gly Arg Asp Ile Gly Ala Thr Thr Val Gln Leu Phe Thr Ala
          20           25           30
Asn Gln Arg Gln Trp Lys Arg Arg Ala Leu Thr Gln Glu Met Val Asp
          35           40           45
Gln Phe Arg Ile Ala Leu Asn Glu Thr Ser Leu Ser Tyr Ile Met Ser
          50           55           60
His Ala Gly Tyr Leu Asn Asn Pro Gly Ala Pro Asn Pro Glu Ile Leu
65           70           75           80
Glu Lys Thr Arg Val Cys Met His Gln Glu Ile Ala Asp Cys Ile Ser
          85           90           95
Leu Gly Ile Ser Phe Val Asn Phe His Pro Gly Ala Ala Leu Ser Asp
          100          105          110
Ser Lys Glu Ser Cys Leu Asp Arg Ala Ile Thr Ser Phe Ser Gln Met
          115          120          125
Ala Pro Leu Phe Glu Asn His Pro Pro Leu Val Val Leu Leu Glu Thr
          130          135          140
Thr Ala Gly Gln Gly Ser Leu Ile Gly Ser Ser Phe Glu Glu Leu Ala
145          150          155          160
Tyr Leu Ile Gln Gly Ile Lys Ala Leu Ile Pro Ile Gly Val Cys Leu
          165          170          175
Asp Thr Cys His Ile Phe Ala Ala Gly Tyr Asp Ile Ser Ser Val Ala
          180          185          190
Gly Trp Glu Gln Val Leu Lys His Phe Asp Ala Val Ile Gly Leu Ser
          195          200          205
Phe Leu Arg Ala Ile His Leu Asn Asp Ser Val Phe Ala Leu Gly Lys
          210          215          220
Asn Lys Asp Arg His Ala Pro Ile Gly Glu Gly Cys Ile Gly Ser Asp
225          230          235          240
Ser Phe Cys Phe Leu Met Gln Asp Glu Arg Thr Arg Met Leu Pro Lys
          245          250          255
Tyr Leu Glu Thr Pro Gly Gly Pro Asp Leu Trp Thr Lys Glu Ile Arg
          260          265          270
Tyr Leu Gln Lys Val Cys
          275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 815:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 355 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 801065..802129

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 815:

Met Arg Lys Asp Asp Glu Gly Ser Leu Val Arg Ser Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ser Gly Thr Phe Phe Ser Arg Leu Thr Gly Met Leu Arg Glu Ile  
 20 25 30  
 Val Met Ala Thr Tyr Phe Gly Ala Asp Pro Leu Val Ala Ser Phe Trp  
 35 40 45  
 Leu Ala Phe Arg Thr Ile Phe Phe Leu Arg Lys Leu Leu Gly Gly Pro  
 50 55 60  
 Ile Leu Gly Leu Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala Gln  
 65 70 75 80  
 Asn Ile Ser Arg Ala Thr Phe Phe Phe Lys Ser Phe Ser Arg Phe Phe  
 85 90 95  
 Cys Tyr Ser Ala Ile Leu Phe Thr Leu Ile Ile Glu Leu Gly Leu Cys  
 100 105 110  
 Val Trp Cys Ser Cys Val Thr Gly Ser Leu Phe Asp Thr Leu Phe Leu  
 115 120 125  
 Thr Ile Ile Leu Leu Pro Ser Gly Ile Phe Leu Met Met Tyr Thr Val  
 130 135 140  
 Asn Ser Thr Leu Leu His Cys Glu Lys Lys Phe Phe Ser Val Gly Leu  
 145 150 155 160  
 Ala Pro Ser Val Val Asn Val Leu Trp Ile Gly Thr Val Phe Leu Ala  
 165 170 175  
 Arg Asn Tyr Asp Pro Arg Asn Arg Ile Phe Gly Leu Ala Val Val Leu  
 180 185 190  
 Val Val Gly Phe Ile Leu Glu Trp Ala Ile Thr Leu Pro Gly Val Met  
 195 200 205  
 Lys Phe Leu Gly Gln Ser Lys Glu Val Pro Gln Glu Arg Asp Ser Ile  
 210 215 220  
 Arg Ala Leu Ile Ala Pro Leu Ser Leu Gly Leu Leu Ser Met Gly Ile  
 225 230 235 240  
 Phe Gln Leu Asn Leu Leu Cys Asp Met Trp Leu Ala Arg Tyr Ile Asn  
 245 250 255  
 Glu Val Gly Pro Leu Tyr Leu Met Tyr Ser Val Arg Ile Gln Gln Leu  
 260 265 270  
 Pro Val His Leu Phe Gly Leu Gly Val Phe Thr Val Leu Leu Pro Ala  
 275 280 285  
 Ile Ser Arg Cys Val Gln Asp Gln Glu His Gln Gln Gly Tyr Asp Leu  
 290 295 300  
 Leu Arg Phe Ser Leu Lys Leu Thr Val Ala Val Met Val Val Ile Thr  
 305 310 315 320  
 Met Gly Leu Leu Leu Phe Ala Leu Pro Gly Val Arg Val Leu Tyr Glu  
 325 330 335  
 His Gly Val Phe Pro Tyr Asn Ser Cys Ala Arg Tyr Cys Arg Ser Ser  
 340 345 350  
 Lys Arg Val  
 355

## (2) INFORMATIONS POUR LA SEQ ID NO: 816:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 217 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 802023..802673

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 816:

```

Arg Trp Gly Tyr Cys Phe Leu Leu Cys Leu Gly Tyr Glu Cys Tyr Met
1      5      10      15
Ser Thr Glu Cys Phe Leu Thr Thr Ala Val His Ala Ile Val Glu Val
20      25      30
Leu Arg Gly Tyr Ser Gly Ser Ile Pro Met Ala Leu Ala Pro Leu
35      40      45
Val Ser Ala Leu Phe Tyr Ala Arg Arg Asn Tyr Lys Val Pro Met Leu
50      55      60
Val Gly Ile Ile Ala Ala Val Val Asn Met Val Leu Asn Val Ile Gly
65      70      75      80
Cys Leu Val Cys Lys Gln Val Ala Val Leu Ala Tyr Ala Thr Ser Leu
85      90      95
Ala Ser Trp Gly Gln Leu Ala Met Leu Trp Tyr Cys Ala Gly Lys Ser
100     105     110
Leu Pro Thr Tyr Lys Gly Leu Met Trp Arg Thr Phe Lys Glu Ser Gly
115     120     125
Lys Thr Val Ile Thr Thr Ile Leu Ala Ala Val Ile Thr Ile Gly Val
130     135     140
Asn Ile Val Thr His Thr Thr Tyr Val Val Phe Ile Glu Pro Leu Thr
145     150     155     160
Val Pro Thr Lys Pro Leu Val Ser Phe Leu Asp Gln Cys Gly Val Phe
165     170     175
Phe Ala Glu Ser Ala Leu Phe Leu Ser Val Leu Phe Gly Leu Ala Lys
180     185     190
Leu Leu Lys Thr Glu Asp Leu Val Asn Leu Thr Ser Phe Gln Tyr Trp
195     200     205
Lys Gly His Gln Ser Ile Leu Arg Asn
210     215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 817:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui.

(viii) POSITION DANS LE GENOME: 802920..803246

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 817:

```

Met Lys Lys Tyr Phe Tyr Lys Gly Phe Val Gly Ala Leu Leu Leu Ala
1      5      10      15
Cys Gly Ser Thr Asn Leu Ala Phe Ala Gln Ala Ser Ser Met Asp Ser
20      25      30
Gln Leu Trp Ser Val Glu Asp Leu Asp Ser Tyr Leu Ser Ser Lys Gly
35      40      45
Phe Val Glu Thr Arg Lys Arg Arg Trp Ser Phe Thr Phe Ser Trp Arg
50      55      60
Cys Pro Arg Ser Met Asp Leu Cys Lys Arg Gly Ile Leu Arg Gln Leu

```

```

65              70              75              80
Arg Leu Leu Leu Asn Leu Phe Tyr Leu Ser Ile Val Ile Val Val Asn
      85              90              95
Ser Ile Cys Met Trp Ile Thr Pro Leu Leu Ile Val Gly
      100              105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 818:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 372 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 803105..804220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 818:

```

Leu Glu Met Ser Ala Leu Asp Gly Phe Met Gln Lys Arg His Leu Glu
1              5              10              15
Thr Thr Gln Thr Pro Thr Lys Pro Ile Leu Pro Ile Asn Arg Tyr Arg
      20              25              30
Ser Glu Phe Asn Leu Tyr Val Asp Tyr Thr Ala Ala Asn Ser Trp Met
      35              40              45
Thr Ser Lys Met Asn Trp Val Thr Ile Ala Gly Gly Glu Ser Ser Ala
      50              55              60
Ala Gly Leu Asp Ile Asn Arg Ala Phe Leu Gly Tyr Arg Phe Tyr Lys
65              70              75              80
Asn Pro Glu Thr Gln Ala Glu Val Phe Ala Glu Ile Gly Arg Ser Gly
      85              90              95
Leu Gly Asp Ile Phe Asp Ser Asp Val Gln Phe Asn Ser Asn Phe Asp
      100              105              110
Gly Ile His Leu Tyr Ala Ala Arg Arg Ile Ser Glu Lys Leu Pro Phe
      115              120              125
Thr Met Ile Val His Gly Gly Pro Phe Val Val Asn Met Ala Glu Lys
      130              135              140
Glu Tyr Ala Trp Val Val Glu Ala Ile Leu Asn Lys Leu Pro Gly Asn
145              150              155              160
Phe Val Val Lys Thr Ser Val Ile Asp Trp Asn Thr Leu Thr Ala Lys
      165              170              175
Thr Asn Asp Pro Ala Asp Ala Ser Thr Ala Gln Pro Ala Lys Pro Asn
      180              185              190
Thr Lys Tyr Asp Tyr Leu Val Trp Gln Trp Leu Val Gly Lys Ser Thr
      195              200              205
Ala Met Pro Trp Phe Asn Gly Gln Thr Lys Asn Leu Tyr Thr Tyr Gly
      210              215              220
Ala Tyr Leu Phe Asn Pro Leu Ala Glu Ile Pro Glu Asn Trp Lys Gln
225              230              235              240
Ser Thr Thr Thr Pro Ala Thr Lys Ile Thr Asn Gly Lys Glu Asn His
      245              250              255
Ala Trp Phe Ile Gly Cys Ser Leu Gly Gly Val Arg Arg Ala Gly Asp
      260              265              270
Trp Ser Ala Thr Val Arg Tyr Glu Tyr Val Glu Ala Leu Ala Ile Pro
      275              280              285
Glu Ile Asp Val Ala Gly Ile Gly Arg Gly Asn Gln Met Lys Tyr Gly
290              295              300

```



```

Phe Ala Gln Ala Ile Lys Gln Gly Leu Asp Pro Lys Glu Ser Asn Gly
305                      310                      315                      320
Phe Thr Asn Tyr Lys Xaa Val Ser Tyr Gln Phe Val Met Gly Leu Thr
                      325                      330                      335
Asp Ser Val Ser Phe Arg Ala Tyr Ala Ala Tyr Ser Lys Pro Ala Asn
                      340                      345                      350
Asp Asn Leu Gly Ser Asp Phe Thr Tyr Arg Lys Tyr Asp Leu Gly Leu
                      355                      360                      365
Ile Ser Ser Phe
                      370

```

(2) INFORMATIONS POUR LA SEQ ID NO: 819:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 350 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 804307..805356

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 819:

```

Gly Phe Phe Ile Phe Leu Tyr Cys Met Glu Ser Gly Pro Glu Ser Val
1      5      10      15
Ser Ser Asn Gln Ser Ser Met Asn Pro Ile Ile Asn Gly Gln Ile Ala
      20      25      30
Ser Asn Ser Glu Thr Lys Glu Ser Thr Lys Ala Ser Glu Ala Ser Ser
      35      40      45
Ser Ala Ser Ser Ser Val Ser Ser Trp Ser Phe Leu Ser Ser Ala Lys
      50      55      60
Asn Ala Leu Ile Ser Leu Arg Asp Ala Ile Leu Asn Lys Asn Ser Ser
      65      70      75      80
Pro Thr Asp Ser Leu Ser Gln Leu Glu Ala Ser Thr Ser Thr Ser Thr
      85      90      95
Val Thr Arg Val Ala Ala Lys Asp Tyr Asp Lys Ala Lys Ser Asn Phe
      100     105     110
Asp Thr Ala Lys Ser Gly Leu Glu Asn Ala Lys Thr Leu Ala Glu Tyr
      115     120     125
Glu Thr Lys Met Ala Asp Leu Met Ala Ala Leu Gln Asp Met Glu Ala
      130     135     140
Asn Ser Asp Pro Ser Asn Asp His Thr Glu Glu Leu Asn Asn Ile Lys
      145     150     155     160
Lys Ala Leu Glu Ala Gln Lys Asp Thr Ile Asp Lys Leu Asn Lys Leu
      165     170     175
Val Thr Leu Gln Asn Gln Asn Lys Ser Leu Thr Glu Ala Leu Lys Thr
      180     185     190
Thr Asp Ser Ala Asp Gln Ile Pro Ala Ile Asn Ser Arg Leu Glu Ile
      195     200     205
Asn Lys Asn Ser Ala His Gln Ile Ile Lys Glu Leu Lys Glu Gln Ile
      210     215     220
Ser Asn Tyr Lys Ala Val Leu Thr Asp Val Glu Lys Val Ile Lys Glu
      225     230     235     240
Phe Ser Glu Ala Gly Ile Lys Leu Gly Gln Ala Leu Gln Ser Ile Val
      245     250     255
Asp Ala Gly Asp Gln Ser Gln Ala Ala Val Leu Gln Ala Arg Gln Ser

```

Asn	Ser	Pro	Asp	Asn	Ile	Ala	Ala	Thr	Lys	Lys	Leu	Ile	Asp	Ala	Ala
		275					280						285		
Lys	Thr	Lys	Val	Asn	Glu	Leu	Lys	Gln	Glu	His	Gln	Glu	Ile	Ala	Asp
	290					295					300				
Ser	Pro	Leu	Val	Lys	Lys	Ala	Glu	Glu	Gln	Ile	Asn	Gln	Ala	Gln	Gln
305					310					315				320	
Asp	Ile	Gln	Thr	Ile	Thr	Pro	Ser	Gly	Leu	Asp	Ile	Pro	Ile	Val	Gly
				325					330					335	
Pro	Ser	Gly	Ser	Gly	Xaa	Pro	Gln	Glu	Val	Arg	Gln	Glu	Arg		
		340						345					350		

(2) INFORMATIONS POUR LA SEQ ID NO: 820:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 331 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 805290..806282

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 820:

Trp	Phe	Gly	Tyr	Ser	Tyr	Arg	Trp	Ser	Glu	Trp	Val	Arg	Xaa	Ser	Ala
1				5				10						15	
Gly	Ser	Ala	Ala	Gly	Ala	Leu	Lys	Ser	Ser	Asn	Asn	Ser	Gly	Arg	Ile
			20					25					30		
Ser	Leu	Leu	Leu	Asp	Asp	Val	Asp	Asn	Glu	Met	Ala	Ala	Ile	Ala	Met
		35				40						45			
Gln	Gly	Phe	Arg	Ser	Met	Ile	Glu	Gln	Phe	Asn	Val	Asn	Asn	Pro	Ala
	50				55					60					
Thr	Ala	Lys	Glu	Leu	Gln	Ala	Met	Glu	Ala	Gln	Leu	Thr	Ala	Met	Ser
65					70				75					80	
Asp	Gln	Leu	Val	Gly	Ala	Asp	Gly	Glu	Leu	Pro	Ala	Glu	Ile	Gln	Ala
			85					90					95		
Ile	Lys	Asp	Ala	Leu	Ala	Gln	Ala	Leu	Lys	Gln	Pro	Ser	Ala	Asp	Gly
		100					105						110		
Leu	Ala	Thr	Ala	Met	Gly	Gln	Val	Ala	Phe	Ala	Ala	Ala	Lys	Val	Gly
		115				120						125			
Gly	Gly	Ser	Ala	Gly	Thr	Ala	Gly	Thr	Val	Gln	Met	Asn	Val	Lys	Gln
	130				135						140				
Leu	Tyr	Lys	Thr	Ala	Phe	Ser	Ser	Thr	Ser	Ser	Ser	Ser	Tyr	Ala	Ala
145				150					155					160	
Ala	Leu	Ser	Asp	Gly	Tyr	Ser	Ala	Tyr	Lys	Thr	Leu	Asn	Ser	Leu	Tyr
			165					170					175		
Ser	Glu	Ser	Arg	Ser	Gly	Val	Gln	Ser	Ala	Ile	Ser	Gln	Thr	Ala	Asn
		180					185						190		
Pro	Ala	Leu	Ser	Arg	Ser	Val	Ser	Arg	Ser	Gly	Ile	Glu	Ser	Gln	Gly
	195					200						205			
Arg	Ser	Ala	Asp	Ala	Ser	Gln	Arg	Ala	Ala	Glu	Thr	Ile	Val	Arg	Asp
	210				215						220				
Ser	Gln	Thr	Leu	Gly	Asp	Val	Tyr	Ser	Arg	Leu	Gln	Val	Leu	Asp	Ser
225				230					235					240	
Leu	Met	Ser	Thr	Ile	Val	Ser	Asn	Pro	Gln	Ala	Asn	Gln	Glu	Glu	Ile
			245					250					255		

```

Met Gln Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr
                260                      265                      270
Pro Ala Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln
                275                      280                      285
Leu Glu Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln
                290                      295                      300
Glu Asn Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val
305                      310                      315                      320
Asn Ile Ala Ser Leu Phe Ser Gly Tyr Leu Ser
                325                      330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 821:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 543 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 806453..808081

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 821:

```

Lys Lys Tyr Tyr Trp Asp Arg Phe Ala Thr Ser Thr Thr Val Glu Leu
1      5      10
Arg Glu Leu Ala Met Asn Arg Ile His Arg Thr Gln Gly Ser Leu Thr
20     25     30
Asp Tyr Asn Ser Thr Leu Glu Ala Ile Ala Lys Lys Ile Ala Lys Pro
35     40     45
Asp Ser Ala Thr Ile Val Ser Gln Val Ala Gln Tyr Glu Gln Phe Lys
50     55     60
Met Glu Gln Glu Ala Leu Lys Ala Leu Leu Val Ser Phe Asp Gln Lys
65     70     75     80
Ala Asp Gln Arg Tyr Arg Asn Leu Ile Gln Arg Leu Glu Gln Leu Asp
85     90     95
Val Asp Arg Gln Thr Gly Arg Ser Ile Glu Ser Pro His Ile Gln Glu
100    105    110
Lys Pro Met Ala Ser Leu Gln Ser Glu Asn Gln Val Val Ala Gln Ala
115    120    125
Val Val Gln Ser Asp Ser Ser Met Pro Ile Phe Thr Gly Ile Lys Gln
130    135    140
Ser Trp Ala Val Arg Leu Val Gln Gly Ile Arg Glu Ile Leu Asp Gln
145    150    155    160
Leu Leu Val Asp Thr Ser Leu Phe Thr Glu Glu Glu Arg Gly Asp Leu
165    170    175
Leu Ala Ile Arg Met Asp Ala Ala Ser Leu Gln Asp Lys Gln Glu Arg
180    185    190
Leu Ser Ala Glu Asp Ile Arg Ser Leu Leu Ser Leu Ser Asn Asp Val
195    200    205
Met Arg Val Leu Gln Lys Ala Ser Val Ser Ser Thr Arg Gln Leu Glu
210    215    220
Leu Ile Gln Ser Leu Ile Asp Ile Phe Gly Thr Glu Glu Asn Leu Glu
225    230    235    240
Gln Ser Phe Ala Gln Val Arg Leu Glu Asn Phe Gln Ala Ile Leu Ser
245    250    255
Val Ile Lys Glu Arg Leu Thr Glu Glu Glu Phe Arg Val Phe Gln Glu

```

Val	Ser	Glu	Ile	Ser	Ser	Ile	Gln	Arg	Thr	Ser	Glu	Ser	His	Leu
		275				280					285			
Ser	Pro	Glu	His	Ile	Glu	Ala	Ile	Ala	Arg	Val	Gly	Gly	Tyr	Leu
	290					295					300			
Ala	Lys	Ile	Val	Glu	Ser	Glu	Leu	Lys	Ala	Ser	Gln	Lys	Val	Asp
305					310					315				320
Cys	Gln	Arg	Ile	Ala	Ala	Met	Tyr	Gln	Glu	Gln	Val	Asp	Ala	Val
				325					330					335
Ala	Tyr	His	Ser	Leu	Glu	Gln	Asp	Ala	Leu	Phe	Val	Asn	Ser	Arg
			340					345					350	
His	Gly	Tyr	Phe	Val	Gln	Val	Ile	Ser	Leu	Val	Ser	Ser	Leu	Met
	355					360						365		His
Ser	Leu	Ser	Pro	Thr	Ser	Glu	Glu	Glu	Arg	Ile	Leu	Leu	Asn	Pro
	370					375					380			Ala
Met	Met	Val	Ser	Val	Leu	Pro	Thr	Val	Arg	Ala	Ile	Gly	Leu	Arg
385					390					395				400
Asp	Phe	Leu	Thr	Ala	Glu	Gln	Gln	Gln	Met	Val	Asn	Ala	Ala	Val
				405					410					415
Ser	Leu	Gln	Gln	Gln	Gln	Leu	Asp	Glu	Phe	Leu	Gly	Val	Leu	Cys
			420					425					430	Ala
His	Leu	Val	Val	Val	Asn	Cys	Gln	Asn	Lys	Glu	Thr	Gly	Leu	Leu
	435						440					445		Glu
Gly	Leu	Glu	Glu	Ser	Phe	Ser	Glu	Thr	Leu	Ser	Gly	Leu	Ser	Asn
	450					455				460				Asn
Phe	Val	Leu	Thr	Ala	Lys	Met	Gln	Asp	Ile	Leu	Gln	Val	Cys	Ser
465					470					475				480
Gln	Gly	Phe	Val	Thr	Leu	Ala	Asn	Gly	Asp	Arg	Tyr	Glu	Leu	Phe
				485					490					495
Tyr	Asn	Asp	Ser	Gly	Glu	Ala	Val	Cys	Asp	Glu	Ile	Ala	Leu	Gly
			500					505					510	Asp
Gly	Phe	His	Lys	Val	Leu	Gly	Thr	Met	Leu	Ala	Val	Ala	Leu	Ser
		515					520					525		Gln
Ala	Glu	Val	Phe	Lys	Ala	Arg	Val	Arg	Ser	Ile	His	Ser	Ala	Ser
	530					535						540		

(2) INFORMATIONS POUR LA SEQ ID NO: 822:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 328 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 808026..809009

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 822:

Arg	Phe	Leu	Lys	Gln	Arg	Tyr	Leu	Lys	Gln	Glu	Cys	Asp	Arg	Phe	Ile
1			5						10					15	
Leu	Gln	Ala	Asp	Ser	Glu	Lys	Asn	Met	Ile	His	Lys	Arg	Met	Val	Gln
		20					25						30		
Gly	Glu	Gln	Lys	Ser	Leu	Phe	Leu	Thr	Lys	Met	Gln	Thr	Glu	Leu	Asn
		35					40					45			
Ala	Gly	Lys	Thr	Ile	Ala	Gln	Thr	Lys	Glu	Val	Glu	Ala	Ser	Pro	Leu
	50					55					60				

```

Pro Ser Ala Val Ala Ser Val Leu Ile Asp His Tyr Met Pro Lys Glu
65          70          75          80
Val Glu Phe Leu Glu Lys Ile Ser Ser Arg Leu Tyr Tyr Gly Asn Lys
          85          90          95
Gly Ser Asp Ile Gly Asn Thr Ile Leu Asp Ala Ile Ser Leu Tyr Val
          100          105          110
Asn Ser Ala Thr Tyr Phe Gly Phe Ala Asn Tyr Ile Gly Gln Pro Pro
          115          120          125
Val Val Gly Lys Thr Gly Glu Asn Ile Phe Ala Gly Ser Ala Asp Asn
          130          135          140
Ala Lys Ala Lys Leu Asp Glu Glu Arg Lys Gln Val Asp Val Phe Leu
145          150          155          160
Glu Ile Thr Lys Ala Ala Lys Thr Thr Val Thr Asn Gln Gln Ser Ala
          165          170          175
Val Thr Asp Asp Asp Lys Leu Ser Thr Glu Gln Lys Ala Lys Ile Asn
          180          185          190
Ala Glu Leu Thr Gln Tyr Thr Asp Met Leu Asn Ala Ile Asn Asn Ser
          195          200          205
Leu Thr Ser Leu Lys Thr Gln Leu Ala Pro Leu Ser Val Ser Thr Val
          210          215          220
Glu Gly Val Asp Gly Val Phe Glu Val Lys Asn Gly Lys Pro Gly Glu
225          230          235          240
Asn Gly Lys Asn Trp Arg Leu Val Leu Gln Thr Leu Glu Asp Thr Val
          245          250          255
Val Ser Gly Glu Val Gly Ser Pro Thr Asn Ile Gly Met Phe Gln Met
          260          265          270
Gln Ala Leu Val His Ser Asn Gln Gln Ala Tyr Ala Asp Met Gly Gln
          275          280          285
Asn Phe Gln Leu Glu Leu Gln Met His Leu Thr Ser Met Gln Gln Glu
          290          295          300
Trp Met Val Val Ala Thr Ser Leu Gln Leu Leu Asn Gln Ile Tyr Leu
305          310          315          320
Gly Leu Ala Arg Asn Leu Leu Arg
          325

```

(2) INFORMATIONS POUR LA SEQ ID NO: 823:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 461 acides aminés.

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(809079..810461)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 823:

```

Leu Leu Asn Arg Lys Ile Ser Ser Met Lys Arg Ser Arg Asn Leu Met
1          5          10          15
Thr Ser Gln Glu Val Thr Thr Ser Val Pro Phe Gly Leu Thr Leu Arg
          20          25          30
Leu Gln Gln Ser Ser Arg Leu Lys Thr Val Thr Thr Asp Glu Val Lys
          35          40          45
Gln Ala Leu Thr Ser Gln Ala Asn Thr Ile Val Ser Asp Phe Ser Leu
          50          55          60
Ala Gln Thr Leu Lys Ser Thr Ile Asn Lys Ile Val Gln Glu Asn Gly

```

65					70					75				80
Glu	Phe	Lys	Ala	Lys	Val	Asp	Gly	Ile	Glu	Arg	Gln	Tyr	Thr	Ile Phe
				85					90					95
Gly	Pro	Leu	Lys	Asn	Asp	Thr	Ser	Ser	Asn	Lys	Ala	Thr	Leu	Asn Pro
			100					105					110	
Ile	Leu	Leu	Asn	Phe	Gly	Ser	Ile	Gly	Phe	Leu	Pro	Asn	Ile	Thr Leu
			115				120					125		
Ala	Ala	Asn	Asn	His	Ala	Glu	Thr	Ser	Ala	Arg	Ala	Phe	Phe	Lys Phe
			130				135				140			
Arg	Ala	Leu	Ala	Gln	Val	Glu	Ser	Thr	Lys	Leu	Asp	Gly	Thr	Leu Gln
145					150					155				160
Gly	Ser	Glu	Asn	Phe	Leu	Gln	Lys	Ile	Asn	Gln	Leu	Arg	Lys	Asp Leu
			165						170					175
Phe	Ser	Tyr	Gln	Leu	Leu	Ala	Gln	Ser	Tyr	Glu	Ile	Arg	Ser	Leu Pro
			180					185					190	
Leu	Pro	Ser	Ala	Val	Ala	Ser	Val	Leu	Ile	Asp	Arg	Tyr	Met	Pro Gln
		195					200					205		
Glu	Ile	Asp	Tyr	Leu	Xaa	Gln	Met	Lys	Ser	Asp	Leu	Tyr	Tyr	Ser Asn
210						215					220			
Phe	Xaa	Ser	Ser	Val	Gly	Asn	Ala	Met	Ile	Glu	Ala	Ile	Ala	Gln Phe
225					230					235				240
Val	Asn	Gly	Ala	Thr	Tyr	Phe	Asn	Phe	Ala	Ser	Phe	Val	Gly	Gln Gln
				245					250					255
Pro	Met	Thr	Ala	Met	Ala	Xaa	Asp	Thr	Phe	Ser	Gly	Ser	Lys	Glu Thr
			260					265					270	
Ala	Glu	Ala	Lys	Leu	Ala	Leu	Glu	Lys	Gln	Gln	Ala	Lys	Leu	Tyr Leu
		275					280					285		
Gln	Tyr	Ala	Thr	Gln	Ala	Leu	Lys	Val	Val	Gln	Glu	Gln	Met	Glu Arg
290						295					300			
Val	Gln	Asn	Asp	Lys	Val	Ile	Thr	Asn	Glu	Gln	Arg	Leu	Arg	Ile Thr
305					310					315				320
Asp	Ala	Leu	Lys	Gly	Tyr	Ala	Asp	Asn	Leu	Asn	Ala	Ile	Ser	Gly Ser
			325						330					335
Leu	Val	Leu	Leu	Gln	Val	Tyr	Leu	Asn	Pro	Leu	Ser	Val	Gly	Val Arg
			340					345					350	
Asn	Gly	Asn	Gln	Arg	Gly	Asn	Asp	Thr	Gly	Thr	Asn	Pro	Lys	Gly Thr
		355					360					365		
Phe	His	Val	Phe	Arg	Gly	Lys	Asp	Gln	Trp	Gln	Ala	Arg	Leu	Glu Ile
		370				375					380			
Leu	Glu	Asp	Ala	Leu	Val	Ser	Gly	Leu	Pro	Ser	Asn	Ile	Ile	Ser Gly
385					390					395				400
Gly	Leu	Phe	Pro	Leu	Gln	Ala	Ser	Val	Gln	Ser	Asp	Gln	Gln	Ala Tyr
			405						410					415
Ala	Asp	Met	Gly	Gln	Asn	Tyr	Gln	Leu	Glu	Met	Gln	Met	His	Met Thr
			420					425					430	
Ala	Met	Gln	Gln	Glu	Trp	Thr	Val	Val	Ala	Thr	Ser	Leu	Gln	Ile Leu
		435					440					445		
Asn	Gln	Ile	Tyr	Leu	Gly	Leu	Thr	Arg	Lys	Leu	Ala	Ser		
450						455					460			

(2) INFORMATIONS POUR LA SEQ ID NO: 824:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 426 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(810328..811605)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 824:

Lys	Thr	Leu	Val	Glu	Met	Cys	Ser	Met	Asn	Ile	Phe	Asn	Lys	Ile	Asn	1	5	10	15
Ser	Val	Ser	Lys	Asp	Tyr	Thr	Lys	Ile	Glu	Glu	Leu	Phe	Leu	Pro	Thr	20	25	30	
His	Lys	Asn	Lys	Thr	Phe	Cys	Met	Asn	Gln	Val	Met	Gln	Phe	Gln	Lys	35	40	45	
Thr	Glu	Ile	Glu	Arg	Ser	Ala	Ile	Gln	Asn	Val	Leu	Ser	Leu	Leu	Asp	50	55	60	
Leu	Asp	Asn	Asp	Val	Lys	Gly	Lys	Tyr	Glu	Gln	Leu	Val	Ala	Ser	Leu	65	70	75	80
Ser	Ser	Ser	Ala	Pro	Thr	Thr	Thr	Ser	Gln	Pro	Ser	Asp	Glu	Ser	Ala	85	90	95	
Val	Ile	Thr	Tyr	Asp	Pro	Pro	Ser	Ser	Asn	Pro	Leu	Tyr	Asn	Ala	Ser	100	105	110	
Lys	Gln	Ala	Trp	Val	His	Asn	Val	Leu	Val	Gly	Phe	Leu	Ser	Val	Val	115	120	125	
Asn	Glu	Ala	Lys	Thr	Lys	Ala	Thr	Glu	Ile	Ala	Gly	Gln	Gln	Asn	Pro	130	135	140	
Pro	Gln	Thr	Asp	Leu	Lys	Pro	Leu	Thr	Asp	Leu	Phe	Asp	Ser	Leu	Thr	145	150	155	160
Thr	Leu	Val	Asp	Lys	Ala	Asn	His	Arg	Glu	Leu	Ser	Asn	Glu	Asp	Leu	165	170	175	
Glu	Thr	Phe	Tyr	Leu	Leu	Pro	Asp	Gln	Ile	Phe	Ser	Ala	Ile	Gln	Thr	180	185	190	
Phe	Pro	Phe	Glu	Gly	Asn	Gln	Lys	Val	Leu	Phe	Ser	Asn	Gln	Leu	Leu	195	200	205	
Asp	Ser	Phe	Gly	Glu	Asp	Ala	Ser	Ile	Glu	Gln	Val	Phe	Ala	Asp	Ile	210	215	220	
Arg	Ile	Glu	Gly	Leu	Gln	Asp	Thr	Leu	Asn	Met	Val	Gln	Ser	Arg	Leu	225	230	235	240
Ser	Ala	Thr	Glu	Phe	Glu	Ser	Phe	Lys	Glu	Leu	Gln	Met	Ile	Ile	Asp	245	250	255	
Thr	Leu	Arg	Glu	Tyr	Val	Glu	Pro	Phe	Asn	Asp	Glu	Gly	Phe	Asp	Thr	260	265	270	
Ile	Leu	Gln	Thr	Ser	Lys	Asp	Leu	Ser	Ser	Ala	Ile	Ile	Asn	Ser	Ser	275	280	285	
Leu	Ser	Ser	Asn	Asp	Lys	Ile	Glu	Leu	Cys	Arg	Asn	Ile	Ala	Asp	Leu	290	295	300	
Tyr	Arg	Asp	Gln	Val	Leu	Ser	Ile	Lys	Asn	Leu	Asp	Asn	Val	Leu	Asn	305	310	315	320
Glu	Thr	Ile	Tyr	Ile	Asn	Ala	Arg	Asn	Ser	Ser	Leu	Phe	Ser	Asn	Ile	325	330	335	
Cys	Ser	Leu	Val	Glu	Phe	Ile	Met	Gly	Ser	Phe	Ala	Pro	Ile	Gly	Leu	340	345	350	
Asn	Glu	Thr	Thr	Ile	Glu	Val	Thr	Asn	Ala	Ser	Ile	Ala	Gly	Ala	Leu	355	360	365	
Gln	Ala	Val	Arg	Ala	Ile	Asp	Thr	Arg	Phe	His	Glu	Leu	Thr	Pro	Glu	370	375	380	
Gln	Lys	Asn	Leu	Val	Asn	Glu	Thr	Val	Lys	Lys	Leu	Asp	Asp	Phe	Ser	385	390	395	400
Gly	Gly	Asn	Tyr	Ile	Gly	Ala	Phe	Trp	Ala	Tyr	Phe	Thr	Ser	Ala	Thr	405	410	415	
Val	Val	Ser	Ser	Lys	Asp	Cys	Asp	Asn	Arg										

420

425

(2) INFORMATIONS POUR LA SEQ ID NO: 825:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 811725..812342

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 825:

```

Ile Leu Gly Gln Leu Leu Tyr Leu Glu Arg Val Tyr Leu Arg Leu Asn
1           5           10           15
Ser Ala Asn Pro Cys Ser Asp Phe Lys Asn Gln Ala Arg Pro Ala Ile
20           25           30
Asp Met Glu Glu Leu Asn Ser Gly Leu Tyr Val Leu Arg Arg Leu Ala
35           40           45
Val Ala Leu Glu Ala Gly Tyr Xaa Gly Val Xaa Ser Val Val Asn Pro
50           55           60
Ser Asn Arg Val Phe Pro Gly Gly Asp Trp Gly Val Arg Arg Ala Ala
65           70           75           80
Gly Gly Ser Thr Pro Ala Ala Gly Thr Ile Ser Gly Ser Thr Xaa Ala
85           90           95
Asp Ile Lys Gln Ser Thr Ala Lys Val Leu Val Thr Thr Ile Thr Asp
100          105          110
Ser Leu Asn Ala Leu Ile Glu Asp Val Pro Glu Val Pro Met Thr Gln
115          120          125
Val Thr Gly Val Ser Ser Asn Leu Val Leu Met Glu Ser Tyr Gln Gln
130          135          140
Lys Asp Ser Leu Asn Asp Thr Glu Gln Ala Ser Val Phe Ala Ser Ala
145          150          155          160
Tyr Ala Pro Ser Asp Glu Ser Ile Lys Thr Val Ile Lys Lys Glu Gln
165          170          175
Glu Lys Glu Leu Gln Glu Gly Lys Asp Arg Val Thr Ala Gln Leu Thr
180          185          190
Ala Gln Gly Ala Ser Asp Gln Val Ile Glu Lys Ser Leu Gly
195          200          205

```

(2) INFORMATIONS POUR LA SEQ ID NO: 826:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 398 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 812329..813522

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 826:



Arg	Ser	Leu	Trp	Ala	Asp	Tyr	Glu	Lys	Tyr	Tyr	Val	Asp	Glu	Tyr	Phe
1				5					10					15	
Asp	Thr	His	Val	Lys	Glu	Ala	Leu	Trp	Lys	His	Arg	Ala	Ser	Ile	Gly
			20					25					30		
Glu	Asn	Ile	Gln	Glu	Met	Leu	Asp	Gln	Cys	Leu	Asn	Leu	Gly	Leu	Asp
		35					40					45			
Val	Pro	Asp	Ser	Leu	Thr	Lys	Glu	Asn	Ile	Asn	Asp	Ala	Asn	Ala	Lys
	50					55					60				
Leu	Val	Leu	Gln	Ala	Trp	Met	Glu	Ala	Phe	Asn	Asn	Ala	Met	Glu	Val
65					70				75					80	
Glu	Pro	Ala	Leu	Gly	Gly	Ser	Lys	Glu	Val	Ile	Asp	Ser	Val	Leu	Lys
			85						90					95	
Met	Ile	Pro	Phe	Ala	Lys	Gln	Ser	Ser	Asn	Leu	Ser	Asp	Thr	Asp	Ile
			100					105					110		
Asn	Thr	Ile	Tyr	Thr	Gln	Ala	Ala	Leu	Pro	Pro	Pro	Glu	Val	Met	Asp
		115				120						125			
Tyr	Tyr	Leu	Thr	Arg	Gln	Asp	Ala	Gly	Ile	Cys	Lys	Gly	Glu	Val	Val
	130					135					140				
Lys	Ala	Phe	Gln	Gln	Ala	Thr	Gln	Asn	Leu	Gln	Ser	Val	Arg	Ser	Asn
145					150				155					160	
Val	Glu	Glu	Gln	Ile	Lys	Glu	Leu	Glu	Val	Lys	Lys	Thr	Ser	Phe	Leu
			165						170					175	
Gln	Ala	Gln	Ala	Ser	Leu	Glu	Ser	Met	Leu	Glu	Gly	Val	Lys	Arg	Leu
			180					185					190		
Asn	Asp	Asn	Gln	Lys	Phe	Thr	Ser	Val	Arg	Leu	Thr	Ser	Val	Met	Glu
		195					200					205			
Cys	Tyr	Ala	Gly	Leu	Ile	Ala	Leu	Ser	Gln	Ile	Thr	Asp	Val	Leu	Asp
	210					215					220				
Ser	Ala	Gly	Ile	Ser	Leu	Ile	Thr	Gln	Tyr	Val	Asp	Lys	Phe	Leu	Lys
225					230				235					240	
Leu	Asn	Asn	Ala	His	Thr	Ala	Gln	Thr	Leu	Ala	His	Val	Ile	Ser	Tyr
			245						250				255		
Met	Ala	Ala	Tyr	Cys	Glu	Val	Ala	Glu	Cys	Thr	Met	Ala	Ser	Thr	Ile
		260						265					270		
Val	Ser	Glu	Asp	Thr	Val	Leu	Gln	Lys	Val	Lys	Asp	Lys	Trp	Asn	Glu
		275					280					285			
Leu	Lys	Lys	Glu	Lys	Phe	Phe	Glu	Ser	Phe	Thr	Leu	Pro	Asp	Asp	Asn
	290					295					300				
Glu	Leu	Lys	Thr	Asn	Tyr	Ile	Thr	Ser	Thr	Asn	Asn	Val	Cys	Arg	Ala
305					310					315				320	
Asn	Phe	Ser	Asn	Phe	Val	Asn	Thr	Val	Ile	Thr	Glu	Lys	Ile	Asn	Leu
			325						330					335	
Thr	Val	Ala	Val	Arg	Glu	Ala	Gln	Ser	Leu	Leu	Thr	Glu	Phe	Gln	Gly
		340						345					350		
Lys	Ala	Ser	Glu	Tyr	Leu	Asn	Thr	Phe	Gln	Ser	Glu	Ile	Asn	Thr	Leu
		355					360					365			
Asn	Gln	Thr	Tyr	Asp	Thr	Leu	Asp	Pro	Ala	Lys	Ala	Ser	Phe	Asn	Tyr
	370					375					380				
Phe	Tyr	Arg	Glu	Tyr	Thr	Phe	Phe	Thr	Cys	Thr	Gly	Cys	Arg		
385					390					395					

## (2) INFORMATIONS POUR LA SEQ ID NO: 827:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 106 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 813455..813772

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 827:

Ile	Gln	Pro	Lys	Leu	Leu	Leu	Ile	Thr	Ser	Thr	Gly	Ser	Thr	Pro	Ser
1			5						10					15	
Leu	Arg	Ala	Gln	Ala	Val	Asp	Ser	Trp	Ile	Asp	Ser	Thr	Ser	Leu	Gly
		20						25					30		
Ser	Ala	Phe	Ile	His	Leu	Ile	Leu	Asn	Thr	Gln	Ile	Pro	Lys	Gln	Glu
		35					40					45			
Asn	Phe	Leu	Asn	Pro	Leu	Ile	Gln	Glu	Val	Asn	Phe	Asn	Asn	Val	Ala
	50					55					60				
Ala	Asn	Ala	Val	Asn	Asp	Leu	Leu	Ser	Ile	Thr	Asn	Asn	Phe	Ser	Thr
65				70						75				80	
Ser	Ser	Val	Tyr	Tyr	Asn	Leu	Ser	Ser	Tyr	Leu	Val	Glu	Ser	Lys	Ala
			85						90					95	
Arg	Lys	Arg	Phe	Ile	Leu	Trp	Gly	Phe	Leu						
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 828:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 201 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 813732..814334

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 828:

Lys	Ala	Arg	Gln	Gly	Lys	Asp	Leu	Phe	Cys	Gly	Asp	Phe	Phe	Glu	Phe
1			5						10					15	
Met	Gly	Ala	Leu	Ala	Lys	Glu	His	Glu	Tyr	Ile	Val	Arg	Asp	Ile	Lys
		20						25					30		
Ser	Cys	Tyr	Arg	Ala	Glu	Val	Phe	Gly	Glu	Ala	Leu	Leu	Ala	Arg	Val
		35					40					45			
Glu	Ala	Leu	Ala	Gln	Gly	His	Lys	Val	Thr	Asp	Ala	Lys	Ala	Asn	Ser
	50					55					60				
Met	Arg	Thr	Gln	Ala	Asn	Leu	Tyr	Leu	Ser	Phe	Ile	Arg	Ile	Ile	Val
65				70						75				80	
Glu	Gln	Leu	Ala	Val	Leu	Asp	Ser	Leu	Leu	Arg	Ser	Leu	Asn	Tyr	Glu
			85						90					95	
Val	Glu	Lys	Lys	Asp	Asn	Asn	Tyr	Asp	Lys	Asp	Lys	Tyr	Lys	Ile	Thr
			100					105					110		
Gly	Pro	Thr	Asp	Trp	Ile	Ser	Thr	Leu	Ala	Ser	Leu	Glu	Gly	Tyr	Ala
		115					120					125			
Val	Asn	Gly	Phe	Asp	Asn	Ala	Ser	Leu	Ser	Gly	Gly	Leu	Gly	Pro	Met
	130					135					140				
His	Thr	Leu	Val	Gln	Thr	Asp	Gln	His	Asp	Tyr	Leu	Thr	Gln	Ser	Gln
145				150						155				160	
Thr	Gln	Gln	Leu	Asn	Leu	Gln	Asn	Gln	Met	Thr	Asn	Ile	Gln	Gln	Glu
			165						170					175	

Trp Thr Leu Val Ser Thr Ser Met Gln Val Leu Asn Gly Ile Leu Ser  
                     180                    185                    190  
 His Leu Ala Ala Glu Ile Tyr Ser Asn  
                     195                    200

(2) INFORMATIONS POUR LA SEQ ID NO: 829:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 300 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(814314..815213)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 829:

Phe Phe Leu Glu Val Ser Thr Met Ala Ala Thr Val Pro Ile Ala Ser  
 1                    5                    10                    15  
 Pro Val Gly Arg Leu Leu Ser Ser Ala Thr Ala Thr Thr Leu Arg Gly  
                     20                    25                    30  
 Asn Ala Thr Ser Leu Arg Ser Lys Leu Ser Ser Val Asn Asp Leu Phe  
                     35                    40                    45  
 Asp Leu Ile Ser Ser Ser Cys Thr Leu Ala Arg Val Thr Pro Arg Thr  
                     50                    55                    60  
 Thr Val Ser Xaa Thr Gln Gln Gln Leu Ser Thr Ile Glu Thr Thr  
 65                    70                    75                    80  
 Leu Gly Ser Ala Lys Ser Ala Ser Asn Ala Val Gln Ala Xaa Cys Gly  
                     85                    90                    95  
 Ile Val Gln Leu Leu Thr Gly Gly Leu Phe Phe Lys Thr Asn Pro Asp  
                     100                    105                    110  
 Gly Ser Phe His Leu Asp Leu Val Ser Gln Gln Arg Thr Leu Leu Ser  
                     115                    120                    125  
 Pro Leu Ser Leu Val Ser Lys Val Thr Arg Leu Ala Ser Lys Val Leu  
                     130                    135                    140  
 Gly Thr Val Lys Phe Met Gly Ser Gln Thr Phe Pro Val Tyr Gln Leu  
 145                    150                    155                    160  
 Gly Ala His Ala Thr Gly Ile Gly Leu Ser Ala Ser Ala Phe Gly Thr  
                     165                    170                    175  
 Val Ser Pro Pro Ser Met Ser Gln Lys Thr Gln Glu Lys Phe Ser Gly  
                     180                    185                    190  
 Thr Ser Asn Arg Ile Asn Leu Gln Lys Glu His Leu Lys Lys Thr Ala  
                     195                    200                    205  
 Ser Trp His Val Leu Lys Glu Leu Val Gln Val Cys Ser Thr Cys Phe  
                     210                    215                    220  
 Ala Ala Ser Trp Thr Cys Trp Leu Arg Leu Ser Val Ser Ser Ala Met  
 225                    230                    235                    240  
 Gln Phe Leu Gln His Leu Trp Glu Cys Thr Pro Leu Leu Leu Trp Val  
                     245                    250                    255  
 Ser Ser Ala Ser Tyr Leu Leu Trp Glu Met Leu Phe Phe Leu Ser Leu  
                     260                    265                    270  
 Phe Lys Val Cys Lys His His Ile Leu Glu Ala Arg Arg Tyr Ile Ser  
                     275                    280                    285  
 Ala Ser Xaa Phe Leu Ile Arg Ile Asn Phe Arg Cys  
                     290                    295                    300

## (2) INFORMATIONS POUR LA SEQ ID NO: 830:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 161 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(814396..814878)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 830:

```

Trp Ile Phe Pro Pro Arg Ser Cys Phe Ala Thr Lys Asn Pro Pro Val
1           5           10           15
Ser Thr Ile Thr Cys Gln Gln Ser Asn Ser Phe Ser Gln Gln Ser Ser
          20           25           30
Arg Asn Arg Glu Ile His Gly Leu Pro Asn Phe Pro Cys Leu Pro Val
          35           40           45
Gly Cys Thr Arg Asn Trp Tyr Trp Leu Ile Cys Phe Cys Val Trp Asn
          50           55           60
Cys Gln Ser Ala Phe Asp Val Ala Glu Asn Ser Arg Glu Val Leu Gly
65           70           75           80
Asn Leu Lys Gln Asn Lys Pro Thr Glu Gly Thr Ser Lys Glu Asn Gly
          85           90           95
Phe Met Ala Arg Leu Lys Arg Ala Arg Ala Ser Met Phe Asn Leu Leu
          100          105          110
Cys Ser Ile Leu Asp Leu Leu Ala Gln Ala Phe Cys Phe Ile Ser Asp
          115          120          125
Ala Val Ser Thr Ala Phe Met Gly Val His Thr Ala Phe Ile Val Gly
          130          135          140
Ile Phe Cys Phe Leu Ser Ala Leu Gly Asn Val Ile Leu Ser Ile Ala
145           150           155           160
Phe

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 831:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 87 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(815428..815688)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 831:

```

Pro Gln Lys Arg Pro Ser Ala Glu Lys Arg Val Ile Thr Ser Lys Lys
1           5           10           15
Lys Gln Leu Arg Asn Gln Ser Phe Lys Ser Lys Val Arg Thr Ile Leu
          20           25           30
Lys Lys Phe Glu Leu Ala Val Gln Ser Gly Asp Val Glu Ser Ile Ser
          35           40           45

```

Ala Gly Leu Arg Ser Val Tyr Ser Ile Ala Asp Lys Ala Val Lys Arg  
 50 55 60  
 Gly Ile Phe Lys Lys Gly Lys Ala Asp Arg Val Lys Ser Arg Ala Ser  
 65 70 75 80  
 Glu Arg Ala Cys Pro Ala Ala  
 85

(2) INFORMATIONS POUR LA SEQ ID NO: 832:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 447 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 816116..817456

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 832:

Ser Ile Pro Lys Phe Ala Ile Cys Arg Asp Ile Val Trp Gly Cys Thr  
 1 5 10 15  
 Ala Gly Met Gln Tyr Val Met Gly Arg Thr Asn Ser Met Thr Arg Gly  
 20 25 30  
 Phe Leu Asn Lys Arg Arg Val Leu Glu Lys Cys Arg Thr Ala Lys Gln  
 35 40 45  
 Lys Ile His Tyr Cys Ile Ser Arg Tyr Phe His Tyr Leu Pro Pro Val  
 50 55 60  
 Leu Ala Ile Leu Leu Pro Ile Gly Ser Trp Pro Phe Leu Ser Glu Gln  
 65 70 75 80  
 Gln Trp Trp Cys Gly Ser Phe Leu Phe Pro Val Val Ser Ser Leu Gly  
 85 90 95  
 Trp Leu Phe Ala Ile Gly Arg Arg Glu Arg Gln Leu Arg Ala Ala Ala  
 100 105 110  
 Gly Gln Leu Leu Glu Ala Lys Ile Arg Lys Leu Thr Glu Gln Asp Glu  
 115 120 125  
 Gly Leu Lys Asn Ile Arg Glu Thr Ile Glu Lys Arg Gln Lys Glu Thr  
 130 135 140  
 Asp Arg Leu Lys Leu His Asn Asp Lys Leu Val Glu Gln Leu Gly Gln  
 145 150 155 160  
 Ala Arg Glu Val Phe Ile Gln Ala Lys Gly Arg Tyr Asp His Met Glu  
 165 170 175  
 Glu Leu Ser Arg Arg Leu Lys Glu Glu Asn Gln Gln Leu Gln Met Gln  
 180 185 190  
 Leu Glu Ala Ala Val Arg Glu Arg Asn Glu Lys Ile Leu Glu Asn Gln  
 195 200 205  
 Glu Leu Leu Gln Glu Leu Lys Glu Thr Leu Ala Tyr Gln Gln Glu Leu  
 210 215 220  
 His Asp Glu Tyr Gln Ala Thr Phe Val Glu Gln His Ser Met Leu Asp  
 225 230 235 240  
 Lys Arg Gln Ala Tyr Ile Gly Asn Leu Glu Ala Lys Val Gln Asp Leu  
 245 250 255  
 Met Cys Glu Leu Arg Asn Leu Leu Gln Leu Glu Met Gly Ala Lys Thr  
 260 265 270  
 Asn Leu Pro Gly Lys Pro Val Ala Ser Arg Asp Val Val Ala Gln Leu  
 275 280 285  
 Val Leu Glu Phe Arg Lys Ile Val Phe Arg Val Glu Thr Thr Glu Ala

290	295	300
Ala Asp Ser Leu Thr	Ala Leu Arg Tyr Thr	Arg Thr Asp Pro Ser Ala
305	310	315
His Asn Tyr Ser Leu	Ala Cys Arg Gln Leu	Phe Asp Gly Leu Arg Glu
325	330	335
Glu Asn Leu Gly Met Leu	Phe Ile Tyr Ala Pro	Phe Ala Gln Arg Ser
340	345	350
Phe Leu Pro Met Leu Cys	Leu Thr Asp Trp Thr	Gly Tyr Gly Leu Glu
355	360	365
Asp Phe Leu Asn Arg Glu	Ser Asp Val Val Leu	Glu Gly Phe Ala Gln
370	375	380
Trp Glu Arg Asp Leu Leu	Thr Glu Ser Arg Val	Glu Arg Ser Gly Lys
385	390	395
Ile Val Ile Lys Thr Lys	Ala Phe Gly Ala Thr	Pro Phe Tyr Tyr Cys
405	410	415
Val Val Thr Leu Asp Lys	Gly Pro Phe Ala Gln	His Ile Leu Gly Val
420	425	430
Leu Tyr Pro Ala Lys Ala	Ser Phe Phe Thr Asn	Leu Ser Tyr Ile
435	440	445

(2) INFORMATIONS POUR LA SEQ ID NO: 833:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 571 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 817608..819320

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 833:

Met Arg Met Asp Thr Leu Asp Ser Gln Ala Ala Glu Ala Ala Gln Glu	
1	15
Glu Glu Ile Gln Arg Lys Leu Glu Glu Leu Val Thr Leu Ala Lys Asp	
20	30
Gln Gly Phe Ile Thr Tyr Glu Glu Ile Asn Glu Ile Leu Pro Pro Ser	
35	45
Phe Asp Thr Pro Glu Gln Ile Asp Gln Val Leu Ile Phe Leu Ala Gly	
50	60
Met Asp Val Gln Val Leu Asn Gln Ala Asp Val Glu Arg Gln Lys Glu	
65	80
Arg Lys Lys Glu Ala Lys Glu Leu Glu Gly Leu Ala Lys Arg Ser Glu	
85	95
Gly Thr Pro Asp Asp Pro Val Arg Met Tyr Leu Lys Glu Met Gly Thr	
100	110
Val Pro Leu Leu Thr Arg Glu Glu Val Glu Ile Ser Lys Arg Ile	
115	125
Glu Lys Ala Gln Val Gln Ile Glu Arg Ile Ile Leu Arg Phe Arg Tyr	
130	140
Ser Thr Lys Glu Ala Val Ser Ile Ala Gln Tyr Leu Ile Asn Gly Lys	
145	160
Glu Arg Phe Asp Lys Ile Val Ser Glu Lys Glu Val Glu Asp Lys Thr	
165	175
His Phe Leu Asn Leu Leu Pro Lys Leu Ile Ser Leu Leu Lys Glu Glu	
180	190

Asp	Ala	Tyr	Leu	Glu	Glu	Arg	Leu	Leu	Ala	Leu	Lys	Asp	Pro	Ala	Leu
	195						200					205			
Ser	Lys	Pro	Asp	Gln	Ala	Arg	Leu	Asn	Asp	Glu	Leu	Glu	Lys	Cys	Arg
	210					215					220				
Ile	Arg	Thr	Gln	Ala	Tyr	Leu	Arg	Cys	Phe	His	Cys	Arg	His	Asn	Val
225					230					235					240
Thr	Glu	Asp	Phe	Gly	Glu	Val	Val	Phe	Lys	Ala	Tyr	Asp	Ser	Phe	Leu
				245					250					255	
Gln	Leu	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Lys	Ala	Arg	Ala	Glu	Arg	Asn
			260					265					270		
Lys	Phe	Ala	Ala	Ala	Lys	Leu	Ala	Ala	Ala	Arg	Arg	Lys	Leu	His	Lys
	275						280					285			
Arg	Glu	Val	Ala	Ala	Gly	Arg	Thr	Leu	Glu	Glu	Phe	Lys	Lys	Asp	Val
	290					295					300				
Arg	Met	Leu	Gln	Arg	Trp	Met	Asp	Lys	Ser	Gln	Glu	Ala	Lys	Lys	Glu
305					310					315					320
Met	Val	Glu	Ser	Asn	Leu	Arg	Leu	Val	Ile	Ser	Ile	Ala	Lys	Lys	Tyr
				325					330					335	
Thr	Asn	Arg	Gly	Leu	Ser	Phe	Leu	Asp	Leu	Ile	Gln	Glu	Gly	Asn	Met
			340					345					350		
Gly	Leu	Met	Lys	Ala	Val	Glu	Lys	Phe	Glu	Tyr	Arg	Arg	Gly	Tyr	Lys
	355						360					365			
Phe	Ser	Thr	Tyr	Ala	Thr	Trp	Trp	Ile	Arg	Gln	Ala	Val	Thr	Arg	Ala
	370					375					380				
Ile	Ala	Asp	Gln	Ala	Arg	Thr	Ile	Arg	Ile	Pro	Val	His	Met	Ile	Glu
385					390					395					400
Thr	Ile	Asn	Lys	Val	Leu	Arg	Gly	Ala	Lys	Lys	Leu	Met	Met	Glu	Thr
				405					410					415	
Gly	Lys	Glu	Pro	Thr	Pro	Glu	Glu	Leu	Gly	Glu	Glu	Leu	Gly	Phe	Thr
			420					425					430		
Pro	Asp	Arg	Val	Arg	Glu	Ile	Tyr	Lys	Ile	Ala	Gln	His	Pro	Ile	Ser
	435						440					445			
Leu	Gln	Ala	Glu	Val	Gly	Asp	Gly	Gly	Glu	Ser	Ser	Phe	Gly	Asp	Phe
	450					455					460				
Leu	Glu	Asp	Thr	Ala	Val	Glu	Ser	Pro	Ala	Glu	Ala	Thr	Gly	Tyr	Ser
465					470					475					480
Met	Leu	Lys	Asp	Lys	Met	Lys	Glu	Val	Leu	Lys	Thr	Leu	Thr	Asp	Arg
				485					490					495	
Glu	Arg	Phe	Val	Leu	Ile	His	Arg	Phe	Gly	Leu	Leu	Asp	Gly	Arg	Pro
			500					505					510		
Lys	Thr	Leu	Glu	Glu	Val	Gly	Ser	Ala	Phe	Asn	Val	Thr	Arg	Glu	Arg
	515						520					525			
Ile	Arg	Gln	Ile	Glu	Ala	Lys	Ala	Leu	Arg	Lys	Met	Arg	His	Pro	Ile
	530					535					540				
Arg	Ser	Lys	Gln	Leu	Arg	Ala	Phe	Leu	Asp	Leu	Leu	Glu	Glu	Glu	Lys
545					550					555					560
Ile	Gly	Ser	Gly	Lys	Ile	Lys	Ser	Tyr	Lys	Asn					
				565					570						

## (2) INFORMATIONS POUR LA SEQ ID NO: 834:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 130 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 819324..819713

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 834:

Ser	Cys	Cys	Leu	Gln	Gly	Val	Leu	Leu	Tyr	Arg	Leu	Asp	Ile	Ala	Asp
1				5					10					15	
Phe	Arg	Val	Trp	Val	Ser	Ile	Gly	Val	Ser	Glu	Gln	Glu	Arg	His	Tyr
			20					25					30		
Pro	Gln	Pro	Val	Leu	Val	Ser	Leu	Ser	Leu	Phe	Phe	Lys	Glu	Glu	Pro
		35					40					45			
Lys	Ala	Trp	Ser	Thr	Asp	Lys	Val	Ser	Asp	Ser	Val	Cys	Tyr	Ala	Glu
	50					55					60				
Leu	Val	Ser	Leu	Ile	Glu	Glu	Val	Ala	Thr	Asn	Asn	Pro	Cys	Ala	Leu
65				70					75						80
Ile	Glu	Arg	Leu	Ala	Lys	Val	Leu	Leu	Glu	Lys	Ile	Glu	Lys	Ala	Leu
				85					90					95	
Ala	Gly	Gln	Val	Ser	Arg	Ile	Asp	Leu	Arg	Val	Ser	Lys	Glu	Arg	Pro
			100					105					110		
Pro	Ile	Pro	Asp	Leu	Leu	Ser	Pro	Val	Ser	Phe	Ser	Ile	Ser	Arg	Glu
		115					120					125			
Val	Pro														
	130														

(2) INFORMATIONS POUR LA SEQ ID NO: 835:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 233 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 819704..820402

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 835:

Arg	Gly	Ala	Met	Thr	Ser	Trp	Asn	Phe	Val	Cys	Leu	Ser	Leu	Gly	Ser
1				5					10					15	
Asn	Leu	Gly	Asn	Arg	His	Glu	His	Ile	Arg	Arg	Ala	Tyr	Ala	Ser	Leu
			20					25					30		
Lys	Lys	Ala	Gly	Ile	Arg	Asn	Leu	Lys	Ser	Ser	Val	Ile	Leu	Glu	Thr
		35					40					45			
Lys	Ala	Leu	Leu	Leu	Glu	Gly	Ala	Pro	Lys	Glu	Trp	Asp	Leu	Pro	Tyr
	50					55					60				
Phe	Asn	Ser	Val	Val	Ile	Gly	Glu	Thr	Gln	Leu	Ser	Pro	Asp	Glu	Leu
65				70					75						80
Ile	Glu	Glu	Ile	Lys	Met	Ile	Glu	Ser	Arg	Phe	Gly	Gln	Asp	Ala	Ser
				85				90					95		
Leu	Lys	Trp	Gly	Pro	Arg	Pro	Ile	Asp	Ile	Asp	Val	Leu	Phe	Tyr	Gly
			100					105					110		
Asp	Glu	Ala	Phe	Ser	Tyr	His	Ser	Asp	Lys	Cys	Thr	Ile	Pro	His	Pro
		115					120					125			
Lys	Val	Leu	Glu	Arg	Pro	Phe	Ile	Leu	Ser	Met	Met	Ala	Ser	Leu	Cys
	130					135					140				
Pro	Tyr	Arg	Arg	Phe	Arg	Leu	Glu	Gly	Ser	Ser	Cys	Asn	Gly	Lys	Thr
145					150					155					160



```

Phe Ala Glu Leu Ala Ala Ile Tyr Pro Leu Thr Glu Glu Asp Ala Leu
      165      170      175
Gly Ser Phe Gly Ser Ala Thr Gln Ile Met Gly Ile Val Asn Ile Thr
      180      185      190
Asp Asn Ser Ile Ser Asp Thr Gly Leu Phe Leu Glu Ala Ser Arg Ala
      195      200      205
Ala Ala His Ala Glu Arg Leu Phe Ala Glu Gly Ala Ser Ile Ile Asp
      210      215      220
Leu Gly Ala Gln Gln Pro Ile Leu Val
225      230

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 836:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 229 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 820375..821061

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 836:

```

Phe Arg Gly Ala Thr Thr Asn Pro Arg Val Lys Asp Leu Gly Ser Val
1      5      10      15
Glu Gln Glu Trp Glu Arg Leu Glu Pro Val Leu Arg Leu Leu Ala Glu
      20      25      30
Gly Trp Gly Ala Ala Gln Gln Cys Pro Asp Val Ser Ile Asp Thr Phe
      35      40      45
Arg Pro Glu Ile Ile Arg Arg Ala Val Glu Val Phe Pro Ile Arg Trp
      50      55      60
Ile Asn Asp Val Ser Gly Gly Ser Leu Glu Met Ala His Leu Ala Lys
      65      70      75      80
Glu Phe Gly Leu Arg Leu Leu Ile Asn His Ser Cys Ser Leu Pro Pro
      85      90      95
Arg Pro Asp Cys Val Leu Ser Tyr Glu Glu Ser Pro Ile Glu Gln Met
      100      105      110
Leu Arg Trp Gly Glu Ser Gln Leu Glu Gln Phe Ala Gln Val Gly Leu
      115      120      125
Asp Thr Ser Trp Gln Val Val Phe Asp Pro Gly Ile Gly Phe Gly Lys
      130      135      140
Thr Pro Val Gln Ser Met Leu Leu Met Asp Gly Val Lys Gln Phe Lys
      145      150      155      160
Arg Val Leu Glu Cys Pro Val Leu Ile Gly His Ser Arg Lys Ser Cys
      165      170      175
Leu Ser Met Leu Gly Arg Phe Asn Ser Asp Asp Arg Asp Trp Glu Thr
      180      185      190
Ile Gly Cys Ser Val Ser Leu His Asp Arg Gly Val Asp Tyr Leu Arg
      195      200      205
Val His Gln Val Glu Gly Asn Arg Arg Ala Leu Ala Ala Ala Ala Trp
      210      215      220
Ala Gly Met Phe Val
225

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 837:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 159 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 821061..821537

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 837:

```

Met Ile Gln Ala Thr Gly Ile Val Ala Ile Asp Pro Arg Gly Val Met
1           5           10           15
Gly Ala Leu Gly Lys Leu Pro Trp Ser Tyr Pro Glu Asp Leu Arg Phe
          20           25           30
Phe Ala Glu Thr Ile Arg Asn His Pro Ile Ile Met Gly Arg Lys Thr
          35           40           45
Trp Glu Ser Leu Pro Asp Lys Tyr Lys His Gly Arg Asp Ile Val Val
          50           55           60
Phe Ser Arg Arg Met His Pro Pro Gln Cys Ile Gly Val Ser Ser Phe
65           70           75           80
Ala Glu Tyr Gly Thr Leu Ser Leu Asn His Pro Phe Leu Ile Gly Gly
          85           90           95
Ala Glu Leu Phe Glu Ser Phe Phe Gln Gln Asn Leu Leu Lys Ala Cys
          100          105          110
Phe Val Thr His Ile Lys Lys Lys Tyr Trp Gly Asp Thr Phe Phe Pro
          115          120          125
Ile Thr Arg Leu Ser Gly Trp Lys Lys Glu Cys Ile Cys Asn Thr Glu
          130          135          140
Asp Phe Ser Ile Tyr Tyr Tyr Glu Asn Asn Ser Asp Gln Asn Thr
145          150          155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 838:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 198 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 821646..822239

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 838:

```

Ser Ala Val Ala Asp Ala Arg Met Cys Lys Ala Glu Leu Ile Lys Lys
1           5           10           15
Glu Ala Asp Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile Tyr Leu Thr
          20           25           30
Lys Lys Glu Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn
          35           40           45
Thr Asp Gln Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu Gly Ser Cys
          50           55           60
Asn Arg Ile Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val Lys Glu Leu
65           70           75           80

```

Gly	Val	Ile	Ile	Thr	Asp	Ser	His	Thr	Thr	Pro	Met	Arg	Arg	Gly	Val
				85					90					95	
Leu	Gly	Ile	Gly	Leu	Cys	Trp	Tyr	Gly	Phe	Ser	Pro	Leu	His	Asn	Tyr
			100					105					110		
Ile	Gly	Ser	Leu	Asp	Cys	Phe	Gly	Arg	Pro	Leu	Gln	Met	Thr	Gln	Ser
		115					120					125			
Asn	Leu	Val	Asp	Ala	Leu	Ala	Val	Ala	Ala	Val	Val	Cys	Met	Gly	Glu
		130				135					140				
Gly	Asn	Glu	Gln	Thr	Pro	Leu	Ala	Val	Ile	Glu	Gln	Ala	Pro	Asn	Met
145					150					155					160
Val	Tyr	His	Ser	Tyr	Pro	Thr	Ser	Arg	Glu	Tyr	Cys	Ser	Leu	Arg	
			165						170					175	
Ile	Asp	Glu	Thr	Glu	Asp	Leu	Tyr	Gly	Pro	Phe	Leu	Gln	Ala	Val	Thr
			180					185						190	
Trp	Ser	Gln	Glu	Lys	Lys										
			195												

(2) INFORMATIONS POUR LA SEQ ID NO: 839:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 822182..822931

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 839:

Asn	Arg	Gly	Leu	Ile	Arg	Thr	Phe	Phe	Ala	Ser	Gly	Tyr	Val	Glu	Ser
1				5					10					15	
Arg	Lys	Glu	Met	Met	Glu	Val	Phe	Met	Asn	Phe	Leu	Asp	Gln	Leu	Asp
			20					25					30		
Leu	Ile	Ile	Gln	Asn	Lys	His	Met	Leu	Glu	His	Thr	Phe	Tyr	Val	Lys
		35					40					45			
Trp	Ser	Lys	Gly	Glu	Leu	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Tyr	Ala	Lys
	50					55				60					
Asp	Tyr	Tyr	Leu	His	Ile	Xaa	Ala	Phe	Pro	Lys	Tyr	Leu	Asp	Ala	Ile
65				70					75						80
His	Ser	Arg	Cys	Asp	Asp	Leu	Glu	Ala	Arg	Lys	Leu	Leu	Leu	Asp	Asn
			85						90					95	
Leu	Met	Asp	Glu	Glu	Asn	Gly	Tyr	Pro	Asn	His	Ile	Asp	Leu	Trp	Lys
			100					105					110		
Gln	Phe	Val	Phe	Ala	Leu	Gly	Val	Thr	Pro	Glu	Glu	Leu	Glu	Ala	His
		115					120					125			
Glu	Pro	Ser	Glu	Ala	Ala	Lys	Ala	Lys	Val	Ala	Thr	Phe	Met	Arg	Trp
		130				135					140				
Cys	Thr	Gly	Asp	Ser	Leu	Ala	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Ser	Tyr
145					150				155						160
Glu	Ser	Gln	Ile	Pro	Arg	Ile	Ala	Arg	Glu	Lys	Ile	Arg	Gly	Leu	Thr
			165					170						175	
Glu	Tyr	Phe	Gly	Phe	Ser	Asn	Pro	Glu	Asp	Tyr	Ala	Tyr	Phe	Thr	Glu
			180					185					190		
His	Glu	Glu	Ala	Asp	Xaa	Arg	His	Ala	Arg	Glu	Glu	Lys	Ala	Leu	Ile
		195				200						205			
Glu	Met	Leu	Leu	Lys	Asp	Asp	Ala	Asp	Lys	Val	Leu	Glu	Ala	Ser	Gln

(2) INFORMATION POUR LA SEQ ID NO: 840:

(A) LONGUEUR: 437 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(823045..824355)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 840:

Pro 1	Met	Leu	His	Gln 5	His	Gln	Thr	Ala	Ser 10	Val	Ala	Leu	Cys	Pro 15	Ala
Leu	His	Leu	Gln	Gln 20	Gly	Leu	Asp	Met 25	Leu	Gln	Met	Pro	Val 30	Ala	Glu
Leu	Ala	Thr 35	Phe	Val	Ser	Gln	Gln 40	Ile	Thr	Ile	Asn 45	Pro	Cys	Phe	Asp
Leu	Asp 50	Ser	Leu	Asp	Ser 55	Pro	Pro	Glu	Ser	Phe 60	Ser	Phe	Phe	Pro	Ile
Ser 65	Glu	Gln	His	Pro 70	Phe	Thr	Glu	Thr	Leu	Ser 75	Ala	Tyr	Leu	Leu	Arg 80
Gln	Ile	Asp	Thr 85	Asn	Phe	Ala	Ser	Ser 90	Gln	Glu	Arg	Thr	Ile 95	Ala	Gln
Tyr	Ile	Val 100	Gly	Asn	Leu	Ser	Pro 105	Glu	Gly	Leu	Phe	Leu 110	Glu	Asn	Pro
Ser	Leu	Val 115	Ala	Ala	Asp	Leu	Asn 120	Val	Ser	Glu	His 125	Leu	Phe	His	Lys
Val	Trp 130	Gln	Arg	Ile	Gln	Gln 135	Leu	His	Pro	Leu	Gly 140	Val	Gly	Ala	Pro
Ser 145	Leu	Gln	Ser	Tyr 150	Trp	Val	Ser	Leu	Leu	Gln 155	Thr	Ser	Pro	His	Lys 160
Glu	Ala	Leu	Ala 165	Ile	Ile	Arg	Asn	His 170	Phe	Pro	Arg	Leu	Ala 175	Arg	Cys
Asp	Phe	Thr 180	Thr	Ile	Ala	Arg	Lys 185	Met	His	Ala	Thr	Thr 190	Thr	Glu	Ile
Leu	Thr	Phe 195	Leu	Arg	His	Ala	Phe 200	Ala	Ser	Ile	Pro	Trp 205	Cys	Pro	Ala
Ala	Gly 210	Phe	Ser	Glu	Thr	Leu	His 215	Pro	Pro	Ala	Pro	Ala 220	Leu	Pro	Asp
Ala 225	Tyr	Leu	Ser	Phe 230	Ser	Arg	Asn	Ser	Ser	Trp 235	Asp	Val	Ser	Ile	Asn 240
Lys	Asp	Cys	Leu 245	Pro	Ser	Ile	Arg	Leu	Asn 250	Asp	Thr	Val	Leu	Asp 255	Ile
Tyr	Pro	Ser 260	Leu	Pro	Arg	Glu	Glu 265	Lys	Asp	His	Leu	Ser 270	Gln	Gln	Ile
Arg	Ala	Ala 275	Lys	Gln	Leu	Leu	Arg 280	Asn	Val	Lys	Lys	Arg 285	Glu	Glu	Thr
Leu	Leu 290	Ala	Ile	Leu	Arg	Val 295	Leu	Ile	Pro	Tyr	Gln 300	Glu	Glu	Phe	Leu

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Leu Lys Lys Arg Thr Ser Pro Lys Ala Phe Ser Val Lys Gln Ile Ala
305                               310                               315                               320
Arg Glu Leu Ser Leu His Glu Ala Thr Val Cys Arg Ala Ile Asp Asn
                               325                               330                               335
Lys Thr Leu Ala Thr Pro Val Gly Leu Leu Pro Met Arg Ser Leu Phe
                               340                               345                               350
Pro Gln Ala Val Gly Ser Cys Pro Asp Gln Ser Lys Ala Thr Ile Leu
                               355                               360                               365
His Trp Ile His Gln Trp Ile Ser Thr Glu Lys His Pro Leu Ser Asp
                               370                               375                               380
Ala Ala Ile Ser Gln Lys Ile Ile Glu Lys Gly Ile Pro Cys Ala Arg
385                               390                               395                               400
Arg Thr Val Ala Lys Tyr Arg Ser Gln Leu Asn Ile Pro Pro Ala His
                               405                               410                               415
Gln Arg Lys His Leu Cys Ser Val Leu Thr Thr Thr Arg Thr Glu Asn
                               420                               425                               430
Ser Arg His Thr Ile
                               435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 841:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 512 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(824359..825894)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 841:

```

Ala Xaa Leu Arg Lys Leu Asn Leu Asp Lys Lys Leu Cys Asn Ala Met
1                               5                               10                               15
Gln Phe Thr Ile Ser Gln Ala Lys Asn Arg Leu Gln Ser Pro Glu Asp
                               20                               25                               30
Leu Asp Ser Lys Glu Tyr Pro Asp Pro Thr Arg Thr Val Tyr Ala Glu
                               35                               40                               45
Tyr Gln Glu Gln Leu Arg Ala Ala Asn Ala Leu Asp Phe Asp Asp Leu
50                               55                               60
Leu Phe Leu Thr Glu Lys Leu Leu Arg Ile Pro Glu Val Gln Gln Glu
65                               70 -                               75                               80
Tyr Ala Asn His Trp Lys Ala Leu Leu Ile Asp Glu Tyr Gln Asp Thr
                               85                               90                               95
Asn His Ala Gln Tyr Leu Ile Ala Lys Arg Leu Ala Ala Ala His Asn
                               100                               105                               110
Asn Ile Phe Val Val Gly Asp Pro Asp Gln Ser Ile Tyr Ser Trp Arg
                               115                               120                               125
Gly Ala Asn Ile Ser Asn Ile Leu Asn Phe Glu Gln Asp Tyr Ser Gln
130                               135                               140
Ala Leu Val Val Arg Leu Glu Glu Asn Tyr Arg Ser Cys Gly Thr Ile
145                               150                               155                               160
Leu Glu Ala Ala Asn Ala Leu Ile Gln Asn Asn Ser Ala Arg Leu Glu
                               165                               170                               175
Lys Thr Leu Arg Ser Val Lys Gly Pro Gly Asp Lys Ile Phe Cys Phe
                               180                               185                               190
Thr Gly Lys Asn Asp Arg Asp Glu Ala Glu Gln Val Leu Glu Glu Ile

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(2) INFORMATION POUR LA SEQ ID NO: 842:

(A) LONGUEUR: 127 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(825879..826259)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 842:

Met	Leu	Thr	Ser	Glu	Leu	Asn	Ala	Ala	Gln	Val	Thr	Ala	Val	Thr	Ala
1				5					10					15	
Pro	Leu	Gln	Pro	Val	Leu	Val	Leu	Ala	Gly	Ala	Gly	Ala	Gly	Lys	Thr
			20					25					30		

(2) INFORMATION POUR LA SEQ ID NO: 843:

(A) LONGUEUR: 229 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 826340..827026

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 843:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 844:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 79 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 827014..827250

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 844:

Leu	Glu	Asp	Arg	Met	Ile	Asp	Gly	Ile	Gln	Thr	Cys	Ser	Phe	Ser	Pro
1				5				10					15		
Thr	His	Arg	Leu	Thr	Ala	Lys	Ser	Ala	Val	Ser	Ile	Glu	Met	Pro	Leu
			20					25					30		
Ala	Thr	Gln	Asn	Leu	Gln	Glu	Gly	Ala	Leu	Val	Asn	Ala	Lys	Leu	Glu
		35					40					45			
Ala	Asp	Phe	Ala	Arg	Ala	Glu	Gln	Ile	Leu	Thr	Glu	Met	Gln	Glu	Ile
	50					55					60				
Arg	Ser	Ser	Leu	Glu	Arg	Ser	Leu	Glu	Thr	Leu	Phe	Pro	Arg	Glu	
65					70					75					

(2) INFORMATIONS POUR LA SEQ ID NO: 845:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 209 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(827230..827856)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 845:

Met	Lys	Ile	Leu	Ile	Ala	Ser	Ser	His	Gly	Tyr	Lys	Val	Arg	Glu	Thr
1				5				10					15		
Lys	Ala	Phe	Leu	Lys	Lys	Leu	Gly	Glu	Phe	Asp	Ile	Phe	Ser	Leu	Val
			20					25					30		
Asp	Tyr	Pro	Ser	Tyr	Gln	Pro	Pro	Lys	Glu	Thr	Gly	Glu	Thr	Pro	Glu
		35					40					45			
Glu	Asn	Ala	Ile	Gln	Lys	Gly	Leu	Phe	Ala	Ala	Gln	Thr	Phe	Arg	Cys
	50					55					60				
Trp	Thr	Ile	Ala	Asp	Asp	Ser	Met	Leu	Ile	Ile	Pro	Ala	Leu	Gly	Gly
65				70					75					80	
Leu	Pro	Gly	Lys	Leu	Ser	Ala	Ser	Phe	Ala	Gly	Glu	Gln	Ala	Asn	Asp
			85					90						95	
Lys	Asp	His	Arg	Lys	Lys	Leu	Leu	Glu	Asn	Met	Arg	Leu	Leu	Glu	Asn
			100					105					110		
Thr	Ile	Asp	Arg	Ser	Ala	Tyr	Phe	Glu	Cys	Cys	Val	Ala	Leu	Ile	Ser
		115					120					125			
Pro	Phe	Gly	Lys	Ile	Phe	Lys	Ala	His	Ala	Ser	Cys	Glu	Gly	Thr	Ile
	130					135						140			



Ala	Phe	Glu	Glu	Arg	Gly	Ser	Ser	Gly	Phe	Gly	Tyr	Asp	Pro	Leu	Phe
145					150				155						160
Val	Lys	His	Asp	Tyr	Lys	Gln	Thr	Tyr	Ala	Glu	Leu	Pro	Glu	Ala	Ile
			165						170					175	
Lys	Asn	Gln	Val	Ser	His	Arg	Ala	Lys	Ala	Leu	Val	Lys	Leu	Gln	Pro
			180					185					190		
Tyr	Val	Glu	Thr	Val	Leu	Ala	Asn	His	Leu	Leu	Ala	Gly	Lys	Glu	Ser
		195					200					205			
Leu															

(2) INFORMATIONS POUR LA SEQ ID NO: 846:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 828007..829275

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 846:

Arg	Lys	Ile	Arg	Phe	Pro	Leu	Ser	Lys	Arg	Asp	Pro	Lys	Glu	Ile	Met
1				5					10					15	
Lys	Thr	Ile	Cys	Lys	Leu	Val	Ile	Leu	Ala	Leu	Leu	Phe	Pro	Asn	Val
			20					25					30		
Ser	Tyr	Ala	Leu	Val	Gln	Val	Gly	Leu	Glu	Arg	Leu	Phe	Gln	Glu	Glu
		35					40					45			
Lys	Tyr	Leu	Glu	Lys	Ile	Arg	Gly	Lys	Arg	Val	Ala	Leu	Ile	Ser	His
		50				55					60				
Ser	Ala	Ala	Ile	Asn	Arg	Gln	Gly	Glu	His	Ser	Leu	Cys	Val	Phe	Asn
65				70					75					80	
Lys	His	Lys	Gly	Val	Cys	Lys	Leu	Ser	Ala	Leu	Cys	Thr	Leu	Glu	His
			85						90					95	
Gly	Tyr	Phe	Gly	Ala	Ser	Ile	Ala	Glu	Thr	Pro	Gly	Tyr	Asp	Pro	Ile
		100						105					110		
Leu	Glu	Asp	Ile	Pro	Val	Ile	Ser	Leu	Phe	Ala	Ser	Lys	Glu	Ile	Pro
		115					120					125			
Ala	Glu	Val	Ile	Glu	Ala	Cys	Asp	Val	Phe	Val	Tyr	Asp	Val	Gln	Asp
		130				135					140				
Ile	Gly	Val	Arg	Ser	Tyr	Ser	Phe	Ile	Ser	Ala	Leu	Leu	Gln	Val	Val
145					150				155					160	
Lys	Ala	Ser	Ala	Ser	Ser	Lys	Lys	Glu	Leu	Ile	Val	Leu	Asp	Arg	Pro
			165					170						175	
Asn	Pro	Met	Gly	Gly	Asn	Leu	Val	Asp	Gly	Pro	Leu	Pro	Asp	Lys	Glu
		180						185					190		
Ala	Phe	Pro	Ala	Ile	Pro	Tyr	Cys	Tyr	Gly	Met	Thr	Pro	Gly	Glu	Leu
		195					200					205			
Ala	Leu	Leu	Tyr	Arg	Ala	Arg	Tyr	Ala	Pro	Lys	Ala	Ser	Val	Thr	Val
		210				215					220				
Val	Pro	Met	Arg	Gly	Trp	Lys	Arg	Ser	Met	Ile	Phe	Ala	Asp	Thr	Gly
225					230				235					240	
Leu	Ile	Trp	Val	Pro	Thr	Ser	Pro	Gln	Ile	Pro	Asp	Ala	Gln	Ser	Ala
			245					250					255		
Tyr	Phe	Tyr	Ala	Thr	Thr	Gly	Ile	Ile	Gly	Ala	Leu	Ser	Val	Thr	Asn

				260						265					270				
Ile	Gly	Ile	Gly	Tyr	Thr	Leu	Pro	Phe	Lys	Val	Leu	Gly	Ala	Pro	Trp				
		275						280											
Met	Asp	Gly	Cys	Lys	Val	Ala	Gln	Glu	Leu	Asn	Lys	Ala	Arg	Leu	Pro				
	290					295					300								
Gly	Val	His	Phe	Leu	Pro	Phe	Met	Tyr	Glu	Pro	Phe	Phe	Gly	Lys	Phe				
305					310					315					320				
Lys	Met	Glu	Met	Cys	Ser	Gly	Val	Leu	Val	Val	Leu	Gln	Asp	Pro	Lys				
				325					330					335					
Gln	Phe	Leu	Pro	Met	Glu	Thr	Gln	Ser	Val	Ile	Leu	Gly	Val	Leu	Lys				
		340						345					350						
Thr	Leu	Tyr	Pro	Lys	Glu	Val	Glu	Gln	Ala	Phe	Leu	Leu	Leu	Asp	Arg				
	355						360					365							
Leu	Val	Pro	Arg	Arg	Lys	Ala	Ile	Gln	Asn	Leu	Leu	Gly	His	Ser	Glu				
	370					375						380							
Phe	Leu	Asn	Val	Cys	Leu	His	Lys	Lys	Tyr	Ile	Thr	Trp	Pro	Leu	Arg				
385					390					395					400				
Thr	Met	Cys	Ala	Glu	Gly	Arg	Lys	Gln	Phe	Ile	Glu	Gln	Arg	Gln	Pro				
				405					410					415					
Phe	Leu	Leu	Pro	Glu	Tyr	Ala													
				420															

(2) INFORMATIONS POUR LA SEQ ID NO: 847:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 533 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 829355..830953

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 847:

Gly	Leu	Ser	Asn	Ser	Phe	Arg	Asp	Gln	Glu	Gln	Gly	Leu	Gln	Ala	Val				
1				5				10						15					
Leu	Arg	Ala	Ala	Arg	Val	Ile	Ser	His	Met	Phe	Ser	Gln	Thr	Ile	Gly				
		20						25					30						
Pro	Tyr	Gly	Phe	Ser	Thr	Ile	Val	His	Asn	Val	Gln	Asp	Thr	Arg	Thr				
		35					40					45							
Thr	Gln	Asp	Ser	Gln	Ser	Met	Leu	Lys	Asp	Ile	Leu	Phe	Pro	Asp	Val				
	50					55					60								
Phe	Glu	Asn	Ile	Gly	Met	Lys	Leu	Ile	Arg	Asp	Thr	Ala	Leu	Gly	Thr				
65					70					75					80				
Arg	Met	Arg	Phe	Gly	Asp	Gly	Ala	Lys	Thr	Thr	Ala	Leu	Leu	Ile	Glu				
				85					90					95					
Ala	Leu	Leu	Ala	Glu	Gly	Met	Thr	Gly	Ile	Gln	Lys	Gly	Leu	Asp	Pro				
			100					105					110						
His	Glu	Ile	His	Arg	Gly	Met	Leu	Leu	Ala	Glu	Lys	Lys	Ile	Gln	Glu				
		115					120					125							
Val	Phe	Tyr	Arg	Glu	Thr	Phe	Pro	Leu	Ser	Asp	Leu	Glu	His	Thr	Val				
	130					135					140								
Tyr	Val	Ser	Ser	Ile	Ala	Arg	Arg	Phe	Asn	Ser	Glu	Ile	Ala	Ser	Val				
145					150					155					160				
Leu	Ser	Ser	Ala	Val	Gly	Tyr	Gly	Gly	Lys	Asn	Gly	Tyr	Tyr	Ile	Val				
				165					170					175					

(viii) POSITION DANS LE GENOME: 831119..831748

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 848:

Val	Gln	Ile	Leu	Ser	Gly	Ala	Leu	Phe	Leu	Ser	Arg	Arg	Ser	Thr	Met
1				5					10					15	
Gly	Ser	Leu	Val	Gly	Arg	Gln	Ala	Pro	Asp	Phe	Ser	Gly	Lys	Ala	Val
			20					25					30		
Val	Cys	Gly	Glu	Glu	Lys	Glu	Ile	Ser	Leu	Ala	Asp	Phe	Arg	Gly	Lys
		35					40					45			
Tyr	Val	Val	Leu	Phe	Phe	Tyr	Pro	Lys	Asp	Phe	Thr	Tyr	Val	Cys	Pro
	50					55					60				
Thr	Glu	Leu	His	Ala	Phe	Gln	Asp	Arg	Leu	Val	Asp	Phe	Glu	Glu	His
65					70					75					80
Gly	Ala	Val	Val	Leu	Gly	Cys	Ser	Val	Asp	Asp	Ile	Glu	Thr	His	Ser
				85					90					95	
Arg	Trp	Leu	Thr	Val	Ala	Arg	Asp	Ala	Gly	Gly	Ile	Glu	Gly	Thr	Glu
			100					105						110	
Tyr	Pro	Leu	Leu	Ala	Asp	Pro	Ser	Phe	Lys	Ile	Ser	Glu	Ala	Phe	Gly
		115				120						125			
Val	Leu	Asn	Pro	Glu	Gly	Ser	Leu	Ala	Leu	Arg	Ala	Thr	Phe	Leu	Ile
	130					135					140				
Asp	Lys	His	Gly	Val	Ile	Arg	His	Ala	Val	Ile	Asn	Asp	Leu	Pro	Leu
145					150					155					160
Gly	Arg	Ser	Ile	Asp	Glu	Glu	Leu	Arg	Ile	Leu	Asp	Ser	Leu	Ile	Phe
				165					170					175	
Phe	Glu	Asn	His	Gly	Met	Val	Cys	Pro	Ala	Asn	Trp	Arg	Ser	Gly	Glu
			180					185					190		
Arg	Gly	Met	Val	Pro	Ser	Glu	Glu	Gly	Leu	Lys	Glu	Tyr	Phe	Gln	Thr
		195					200					205			
Met	Asp														
	210														

(2) INFORMATIONS POUR LA SEQ ID NO: 849:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(831751..832152)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 849:

Leu	Ala	Cys	Gly	Met	Lys	Phe	Thr	Val	Ala	Val	Phe	Gly	Glu	Ala	Glu
1				5					10					15	
Glu	Gly	Ser	Phe	Glu	Ser	Ala	Tyr	Leu	Cys	Ser	Ser	Leu	Thr	Asp	Leu
			20					25					30		
His	Asn	Asn	Leu	Gly	His	Gly	Arg	Asp	Ser	Pro	Ser	Gly	Ile	Ser	Leu
		35					40					45			
Ala	Val	Gln	Ala	Ile	Met	Gln	Gly	Tyr	Asp	Ile	Leu	Phe	Phe	Arg	Val
	50					55				60					
Lys	Glu	Glu	Gly	Phe	Phe	Ile	Asp	Ser	Tyr	Phe	Phe	Gly	Leu	His	Phe
65					70					75					80
Leu	Asn	Thr	Gln	Thr	Ser	Leu	Thr	Asn	Ile	Val	Ala	Leu	Ala	Leu	Pro
				85					90					95	

Gly Val Gly Asp Phe Asn Ile Ile Glu Ala Ser Leu Ala Leu Cys Arg  
                   100                                  105                  110  
 Lys Leu Lys Ser Leu Leu Leu Phe Ser Asp Gln Asp Leu Tyr Asp Phe  
                   115                                  120                  125  
 Leu Thr Phe Lys Asp Ala  
                   130

(2) INFORMATIONS POUR LA SEQ ID NO: 850:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(832214..832744)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 850:

Ser Ala Val Phe Ala Gly Tyr Ser Ser Arg Ser Arg Arg Thr Ser Ser  
 1                  5                                  10                  15  
 Arg Leu His Ala His His Asn Glu Leu Ala Met Ile Ser Glu Arg Leu  
                   20                                  25                  30  
 Asp Glu Gln Asp Thr Lys Leu Gln Gln Leu Ser Ser Thr Gln Asp His  
                   35                                  40                  45  
 Asn Leu Pro Arg Gln Val Gln Arg Leu Glu Thr Asp Gln Lys Ala Leu  
                   50                                  55                  60  
 Ala Lys Thr Leu Ala Ile Leu Ser Gln Ser Val Gln Asp Ile Arg Ser  
 65                  70                                  75                  80  
 Ser Val Gln Asn Lys Leu Gln Glu Ile Gln Gln Glu Gln Lys Lys Leu  
                   85                                  90                  95  
 Ala Gln Asn Leu Arg Ala Leu Arg Asn Ser Leu Gln Ala Leu Val Asp  
                   100                                  105                  110  
 Gly Ser Ser Pro Glu Asn Tyr Ile Asp Phe Leu Ala Gly Glu Thr Pro  
                   115                                  120                  125  
 Glu His Ile His Ile Val Lys Gln Gly Glu Thr Leu Ser Lys Ile Ala  
                   130                                  135                  140  
 Ser Lys Tyr Asn Ile Pro Val Val Glu Leu Lys Lys Leu Asn Lys Leu  
 145                  150                                  155                  160  
 Asn Ser Asp Thr Ile Phe Thr Asp Gln Arg Ile Arg Leu Pro Lys Lys  
                   165                                  170                  175  
 Lys

(2) INFORMATIONS POUR LA SEQ ID NO: 851:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(832805..833446)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 851:

Glu	Asn	Cys	Tyr	Arg	Ile	Trp	Arg	Glu	Thr	Phe	Pro	Met	Leu	Gly	Ser
1				5					10					15	
Ile	Ser	Phe	Thr	Thr	Tyr	Lys	Glu	Asn	Leu	Met	Arg	Lys	Thr	Ile	Phe
			20					25					30		
Lys	Ala	Phe	Asn	Leu	Leu	Phe	Ser	Leu	Leu	Phe	Leu	Ser	Ser	Cys	Ser
		35					40					45			
Tyr	Pro	Cys	Arg	Asp	Trp	Glu	Cys	His	Gly	Cys	Asp	Ser	Ala	Arg	Pro
	50					55					60				
Arg	Lys	Ser	Ser	Phe	Gly	Phe	Val	Pro	Phe	Tyr	Ser	Asp	Glu	Glu	Ile
65					70					75					80
Gln	Gln	Ala	Phe	Val	Glu	Asp	Phe	Asp	Ser	Lys	Glu	Glu	Gln	Leu	Tyr
				85					90					95	
Lys	Thr	Ser	Ala	Gln	Ser	Thr	Ser	Phe	Arg	Asn	Ile	Thr	Phe	Ala	Thr
			100					105					110		
Asp	Ser	Tyr	Ser	Ile	Lys	Gly	Glu	Asp	Asn	Leu	Thr	Ile	Leu	Ala	Ser
		115					120					125			
Leu	Val	Arg	His	Leu	His	Lys	Ser	Pro	Lys	Ala	Thr	Leu	Tyr	Ile	Glu
	130					135					140				
Gly	His	Thr	Asp	Glu	Arg	Gly	Ala	Ala	Ala	Tyr	Asn	Leu	Ala	Leu	Gly
145					150					155					160
Ala	Arg	Arg	Ala	Asn	Ala	Val	Lys	Gln	Tyr	Leu	Ile	Lys	Gln	Gly	Ile
				165					170					175	
Ala	Ala	Asp	Arg	Leu	Phe	Thr	Ile	Ser	Tyr	Gly	Lys	Glu	His	Pro	Val
			180					185					190		
His	Pro	Gly	His	Asn	Glu	Leu	Ala	Trp	Gln	Gln	Asn	Arg	Arg	Thr	Glu
		195					200					205			
Phe	Lys	Ile	His	Ala	Arg										
		210													

## (2) INFORMATIONS POUR LA SEQ ID NO: 852:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(833368..833802)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 852:

Pro	Asp	Gly	Thr	Arg	Leu	Val	Phe	Val	Ser	Asn	Lys	Asp	Gly	Thr	Pro
1				5					10					15	
Arg	Ile	Tyr	Gln	Met	Gln	Ile	Ser	Pro	Glu	Gln	His	Ser	Pro	Arg	Leu
			20					25					30		
Leu	Thr	Lys	Lys	Tyr	Arg	Asn	Ser	Ser	Cys	Pro	Thr	Trp	Ser	Pro	Asp
		35					40					45			
Gly	Lys	Lys	Ile	Ala	Phe	Cys	Ser	Val	Ile	Lys	Gly	Val	Arg	Gln	Ile
	50					55					60				
Cys	Val	Tyr	Asp	Leu	Ala	Ser	Gly	Arg	Asp	Glu	Gln	Leu	Thr	Thr	Ser
65					70					75					80
Thr	Glu	His	Lys	Glu	Ser	Pro	Ser	Trp	Ala	Ala	Asp	Ser	Asn	His	Leu
				85					90					95	

Val Tyr Ser Ala Gly Ser Ser Asn Thr Ser Glu Leu Phe Leu Leu Ser  
                   100                  105                  110  
 Leu Ile Thr Lys Lys Ser Arg Lys Ile Val Ile Gly Ser Gly Glu Lys  
                   115                  120                  125  
 Arg Phe Pro Cys Trp Gly Ala Phe Pro Ser Gln His Ile Lys Lys Thr  
                   130                  135                  140  
 Ser  
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 853:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(833879..834679)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 853:

Thr Ala Gly Lys Phe Cys Leu Met Lys Gly Ser Val Val Phe Leu Arg  
 1                  5                  10                  15  
 Ser Leu Leu Cys Leu Leu Cys Leu Leu Pro Ser Thr Leu His Cys Glu  
                   20                  25                  30  
 Asp Leu Glu Ile His Val Arg Ser Glu Ser Ser Leu Leu Pro Ile Ala  
                   35                  40                  45  
 Val Ser Leu Leu Ser Ser Pro Lys Asp Ser Arg Gln Ala Ser Tyr Leu  
                   50                  55                  60  
 Ala Ser Leu Arg Asp Leu Phe Ala Arg Asp Leu Ala Leu Gly Asp Leu  
 65                  70                  75                  80  
 Leu Ala Pro Thr Lys Glu Leu Ala Pro Gln Thr Ile Phe Ile Glu Ala  
                   85                  90                  95  
 Ser Tyr Pro Glu Leu Ile Phe Ser Leu Lys Lys Glu Gly Lys Gly Ser  
                   100                  105                  110  
 Gln Lys Ile Phe Ser Leu Glu Leu Ser Gly Asp Pro Ser Lys Asp His  
                   115                  120                  125  
 Gln Ala Ile His Glu Ala Ala Asp Arg Ile His Phe Leu Leu Thr Arg  
                   130                  135                  140  
 Val Pro Gly Ile Ser Ser Gly Lys Ile Ile Phe Ser Leu Cys Ala Thr  
 145                  150                  155                  160  
 Asn Ser Ser Thr Glu Leu Lys Gln Gly Glu Leu Trp Ser Val Asp Tyr  
                   165                  170                  175  
 Asp Gly Gln His Leu Tyr Pro Leu Thr Asn Glu His Ser Leu Ser Val  
                   180                  185                  190  
 Thr Pro Thr Trp Met His Ile Ser His Ile Pro Ala Tyr Met Tyr Val  
                   195                  200                  205  
 Ser Tyr Lys Leu Gly Val Pro Lys Ile Phe Leu Asn Thr Leu Asn Gln  
                   210                  215                  220  
 Pro Ala Gly Lys Lys Ser Leu Leu Cys Lys Gly Ile Ser Leu Cys Arg  
 225                  230                  235                  240  
 Leu Ser Leu Leu Lys Leu Asn Ser Ser Pro Leu Phe Leu Ile Glu Thr  
                   245                  250                  255  
 Ala Ile Leu Ile Phe Leu Tyr Asn His Ser His  
                   260                  265

## (2) INFORMATIONS POUR LA SEQ ID NO: 854:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(834661..835452)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 854:

Tyr	Ser	Phe	Gln	Thr	Val	Ser	Arg	Asp	Gln	Ile	Asp	Tyr	Arg	Arg	Ser
1				5					10					15	
Arg	Ile	Ser	Gly	Thr	Ser	Tyr	Cys	Phe	Glu	Glu	Leu	Thr	Met	Pro	Lys
			20					25					30		
Phe	Gln	Tyr	Ala	Pro	Phe	Leu	Cys	Ala	Ser	Ile	Ile	Ile	His	Ile	Ala
		35					40					45			
Leu	Gly	Gly	Met	Leu	Phe	Phe	Ser	Ala	Pro	Gln	Lys	Lys	Lys	Pro	Arg
	50					55					60				
Leu	Ser	Pro	Phe	Lys	Glu	Arg	Ile	Val	Ala	Leu	Pro	Pro	Glu	Pro	Lys
65					70					75					80
Ile	Thr	Thr	Thr	Leu	Gln	Thr	Pro	Ser	Pro	Gln	Pro	Ile	Arg	Lys	Pro
				85					90					95	
Val	Lys	Asn	Ala	Pro	Ala	Pro	Glu	Lys	Lys	Ala	Ala	Lys	Pro	Pro	Ala
			100					105					110		
Ile	Ser	Asn	Pro	Gln	Lys	Ser	Pro	Gln	Lys	Pro	Asn	Lys	Ala	Ser	Pro
		115					120					125			
Thr	Pro	Arg	Asn	Glu	Thr	Leu	Glu	Lys	Lys	Gln	Ala	Thr	Leu	Lys	Lys
	130					135					140				
Leu	Ala	Gln	Leu	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ala	Glu	Thr	Gln	Glu
145					150					155					160
Ser	His	Ile	Ala	Gln	Phe	Ser	Trp	Pro	Ala	Gln	Ala	Gln	Val	Leu	Thr
			165						170					175	
Glu	Asn	Thr	Ser	Tyr	Gln	Gln	Asp	Ala	Phe	Cys	Ala	Leu	Phe	Gln	Gln
			180					185					190		
Tyr	Val	Ser	Leu	Pro	Phe	Pro	Gly	Glu	Val	Arg	Leu	Lys	Leu	Glu	Phe
		195					200					205			
Ser	Arg	Glu	Gly	Ala	Leu	Leu	His	Cys	Ser	Ile	Leu	Ser	Thr	Ile	Ser
	210					215					220				
His	Ala	Asp	Lys	Gln	His	Ile	Leu	Asn	Gln	Ile	Gln	Lys	Ile	Pro	Phe
225					230					235					240
Gln	Ser	Phe	Phe	Ser	Ala	Tyr	Lys	Thr	Ser	Lys	Asn	Ile	Val	Phe	His
			245						250					255	
Ile	Arg	Leu	Gln	Gly	Asn	Ser	Ala								
				260											

## (2) INFORMATIONS POUR LA SEQ ID NO: 855:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: complement(835371..835778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 855:

```

Leu Met Lys Arg Phe Val Tyr Glu Asp Leu Glu Glu Asp Pro Ser Val
1          5          10          15
Asn Leu Thr Pro Leu Ile Asp Ile Val Phe Val Ile Leu Met Ala Phe
          20          25          30
Met Ile Ala Met Pro Leu Ile Lys Ile Asp Arg Ile Ser Leu Ala Thr
          35          40          45
Gly Ser Ser Ser His Gln Ala Phe Lys Lys Gln Glu Ser Gln Gln Ala
          50          55          60
Glu Ile Lys Val Phe Arg Asn His Thr Ile Thr Leu Asn Asp Leu Pro
65          70          75          80
Val Ser Leu Gln Glu Leu Arg Ser Gln Leu Thr Val Ile His Ala Gln
          85          90          95
His Pro Asn Ile Val Pro Leu Leu Leu Gln Asp Gly Asp Thr Ala Phe
          100          105          110
Lys Leu Tyr Gln Glu Ile Lys Ser Thr Ile Glu Glu Ala Gly Phe Gln
          115          120          125
Glu Leu His Ile Ala Leu Lys Asn
          130          135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 856:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(835775..836482)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 856:

```

Val Tyr Val Leu Met Phe Gln Leu Val Asn Asn Pro Ile Ile Gln Ser
1          5          10          15
Phe Gln Glu Ala Asp Leu Phe Gly Lys Val Ile Phe Phe Ser Leu Phe
          20          25          30
Ala Leu Ser Ile Cys Thr Trp Thr Val Leu His Gln Lys Leu Ser Ile
          35          40          45
Gln Lys Lys Phe Leu Lys Ser Gly Lys Ser Leu Lys Glu Phe Leu Ile
          50          55          60
Lys Asn Arg His Ser Pro Leu Ser Leu Asp Ile His Pro Glu Ser Thr
65          70          75          80
Pro Phe Thr Asp Leu Tyr Phe Thr Ile Lys Arg Gly Thr Leu Glu Leu
          85          90          95
Leu Asp Lys Asn Arg Gln Leu Ala Pro Glu Arg Thr Pro Leu Leu Ser
          100          105          110
Val Glu Asp Ile Gln Ser Leu Glu Thr Leu Phe Asn Ala Val Met Pro
          115          120          125
Lys Tyr Arg Ala Leu Leu Asn Lys Asn Asn Phe Ile Pro Ala Thr Thr
          130          135          140
Ile Ser Leu Ala Pro Phe Leu Gly Leu Leu Gly Thr Val Trp Gly Ile

```

```

145          150          155          160
Leu Leu Ala Phe Ala His Ile Ser Thr Gly Gln Ala Asn Gly Thr Ile
          165          170          175
Met Met Glu Gly Leu Ala Thr Ala Leu Gly Thr Thr Ile Val Gly Leu
          180          185          190
Phe Val Ala Ile Pro Ser Leu Val Gly Phe Asn Tyr Leu Arg Ala His
          195          200          205
Ala Phe Gln Val Ser Leu Glu Ile Glu Gln Thr Ala Phe Leu Leu Leu
          210          215          220
Asn Ser Ile Glu Val Lys Tyr Arg Gln Thr Ser Leu
225          230          235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 857:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 221 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 836602..837264

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 857:

```

Thr Gly Glu Ser Val Val Phe Met Ile Arg Gln Trp Tyr Gly Phe Phe
1          5          10          15
Leu Cys Leu Leu Phe Ser Tyr Thr Ser Cys Phe Gly Val Glu Glu Asn
          20          25          30
Ser Gly Arg Ala Thr Pro Thr Val Glu Leu Val Ser Glu Ser Glu Gln
          35          40          45
Ala Val Glu Gly Glu Val Leu Arg Ile Gly Val Leu Ile Ala Ile Pro
50          55          60
Glu Gly Glu His Ile Tyr Trp Lys Asn Pro Gly Lys Leu Gly Met Pro
65          70          75          80
Leu Arg Ile Ser Trp Asp Leu Pro Ser Gly Cys Arg Leu Leu Glu Glu
          85          90          95
His Trp Pro Thr Pro Glu Ile Phe Glu Glu Asp Gly Val Val Tyr Phe
100          105          110
Gly Tyr Lys His Ser Thr Met Val Ala Asp Ile Arg Val Ser Lys
115          120          125
Glu Ile Glu Thr Arg Pro Leu Glu Ile Lys Ala Gln Val Glu Trp Leu
130          135          140
Ser Cys Gly Ala Ser Cys Leu Pro Gly Ser Ser Ser Arg Val Leu Val
145          150          155          160
Ile Pro Ile Asp Gln Gly Pro Leu Ile Pro Asn Ser Lys Glu Thr Phe
          165          170          175
Thr Phe Ser Arg Ala Leu Ala Ala Gln Pro Arg Pro Leu Asp Ala Ala
180          185          190
Ile Lys Ile Ser Tyr Gln Pro Asp Gly Leu Asp Val Leu Val Pro Ala
195          200          205
Gly Glu Ser Gly Ser Gly Asn Pro Gly Met Val His Cys
210          215          220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 858:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 497 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 837209..838699

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 858:

Met	Phe	Leu	Cys	Gln	Gln	Gly	Lys	Ala	Asp	Arg	Ala	Thr	Gln	Ala	Trp	1	5	10	15
Phe	Ile	Ala	Glu	Asn	Thr	Arg	Asp	Phe	Ala	Tyr	Ala	Gln	Glu	Val	Pro	20	25	30	
Leu	Glu	Gln	Ala	Thr	Thr	Tyr	Ile	Trp	Lys	Leu	Lys	His	Pro	Glu	Gly	35	40	45	
Asn	Met	Pro	Lys	Gly	Val	Gly	Leu	Ser	Arg	Ile	Leu	Ile	Phe	Lys	Asp	50	55	60	
Asp	Ala	Gly	Lys	Val	Val	Ala	Ser	Tyr	Gln	Val	Glu	Xaa	Asn	Gln	Val	65	70	75	80
Glu	Gln	Leu	Ser	Ala	Leu	Ser	Trp	Gly	Phe	Leu	Ser	Ile	Leu	Leu	Met	85	90	95	
Ala	Phe	Ile	Gly	Gly	Ile	Leu	Leu	Asn	Ile	Met	Pro	Cys	Val	Leu	Pro	100	105	110	
Leu	Ile	Thr	Leu	Lys	Val	Phe	Ser	Leu	Ile	Lys	Ser	Ala	Ala	Asp	His	115	120	125	
His	Ser	Ser	Ser	Val	Ile	Gly	Gly	Ile	Trp	Phe	Thr	Leu	Gly	Ala	Ile	130	135	140	
Val	Ser	Phe	Trp	Gly	Leu	Ala	Phe	Cys	Ala	Phe	Leu	Leu	Lys	Val	Leu	145	150	155	160
Gly	Gln	Asn	Ile	Gly	Trp	Gly	Phe	Gln	Leu	Gln	Glu	Pro	Met	Phe	Val	165	170	175	
Ala	Val	Leu	Ile	Ile	Val	Phe	Phe	Leu	Phe	Ala	Leu	Ser	Ser	Leu	Gly	180	185	190	
Val	Phe	Glu	Met	Gly	Met	Ile	Cys	Leu	Ser	Leu	Gly	Glu	Lys	Leu	Gln	195	200	205	
Glu	Glu	Gly	Gly	Ala	Ser	Val	Arg	Lys	Asn	Gln	Ile	Trp	Gly	Ala	Phe	210	215	220	
Phe	Asn	Gly	Met	Leu	Thr	Thr	Leu	Val	Thr	Thr	Pro	Cys	Thr	Gly	Pro	225	230	235	240
Phe	Leu	Gly	Ser	Val	Phe	Gly	Leu	Val	Met	Ala	Val	Ser	Phe	Val	Lys	245	250	255	
Gln	Leu	Ala	Ile	Phe	Thr	Ala	Ile	Gly	Leu	Gly	Met	Ala	Ser	Pro	Tyr	260	265	270	
Leu	Leu	Phe	Ala	Ser	Phe	Pro	Lys	Met	Leu	Ala	Ile	Leu	Pro	Lys	Pro	275	280	285	
Gly	Pro	Trp	Met	Ser	Thr	Phe	Lys	Gln	Leu	Thr	Gly	Phe	Met	Leu	Leu	290	295	300	
Ala	Thr	Ala	Thr	Trp	Leu	Ile	Trp	Ile	Phe	Gly	Val	Glu	Thr	Ser	Ala	305	310	315	320
Thr	Ala	Val	Thr	Ile	Leu	Leu	Val	Gly	Leu	Trp	Leu	Ala	Ala	Val	Gly	325	330	335	
Ala	Trp	Ile	Leu	Gly	Arg	Trp	Gly	Thr	Leu	Val	Ser	Pro	Arg	Asn	Gln	340	345	350	
Arg	Leu	Leu	Ala	Ser	Val	Val	Phe	Ile	Phe	Cys	Ile	Leu	Ser	Ser	Leu	355	360	365	
Val	Ile	Thr	Ser	Ile	Gly	Val	Arg	Tyr	Phe	Asp	Glu	Asn	Val	Pro	Pro				

370		375		380
Ala His Ser Phe Asp Trp	Gln Ser Phe Ser Pro	Glu Lys Leu Ala Asp		
385	390	395		400
Leu Arg Glu Lys Gly Ile	Pro Val Phe Val Asn	Phe Thr Ala Lys Trp		
	405	410		415
Cys Leu Thr Cys Gln Leu	Asn Lys Pro Leu Leu	His Ala Asn Met Gln		
	420	425		430
Ala Phe Ala Ala Lys Gly	Val Val Thr Leu Glu	Ala Asp Trp Thr Lys		
	435	440		445
Lys Asp Pro Lys Ile Thr	Glu Glu Leu Ala Arg	Leu Gly Arg Ala Ser		
	450	455		460
Val Pro Ser Tyr Val Tyr	Tyr Pro Ala Gly Asn	Lys Ala Pro Leu Ile		
465	470	475		480
Leu Pro Glu Arg Leu Ser	Gln Ser Ala Leu Glu	Glu Met Val Phe Ser		
	485	490		495
Gln				

(2) INFORMATIONS POUR LA SEQ ID NO: 859:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 272 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 838760..839575

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 859:

Leu Arg Lys Ile Asp Tyr Glu Gly Ser Met Glu Ile Val Asp Ala His	
1	5 10 15
Val His Leu Ser Ser Glu Glu Phe Ile Glu Asp Phe Gly Asp Val Val	
	20 25 30
Leu Arg Gly Lys Thr Ala Gly Val Thr Arg Val Val Asn Val Thr Thr	
	35 40 45
Thr Lys Ala Glu Leu Leu Arg Ser Phe Ala Tyr Ala Glu Ala Tyr Pro	
	50 55 60
Asp Trp Met Phe Tyr His Val Ala Gly Thr Pro Pro Gln Asp Ala Gln	
65	70 75 80
Asp Asp Ile Glu Glu Asp Phe Gln Glu Phe Cys Arg Ala Ala Glu Asp	
	85 90 95
Gly Lys Leu Ala Ala Ile Gly Glu Val Gly Leu Asp Tyr Leu Phe Ala	
	100 105 110
Val Gln Ala Ser Glu Gln Glu Arg Gln Lys Glu Val Leu Cys Arg Tyr	
	115 120 125
Leu Gln Leu Ala Leu Gln His Glu Leu Pro Leu Val Val His Cys Arg	
	130 135 140
Gly Ala Phe Glu Asp Phe Phe His Ile Leu Asp His Val Tyr Arg Val	
145	150 155 160
Asp Gln Arg Ala Lys Pro Gly Met Leu His Cys Phe Thr Gly Thr Tyr	
	165 170 175
Glu Glu Ala Thr Glu Leu Leu Ala Arg Asp Trp Tyr Ile Ser Ile Ser	
	180 185 190
Gly Ile Val Thr Phe Lys Asn Ala Lys Ser Leu Gln Asp Leu Val Glu	
	195 200 205

```

Lys Ile Pro Leu Glu Arg Leu Leu Val Glu Thr Asp Ala Pro Tyr Leu
  210                      215                      220
Ala Pro Thr Pro Leu Arg Gly Lys Arg Asn Glu Pro Ala Asn Ile Val
225                      230                      235                      240
His Thr Leu Ala Arg Ile Ala Glu Ile Lys Gly Ile Ser Val Tyr Glu
                      245                      250                      255
Leu Gln Asp Ala Val Ser Thr Asn Val Gln Arg Trp Leu Arg Gly Ser
                      260                      265                      270

```

(2) INFORMATIONS POUR LA SEQ ID NO: 860:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 839942..840583

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 860:

```

Leu Phe Arg Leu Val Phe Ile Pro Ser Ser Asp Leu Ala Ile Phe Phe
 1                      5                      10                      15
Glu Gly Glu Arg Ile Phe Ser Leu Gln Met Glu Glu His Leu Arg Tyr
                      20                      25                      30
Gly Arg Asn Leu Ala Tyr Thr Leu Gln Arg Met Thr Ala Trp Ile Leu
                      35                      40                      45
Leu Ala Gly Leu Ala Phe His Val Ile Gln Phe Arg Phe Val Leu Tyr
 50                      55                      60
Pro Ile Gln Val Thr Ile Gln Gly Lys Thr Phe Tyr Ala Val Ser Phe
65                      70                      75                      80
Asp Ala Ala Arg Tyr Pro Ser Val Val Gln Gly Thr Thr Gly Phe Phe
                      85                      90                      95
Ile Met Asn Val Pro Phe Ala Glu Gly Gly Pro Gln Ile Thr Glu Gln
                      100                      105                      110
Phe Leu Gln Glu Lys Asp Arg Ala Leu Phe Ala Ser His Lys Ser Tyr
                      115                      120                      125
Ile Phe Thr Pro Glu Ala Arg Lys Ala Phe Leu Tyr Ala Val Arg Asn
130                      135                      140
Ala Leu Gly Ser Leu Trp Met Ala Ile Phe Tyr Thr Leu Phe Val Ile
145                      150                      155                      160
Ala Ala Val Phe His Gly Phe Asn Gly Val Trp Thr Phe Val Ser Arg
                      165                      170                      175
Trp Gly Ile Ile Ile Ser Ser Arg Tyr Leu Arg Leu Cys Gln Ile Leu
                      180                      185                      190
Cys Tyr Val Gly Met Cys Val Val Met Ala Met Gly Ile Ser Val Ile
                      195                      200                      205
Trp Asn Met Tyr Leu Leu
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 861:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 861:

Trp 1	Ser	Met	Asp	Val 5	Cys	Leu	Ala	Met	Gly 10	Asn	His	Tyr	Leu	Phe 15	Pro
Leu	Ser	Pro	Ile 20	Met	Ser	Asp	Leu 25	Met	Leu	Arg	Arg	Asp	Val 30	Cys	Cys
Asp	Gly	Tyr 35	Gly	Tyr	Gln	Arg	Asn 40	Leu	Glu	Tyr	Val	Phe 45	Val	Met	Met
Asn	Gln 50	Arg	Cys	Arg	Val	Ile 55	Ile	Ile	Gly	Gly	Gly 60	Leu	Ala	Gly	Leu
Ser 65	Ala	Ala	Met	Gln	Leu 70	Ala	Asp	Arg	Gly	Ile 75	Leu	Val	Glu	Leu	Phe 80
Ser	Leu	Thr	Lys 85	Val	Lys	Arg	Ser	His	Ser 90	Val	Cys	Ala	Gln	Gly	Gly
Ile	Asn	Ala	Ala 100	Leu	Asn	Leu	Lys	Gly 105	Glu	Asn	Asp	Ser	Pro 110	Tyr	Ile
His	Ala	Tyr 115	Asp	Thr	Ile	Lys	Gly 120	Gly	Asp	Phe	Leu	Ala 125	Asp	Gln	Pro
Pro	Val 130	Leu	Glu	Met	Cys	Leu 135	Thr	Ala	Ser	Arg	Ile 140	Ile	His	Met	Leu
Asp 145	Arg	Phe	Gly	Cys	Pro 150	Phe	Asn	Arg	Asp	Ala 155	Asp	Gly	Asn	Leu	Asp 160
Val	Arg	Arg	Phe 165	Gly	Gly	Thr	Leu	Tyr	His 170	Arg	Thr	Val	Phe	Cys	Gly
Ala	Ser	Thr 180	Gly	Gln	Gln	Leu	Met 185	Tyr	Thr	Met	Asp	Glu 190	Gln	Val	Arg
Arg	Arg	Glu 195	Trp	Gln	Gly	Lys	Ile 200	Ile	Lys	Arg	Glu	Asn 205	His	Glu	Phe
Val	Arg 210	Leu	Ile	Thr	Asn 215	Thr	Glu	Gly	Arg	Ala 220	Cys	Gly	Val	Val	Val
Met 225	Asn	Leu	Phe	Asn 230	His	Arg	Leu	Glu	Val	Ile 235	Gln	Gly	Asp	Ala	Val 240
Ile	Ile	Ala	Thr 245	Gly	Gly	Leu	Gly	Val	Ile 250	Phe	Gln	Met	Ser	Thr	Asn
Ser	Thr	Ile 260	Cys	Thr	Gly	Ala	Ala 265	Asn	Gly	Arg	Leu	Phe 270	Met	Gln	Gly
Met	His 275	Tyr	Ala	Asn	Pro	Glu	Phe 280	Ile	Gln	Ile	His	Pro 285	Thr	Ala	Ile
Pro	Gly 290	Leu	Asp	Lys	Leu 295	Arg	Leu	Ile	Ser	Glu	Ser 300	Val	Arg	Gly	Glu
Gly 305	Gly	Arg	Val	Trp 310	Val	Pro	Arg	Cys	Ser	Ser 315	Lys	Thr	Ile	Ile	Phe 320
Pro	Asp	Gly	Ser 325	Arg	Arg	Pro	Cys	Gly	Glu 330	Thr	Gly	Lys	Pro	Trp	Tyr
Phe	Leu	Glu 340	Glu	Met	Tyr	Pro	Ala 345	Tyr	Gly	Asn	Leu	Val 350	Ser	Arg	Asp
Val	Gly 355	Ala	Arg	Ala	Ile	Leu	Gln 360	Val	Cys	Glu	Ala	Gly 365	Leu	Gly	Ile
Asp	Gly 370	Arg	His	Glu	Val 375	Phe	Leu	Asp	Val	Thr	His 380	Leu	Pro	Val	Glu
Thr 385	Leu	Asn	Lys	Leu 390	Glu	Ala	Val	Leu	Asp	Ile 395	Tyr	His	Lys	Phe	Thr 400

Gly Glu Asp Pro Lys Lys Val Pro Met Arg Ile Phe Leu Arg Cys Thr  
                                   405                                  410                                  415  
 Ile Leu Trp Glu Ala Pro Gly  
                                   420

(2) INFORMATIONS POUR LA SEQ ID NO: 862:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 841659..842459

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 862:

Lys Ser Pro Tyr Ala His Phe Ser Ala Val His Tyr Ser Met Gly Gly  
 1                                  5                                  10                                  15  
 Ala Trp Val Asp Trp Pro Ala Ser Asp Asp Arg Asp Arg Asp Ser Arg  
                                   20                                  25                                  30  
 Tyr Arg His Met Thr Asn Ile Pro Gly Cys Phe Asn Cys Gly Glu Ser  
                                   35                                  40                                  45  
 Asp Phe Gln Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu  
                                   50                                  55                                  60  
 Ala Cys Leu Tyr Ala Gly Leu Val Ala Gly Asp Glu Ala Ala Arg Phe  
 65                                  70                                  75                                  80  
 Val Glu Ser Phe Gly Ser Cys Ile Tyr Ser Gln Gln Asp Leu Asn Gln  
                                   85                                  90                                  95  
 Ala Leu Gln Gln Glu Gln Glu Ile Ser Arg Glu Ile Leu Ser Arg Gln  
                                   100                                  105                                  110  
 Gly Gly Glu Asn Ala Phe Ala Leu His Glu Glu Ile Ala Arg Val Met  
                                   115                                  120                                  125  
 Val Ser Asn Val Thr Val Lys Arg Glu Asn Lys Ala Leu Glu Glu Thr  
                                   130                                  135                                  140  
 Leu His Lys Leu Lys Glu Phe Arg Glu Arg Ile Lys Lys Val Ser Val  
 145                                  150                                  155                                  160  
 His Asp Ser Ser Arg Phe Ala Asn Lys Thr Phe His Phe Val Arg Gln  
                                   165                                  170                                  175  
 Met Glu Pro Met Leu Glu Leu Ala Leu Ala Ile Thr Thr Gly Ala Leu  
                                   180                                  185                                  190  
 Leu Arg Asn Glu Phe Arg Gly Ser His Tyr Lys Pro Glu Phe Ser Lys  
                                   195                                  200                                  205  
 Arg Asp Asp Val Asn Trp Leu Lys Thr Thr Ile Ala Thr Tyr Ser Val  
                                   210                                  215                                  220  
 Asp Glu Pro Glu Ile Ser Tyr Lys Lys Val Asp Thr Arg His Val Asn  
 225                                  230                                  235                                  240  
 Pro Glu Leu Arg Asp Tyr Thr Arg Gln Gly Ala Lys Asp Val Val Leu  
                                   245                                  250                                  255  
 Glu Asn Ile Pro Ala Asn Ile His Phe Pro Ile  
                                   260                                  265

(2) INFORMATIONS POUR LA SEQ ID NO: 863:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 842523..843068

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 863:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 864:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 155 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(843031..843495)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 864:

Leu	Ala	Asn	Phe	Leu	Ala	Ile	Ala	Arg	Phe	Phe	Phe	Ala	Lys	Ala	Thr
1				5					10					15	
Leu	Leu	Tyr	Val	Val	Lys	Ser	Cys	Arg	Phe	Ser	Pro	His	Lys	Thr	Ser
			20					25					30		
Ser	Ser	Lys	Glu	Ala	Phe	Ser	Leu	Leu	Ala	Lys	Glu	Ser	Asn	Thr	Glu
		35					40					45			
Thr	Ser	Lys	Arg	Asp	Met	Thr	Lys	Lys	Gly	Val	Phe	Ser	Leu	Pro	Leu
	50					55					60				



Pro	Trp	Asn	Lys	Ile	Ala	Met	Gln	Ser	Ser	Lys	Leu	Lys	Ser	Pro	His
65					70					75					80
Leu	Gln	Lys	Thr	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Phe	Leu	Asn	Asn	Glu
				85					90					95	
Glu	Asn	Asn	Ala	Arg	Lys	Glu	Lys	Arg	Glu	Thr	Ser	His	Pro	Ile	Ala
			100					105					110		
Glu	Met	Leu	Ser	Val	Lys	Gly	Asn	Phe	Leu	Gly	His	Thr	Arg	Thr	Gln
		115					120					125			
Leu	Trp	Ala	Cys	Pro	Asp	Pro	Ser	Ile	Pro	Arg	Val	Pro	Ile	Asn	Ala
	130					135					140				
Arg	Asn	Arg	Leu	Ser	Arg	Arg	Phe	Ser	Pro	Gly					
145					150					155					

(2) INFORMATIONS POUR LA SEQ ID NO: 865:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 986 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 843239..846196

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 865:

Gln	Arg	Val	Phe	Trp	Arg	Trp	Gly	Leu	Leu	Ser	Phe	Glu	Asp	Cys	Ile
1				5					10					15	
Ala	Ile	Leu	Phe	His	Gly	Lys	Gly	Arg	Glu	Lys	Thr	Pro	Phe	Phe	Val
			20					25					30		
Met	Ser	Arg	Leu	Asp	Val	Ser	Val	Phe	Asp	Ser	Leu	Ala	Asn	Lys	Glu
		35					40					45			
Lys	Ala	Ser	Leu	Leu	Glu	Glu	Val	Leu	Cys	Gly	Glu	Asn	Leu	Gln	Asp
	50					55					60				
Phe	Thr	Thr	Tyr	Ser	Lys	Val	Ala	Leu	Ala	Lys	Lys	Asn	Leu	Ala	Ile
65					70					75					80
Ala	Arg	Lys	Leu	Ala	Ser	Tyr	Ile	Leu	Asn	Glu	Glu	Gly	Asp	Leu	Glu
				85					90					95	
Leu	Ser	Arg	Val	Val	Glu	Ser	Ile	Gln	Leu	Leu	Thr	Lys	Cys	Leu	Tyr
			100					105					110		
Pro	Leu	Gly	Pro	Tyr	Arg	Gln	Gly	Glu	Gly	Pro	Ile	Arg	Glu	His	Val
		115					120					125			
Leu	Lys	Met	Leu	Glu	Phe	Leu	Arg	Asp	Asp	Gln	Glu	Ile	Lys	Asn	Arg
	130						135				140				
Phe	Arg	Arg	Phe	Phe	Val	Pro	Ser	Tyr	Ala	Arg	Val	Gln	Asp	Leu	Ile
145					150					155					160
Arg	Asn	Thr	Leu	Ala	Leu	Pro	Ala	Ser	Glu	Thr	Val	Thr	Val	Arg	His
				165					170					175	
Val	Arg	Glu	Ala	Ala	Leu	Val	Ala	Leu	Phe	Thr	Tyr	Leu	Arg	Gln	Asp
			180					185					190		
Val	Gly	Ser	Cys	Phe	Ala	Thr	Ala	Leu	Ala	Ile	Leu	Ile	His	Arg	Glu
		195					200					205			
Tyr	Pro	Leu	Leu	Phe	Ile	Arg	Asp	Leu	Glu	Asp	Leu	Leu	Ser	Ser	Gly
	210					215					220				
Lys	Ile	Ser	Arg	Ile	Val	Gly	Asp	Arg	Glu	Ile	Ser	Val	Pro	Ile	Asn
	225				230					235					240
Leu	Leu	Pro	Cys	Val	Gly	Asp	Leu	Phe	Lys	Pro	Ile	Cys	Val	Met	Asp

					245										255
Leu	Tyr	Pro	Asn	Pro	Val	Ala	Thr	Leu	Ala	Ala	Ser	Ser	Asp	Leu	Gln
			260					265					270		
Ala	Ala	Phe	Val	Ala	Ser	Gly	Ile	Phe	Pro	Thr	Thr	Gly	Asp	Ile	Ala
		275					280					285			
Gly	Glu	Val	Gln	Thr	Leu	Leu	Ala	Asn	Glu	Phe	Ile	Tyr	Gln	Lys	Val
	290					295					300				
Gln	Asp	Ile	His	Gly	Lys	Ile	Thr	Ala	His	Asp	Val	Ile	Gln	Asp	Ser
305					310					315					320
Leu	Leu	His	His	Tyr	Gln	Leu	Ser	Leu	Ser	Thr	Val	Gln	Ala	Ser	Val
				325					330					335	
Leu	Gln	Glu	Gly	Phe	Arg	Lys	Glu	Arg	Gly	Asp	Gly	Thr	Val	Leu	Leu
			340					345					350		
Ser	Thr	Asn	Ser	Gln	Arg	Val	Leu	Ser	Tyr	Leu	Glu	Ser	Tyr	Glu	Gln
		355					360					365			
Ala	Lys	Leu	Gly	Phe	Ile	Arg	Asp	Thr	Gln	Asn	Val	Leu	Leu	Lys	Ser
	370					375					380				
Trp	Glu	Tyr	Thr	Leu	Ala	Thr	Leu	Ala	Asp	Ala	Ser	Gln	Thr	Thr	Thr
385					390					395					400
Thr	Lys	His	Leu	Gln	Ile	Ala	Leu	Gly	Trp	Thr	Ser	Asp	Asp	Glu	Asp
				405					410					415	
Gly	Leu	Arg	Glu	Ile	Ile	Arg	Arg	Phe	Leu	Ala	Glu	Glu	Val	Ala	Thr
			420					425					430		
Thr	Gln	Ala	Phe	Ala	Gly	Gln	Cys	Glu	Glu	Thr	Tyr	Gln	Glu	Ala	Lys
		435					440					445			
Ala	Gln	Leu	Glu	Tyr	Val	Glu	Ser	Arg	Met	Arg	Asn	Pro	Ile	Asn	Lys
	450					455					460				
Gln	Asp	Ser	Gln	Ile	Leu	Ala	Met	Asp	His	Val	Arg	Phe	Arg	Gln	Glu
465					470					475					480
Leu	Asn	Gln	Ala	Leu	Gln	Asp	Trp	Asn	Ala	Ala	Gln	Glu	Lys	Leu	Lys
				485					490					495	
Lys	Met	Ile	Met	Leu	Pro	Asp	Phe	Leu	Leu	Ser	Phe	Tyr	Ser	Arg	Glu
			500					505					510		
Ile	Pro	Asn	Tyr	Phe	Arg	Ser	Val	Tyr	Asp	Ala	Phe	Ile	Arg	Glu	Phe
		515					520					525			
Ser	Gly	Asn	Tyr	Gln	Asp	Val	Pro	Ala	Gly	Phe	Arg	Ile	Leu	Phe	Thr
	530					535					540				
Tyr	Gly	Arg	Ser	His	Pro	Asn	Thr	Trp	Glu	Pro	Ile	Tyr	Ser	Ile	Glu
545					550					555					560
Glu	Phe	Ile	His	Ala	Leu	Thr	Glu	Phe	Phe	Thr	Ser	Ile	Glu	Gly	Asp
				565					570					575	
Leu	Leu	Ala	Lys	His	Asn	Val	Ser	Gly	Leu	Glu	Lys	Glu	Thr	Ser	Ile
			580					585					590		
Leu	Leu	His	Arg	Ile	Val	Ser	Ala	Leu	His	Glu	Pro	Arg	Phe	Gln	Glu
		595													

Trp	Thr	Asn	Asp	Trp	Tyr	Ser	Tyr	Thr	Trp	Leu	Arg	Asp	Val	Trp	Leu
				725					730					735	
Ser	Lys	His	Gln	Asp	Phe	Leu	Lys	Arg	Thr	Leu	Phe	Asp	Lys	Ser	Ala
			740					745					750		
Ile	Tyr	Ala	Phe	Ile	Thr	Arg	Phe	Cys	Thr	Arg	Tyr	Tyr	Leu	Gln	Glu
		755					760					765			
Leu	Thr	Gln	Asp	Leu	Leu	Tyr	Phe	Cys	Asp	Asp	Leu	Ser	Leu	Ser	Ile
	770					775					780				
Pro	Glu	Phe	Tyr	Glu	Lys	Ser	Ser	Arg	Phe	Phe	Gln	Ser	Thr	Val	His
785					790					795					800
Asp	Glu	Lys	Val	Val	Ala	Thr	Leu	Gln	Lys	Tyr	Leu	Ala	Ser	Gln	Phe
				805					810					815	
Val	His	Glu	Ala	Pro	Tyr	Val	Ser	Glu	Gln	Gln	Leu	Pro	Gln	Ile	Ile
			820					825					830		
Ser	Asp	Leu	Ser	Ser	Tyr	Leu	Gly	Ile	Ser	Ser	Arg	Ile	Ser	Tyr	Asp
		835					840					845			
Gln	Leu	Ala	Thr	Leu	Leu	Glu	Glu	Asn	Val	Gly	Lys	His	Ser	Leu	Leu
	850					855					860				
Ser	Ser	Ser	Asp	Leu	Arg	His	Leu	Tyr	Lys	Gly	Leu	Leu	Met	Ala	Gly
865					870					875					880
Tyr	Gln	Arg	Val	Tyr	His	Glu	Glu	Asp	Leu	Ser	Met	Arg	Leu	Ile	Ala
				885					890					895	
Ala	Met	Arg	His	Tyr	Gly	Leu	Ala	Tyr	Pro	Ala	Pro	Leu	Leu	Phe	Gly
			900					905					910		
Asp	Thr	Asn	Trp	Ala	Tyr	Arg	Tyr	Phe	Gly	Phe	Ile	Xaa	His	Pro	Gly
		915					920					925			
Thr	Gln	Glu	Met	Asp	Leu	Trp	Glu	Phe	Asn	Tyr	Leu	Gly	Leu	Val	Gly
	930					935					940				
Arg	Pro	Ser	Glu	Asn	Lys	Glu	Arg	Trp	Phe	Ala	Val	Arg	Asp	Pro	Trp
945					950					955					960
Ala	Leu	Tyr	Pro	Glu	Ser	His	Arg	Leu	Arg	Asn	Gly	Pro	Ser	Thr	Arg
				965					970					975	
Leu	Ser	Lys	Trp	Ile	Ala	Glu	Arg	Phe	Phe						
			980					985							

(2) INFORMATIONS POUR LA SEQ ID NO: 866:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 112 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui -

(viii) POSITION DANS LE GENOME: complement(843802..844137)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 866:

Ile	Asn	Ser	Leu	Ala	Ser	Ser	Val	Cys	Thr	Ser	Pro	Ala	Ile	Ser	Pro
1				5					10				15		
Val	Val	Gly	Asn	Met	Pro	Glu	Ala	Thr	Asn	Ala	Ala	Cys	Lys	Ser	Asp
			20					25				30			
Glu	Ala	Ala	Arg	Val	Ala	Thr	Gly	Leu	Gly	Tyr	Lys	Ser	Ile	Thr	Gln
		35					40				45				
Ile	Gly	Leu	Asn	Lys	Ser	Pro	Thr	His	Gly	Arg	Arg	Leu	Ile	Gly	Thr
	50					55				60					
Glu	Ile	Ser	Arg	Ser	Pro	Thr	Ile	Arg	Asp	Ile	Phe	Pro	Glu	Asp	Asn

65		70		75		80									
Lys	Ser	Ser	Lys	Ser	Arg	Ile	Asn	Asn	Asn	Gly	Tyr	Ser	Arg	Trp	Ile
			85					90						95	
Arg	Ile	Ala	Asn	Ala	Val	Ala	Lys	Gln	Asp	Pro	Thr	Ser	Cys	Arg	Lys
			100					105						110	

(2) INFORMATIONS POUR LA SEQ ID NO: 867:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 609 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(846217..848043)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 867:

Asn	Ile	Cys	Phe	Arg	Cys	Gly	Met	Arg	Gln	Thr	Phe	Thr	Lys	Arg	Ile
1			5						10					15	
Leu	Leu	Phe	Leu	Phe	Leu	Val	Ile	Pro	Ala	Pro	Leu	Leu	Leu	Asn	Leu
			20					25					30		
Val	Val	Leu	Ser	Phe	Phe	Ser	Phe	Ala	Ala	Val	Lys	Thr	Thr	Ile	Ile
		35					40					45			
Gln	Asp	Leu	His	Thr	Arg	Thr	Met	Asn	Phe	Asn	Leu	Glu	Leu	Glu	Lys
	50					55					60				
Lys	Ile	Ala	Ile	Gln	Asn	Ile	Phe	Leu	Lys	Arg	Leu	Ala	Glu	Thr	Leu
65					70					75					80
Ala	Leu	Lys	Thr	Leu	Thr	Thr	Ser	His	Asp	Phe	Phe	Thr	Glu	Ala	Tyr
				85					90					95	
Ser	Glu	Met	Ile	Ala	Leu	Gly	Asp	Thr	Asp	Leu	Ser	Leu	Cys	Leu	Leu
			100					105					110		
Ser	Ser	Ala	Asn	Asp	Ser	Ile	Arg	Thr	Lys	Asn	Pro	Arg	Asp	Pro	Phe
		115					120					125			
Val	Arg	Tyr	Ile	Lys	Ala	His	Pro	Glu	Ile	Arg	Asp	Lys	Leu	Ile	Gln
	130					135					140				
Asn	Pro	Gly	Asn	Ala	Ser	Leu	Ile	Ser	Ile	Ser	Glu	Arg	Pro	Asp	Thr
145					150					155					160
Glu	Asp	His	Tyr	Leu	Val	Phe	Ala	Glu	Pro	Leu	Pro	Ile	Tyr	Glu	Asp
				165					170					175	
Pro	Ser	Leu	Ala	Gly	Trp	Val	Ile	Ala	Phe	Tyr	Ser	Met	Gln	Lys	Leu
			180					185					190		
Arg	Asn	Tyr	Leu	Phe	His	Asn	Lys	Gln	Ser	Tyr	Gln	Asp	Leu	Leu	Cys
		195					200					205			
Tyr	Leu	Asn	His	Lys	Gly	Glu	Leu	Leu	Phe	Ser	Asp	Ser	Ser	Pro	Phe
	210					215					220				
Gln	Asn	Gly	Ala	Phe	Ser	Leu	Ser	Met	Glu	Gly	Tyr	Pro	Ala	Leu	Ser
225					230					235					240
Ser	Glu	Lys	Ala	Ser	Tyr	Pro	Leu	Glu	Pro	Ser	Pro	Glu	Leu	Phe	Lys
				245					250					255	
Ala	Lys	Glu	Leu	Leu	Lys	Val	Ser	Asn	Thr	Arg	Glu	Asn	Phe	Leu	Ser
			260					265					270		
Leu	Phe	Ile	Ser	Leu	Ala	Ala	Tyr	Thr	Thr	Tyr	Pro	Phe	Ser	Cys	Ala
		275					280					285			
Asp	Pro	Ser	Ile	His	Leu	His	Tyr	Thr	Ser	Leu	Arg	Leu	Pro	Ile	Asn
	290						295				300				

Val	Ile	Leu	Phe	Tyr	Ile	Leu	Ala	Phe	Ser	Leu	Met	Gly	Trp	Val	Leu
305					310					315					320
Ser	Cys	Thr	Ser	Lys	Arg	Leu	Asn	Arg	Pro	Leu	Gln	Glu	Leu	Ser	Val
				325					330						335
Ser	Met	Glu	Ser	Ala	Trp	Lys	Gly	Asn	His	Asn	Val	Arg	Tyr	Glu	Pro
				340				345						350	
Gln	Pro	Tyr	Gly	Tyr	Glu	Ile	Asn	Glu	Leu	Gly	Asn	Ile	Phe	Asn	Cys
		355					360					365			
Thr	Leu	Leu	Leu	Leu	Leu	Asn	Val	Lys	Glu	Lys	Ala	Glu	Ile	Glu	Tyr
	370					375					380				
Ile	Ser	Gly	Asn	Leu	Leu	Gln	Lys	Glu	Leu	Ala	Leu	Leu	Ser	Ser	Leu
385					390					395					400
Lys	Asp	Thr	Leu	Leu	Cys	Gln	Arg	Ser	Asn	Ser	Leu	Pro	Gly	Gly	Thr
				405					410						415
Phe	Ser	Leu	His	Tyr	Leu	Gln	Gly	Glu	Gln	Gln	Thr	Gly	Tyr	Phe	Tyr
			420					425						430	
Gly	Trp	Val	Ala	Thr	Pro	Glu	Lys	Asp	Arg	Leu	Phe	Gly	Val	Ile	Gly
		435					440					445			
Ile	Ala	Gly	Asp	Ile	Gly	Leu	Pro	Ser	Tyr	Leu	Tyr	Ala	Leu	Ser	Ala
	450					455					460				
Arg	Ser	Leu	Phe	Leu	Thr	Tyr	Ala	Ser	Leu	Gly	Tyr	Ser	Leu	Pro	Ser
465					470					475					480
Ile	Cys	His	Lys	Thr	Met	Arg	Ser	Phe	Asp	Glu	Thr	Thr	Val	Gly	Asn
				485					490						495
Glu	Ala	Ser	Val	Ser	Ile	Ala	Cys	Leu	Glu	Tyr	Asp	Leu	Ser	Ser	Lys
			500					505					510		
Ser	Leu	Ser	Val	Leu	Thr	Glu	Gly	Ala	Asn	Pro	Pro	Thr	Leu	Phe	Ile
		515					520					525			
Lys	Arg	Gln	Glu	His	Leu	Leu	Thr	Met	Ser	Glu	Gln	Gln	Arg	Ile	Glu
	530					535						540			
Thr	Gly	Asp	Ile	Leu	Val	Cys	Leu	Thr	Gly	Gly	Pro	His	Ile	Ile	Gln
545					550					555					560
Tyr	Leu	Lys	Thr	Leu	Pro	Ile	Glu	Ala	Leu	Leu	Lys	Asp	Pro	Leu	Ala
				565					570						575
Pro	Leu	Asn	Ser	Lys	Asn	Phe	Ala	Glu	Met	Leu	Thr	Thr	Met	Leu	Arg
			580					585					590		
Ser	Lys	Asn	Gln	Thr	Gln	Ile	Asp	Gly	Ala	Val	Gly	Phe	Leu	Ser	Phe
		595					600					605			

Ile

(2) INFORMATIONS POUR LA SEQ ID NO: 868:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 658 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(848150..850123)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 868:

Ala	Pro	Leu	Gly	Lys	Lys	Arg	Glu	Met	Thr	Ile	Pro	Ile	His	Glu	Asn
1				5				10					15		
Lys	Tyr	Ser	Met	Ile	Ser	Phe	Thr	Arg	Thr	Ile	Gly	Phe	Arg	Leu	Trp

			20					25					30			
Leu	Ile	Cys	Val	Ala	Ala	Ile	Met	Phe	Pro	Leu	Gly	Ile	Asn	Ile	Leu	
		35					40					45				
Gln	Leu	Asn	Leu	Gln	Gln	Tyr	Lys	Lys	Thr	Leu	Ser	Ser	Ile	Thr	Ser	
	50					55					60					
Asp	Leu	Arg	Glu	Asn	Ala	Leu	Phe	Lys	Ala	His	Thr	Leu	Gln	Gln	Thr	
65					70					75					80	
Ile	Pro	Leu	Asn	Ile	Asp	Ile	Leu	Ala	Leu	Phe	Ser	Glu	Ile	Phe	Asp	
				85					90					95		
Leu	Asp	Arg	Gly	Val	Pro	Ala	Glu	Pro	Asp	Leu	Ala	Leu	Ser	Lys	Glu	
			100					105					110			
Met	Glu	Lys	Ile	Phe	His	Ser	Thr	Tyr	Lys	Glu	Ile	Ser	Leu	Val	Lys	
		115					120					125				
Lys	Glu	Ala	Asp	Gly	Asn	Phe	Arg	Val	Val	Ala	Ser	Ser	Arg	Ile	Glu	
	130					135					140					
Gln	Leu	Gly	Lys	Asn	Tyr	Asn	Gln	Glu	Ile	Phe	Leu	Ser	Asp	Ser	Gln	
145					150					155					160	
Pro	Phe	Leu	Ala	Thr	Leu	Arg	His	Ser	Gly	Ser	Asp	Ser	Gln	Val	Leu	
				165					170					175		
Ala	Val	Leu	Gln	Thr	Asn	Ile	Phe	Asp	Ile	Ser	Ser	Gln	Glu	Val	Leu	
			180					185					190			
Gly	Val	Leu	Tyr	Thr	Leu	Ser	Asp	Thr	Asn	Tyr	Leu	Leu	Asn	Gly	Leu	
	195						200					205				
Leu	Ala	Ala	Lys	Asp	Pro	Leu	Ser	Val	Lys	Thr	Ala	Ile	Leu	Ser	Lys	
	210					215					220					
Asn	Gly	Ile	Ile	Leu	Gln	Ala	Thr	Asp	Ser	Ser	Leu	Asp	Leu	Val	Ser	
225					230					235					240	
Ile	His	Lys	Thr	Val	Ser	Lys	Glu	Gln	Phe	Cys	Asp	Val	Phe	Leu	Arg	
			245						250					255		
Asp	Asp	Ile	Cys	Pro	Pro	His	Leu	Leu	Leu	Arg	Pro	Pro	Leu	Asn	Leu	
			260					265					270			
Asp	Pro	Leu	Pro	Tyr	Gly	Glu	Asn	Phe	Val	Ser	Phe	Cys	Ile	Gly	Asn	
		275					280					285				
Thr	Glu	Met	Trp	Gly	Tyr	Ile	His	Ser	Leu	Pro	Glu	Met	Asp	Phe	Arg	
	290					295					300					
Ile	Leu	Thr	Tyr	Glu	Glu	Lys	Ser	Ile	Ile	Phe	Ala	Ser	Leu	Trp	Arg	
305					310					315					320	
Arg	Thr	Leu	Leu	Tyr	Phe	Ala	Tyr	Phe	Cys	Cys	Val	Leu	Leu	Gly	Ser	
			325						330					335		
Ile	Thr	Ala	Phe	Leu	Val	Ala	Lys	Arg	Leu	Ser	Lys	Pro	Ile	Arg	Lys	
			340					345					350			
Leu	Ala	Thr	Ala	Met	Met	Glu	Thr	Arg	Arg	Asn	Gln	His	Pro	Tyr		
		355					360									

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Ser Ile Gln Glu Ala Val Gln Gln Thr Ala Ala Leu Phe Tyr Gln Gln
      500                      505                      510
Thr Ala Glu Ser Gly Met Phe Val Thr Leu Cys Ile Tyr Cys Tyr His
      515                      520                      525
Tyr Ala Thr Arg Glu Leu Glu Tyr Tyr Ser Cys Gly His Asn Pro Ala
      530                      535                      540
Cys Leu Arg Ala Pro Asn Gly Asp Ile Ser Phe Leu Ser His Pro Gly
545                      550                      555                      560
Met Ala Leu Gly Phe Leu Pro Glu Val Pro Pro His Pro Ala Tyr Thr
      565                      570                      575
Leu Val Leu Glu Glu Glu Ser Leu Leu Val Leu Tyr Thr Asp Gly Val
      580                      585                      590
Thr Glu Ala Ser Asn Lys His Gly Glu Met Phe Gly Glu Glu Arg Leu
      595                      600                      605
Lys Ala Leu Val Ala Ser Leu Thr Lys Gln Ser Ala Glu Glu Ala Ile
      610                      615                      620
Gln Ser Ile Met Phe Ser Ile Lys Ser Phe Val Lys Asp Cys Pro Gln
625                      630                      635                      640
His Asp Asp Ile Thr Leu Leu Val Leu Lys Ile Pro Lys Glu Pro Ser
      645                      650                      655
Ala Tyr

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(2) INFORMATIONS POUR LA SEQ ID NO: 869:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 472 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(850230..851645)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 869:

```

Ile Pro Arg Tyr Asp Pro Phe Leu Leu Arg Glu Ser Pro Ser Glu Pro
1      5      10      15
Ser Leu Cys Ile Ala Val Ile His Ala His Arg Arg Lys Leu Asp Lys
      20      25      30
Thr Ser Glu Leu Leu Ser Leu Thr Val Leu Asp Lys Asp Leu Val Met
      35      40      45
Phe Asp Val Val Ile Ser Asp Ile Glu Ala Arg Glu Ile Leu Asp Ser
50      55      60
Arg Gly Tyr Pro Thr Leu Cys Val Lys Val Ile Thr Asn Thr Gly Thr
65      70      75      80
Phe Gly Glu Ala Cys Val Pro Ser Gly Ala Ser Thr Gly Ile Lys Glu
      85      90      95
Ala Leu Glu Leu Arg Asp Lys Asp Pro Lys Arg Tyr Gln Gly Lys Gly
100      105      110
Val Leu Gln Ala Ile Ser Asn Val Glu Lys Val Leu Val Pro Ala Leu
115      120      125
Gln Gly Phe Ser Val Phe Asp Gln Ile Thr Ala Asp Ala Ile Met Ile
130      135      140
Asp Ala Asp Gly Thr Pro Asn Lys Glu Lys Leu Gly Ala Asn Ala Ile
145      150      155      160
Leu Gly Val Ser Leu Ala Phe Ser Lys Ser Cys Leu Gln Ile Leu Tyr

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(2) INFORMATION POUR LA SEQ ID NO: 870:

(A) LONGUEUR: 676 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(851669..853696)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 870:

Lys Ile Leu Thr Thr Ile His Cys Val Gly Gly Gly Val Leu Lys Gln  
1 5 10 15  
Gln Phe Val Leu His Ala Pro Phe Leu Pro Cys Gly Asp Gln Pro Glu  
20 25 30



Ala	Ile	Arg	Arg	Leu	Ser	Gln	Gly	Ile	Thr	Asp	Gly	Val	Pro	Ala	Gln
		35					40					45			
Val	Leu	Leu	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Thr	Phe	Thr	Met	Ala	Asn
	50					55					60				
Val	Ile	Ala	Asn	Val	Asn	Val	Pro	Thr	Leu	Val	Leu	Ala	His	Asn	Lys
65					70					75					80
Thr	Leu	Ala	Ala	Gln	Leu	Tyr	Gln	Glu	Phe	Lys	Ala	Phe	Phe	Pro	Glu
				85					90					95	
Asn	Ala	Val	Glu	Tyr	Phe	Ile	Ser	Tyr	Tyr	Asp	Tyr	Tyr	Gln	Pro	Glu
			100					105					110		
Ala	Tyr	Ile	Ala	Arg	Ser	Asp	Thr	Tyr	Ile	Glu	Lys	Ser	Leu	Leu	Ile
		115					120					125			
Asn	Asp	Glu	Ile	Asp	Lys	Leu	Arg	Leu	Ser	Ala	Thr	Arg	Ser	Ile	Leu
	130					135					140				
Glu	Arg	Arg	Asp	Thr	Leu	Ile	Val	Ser	Ser	Ile	Ser	Cys	Ile	Tyr	Gly
145					150					155					160
Ile	Gly	Ser	Pro	Asp	Asn	Tyr	Ser	Ser	Met	Ala	Leu	Thr	Leu	Glu	Val
				165					170					175	
Gly	Lys	Glu	Tyr	Pro	Arg	Ser	Gln	Leu	Ser	Ser	Gln	Leu	Val	Arg	Met
			180					185					190		
His	Tyr	Gln	Ala	Ser	Ser	Thr	Pro	Gln	Arg	Ser	Ala	Phe	Arg	Glu	Arg
		195					200					205			
Gly	Ser	Val	Ile	Asp	Ile	Phe	Leu	Ala	Tyr	Glu	Ser	Asp	Leu	Ala	Val
	210					215					220				
Arg	Leu	Glu	Phe	Met	Asn	Asp	Thr	Leu	Ile	Ser	Ile	Glu	Tyr	Val	Asp
225					230					235					240
Pro	Leu	Thr	Met	Ile	Pro	Ser	His	Thr	Thr	Ser	Ser	Ile	Thr	Leu	Tyr
				245					250					255	
Pro	Gly	Ser	His	Tyr	Val	Thr	Pro	Glu	Ala	Val	Arg	Glu	Gln	Ala	Ile
			260					265					270		
Arg	Thr	Ile	Arg	Glu	Glu	Leu	Glu	Gln	Arg	Met	Leu	Phe	Phe	Glu	Gly
		275					280					285			
Arg	Pro	Val	Glu	Gln	Glu	Arg	Leu	Phe	Gln	Arg	Thr	Thr	His	Asp	Ile
	290					295					300				
Glu	Met	Ile	Lys	Glu	Ile	Gly	Phe	Cys	Lys	Gly	Ile	Glu	Asn	Tyr	Ser
305					310					315					320
Arg	His	Phe	Thr	Gly	Ala	Ala	Pro	Gly	Glu	Pro	Pro	Thr	Cys	Leu	Leu
				325					330					335	
Asp	Tyr	Phe	Pro	Asp	Asp	Phe	Leu	Leu	Ile	Ile	Asp	Glu	Ser	His	Gln
			340					345					350		
Thr	Leu	Pro	Gln	Leu	Arg	Ala	Met	Tyr	Arg	Gly	Asp	Gln	Ser	Arg	Lys
		355					360					365			
Gln	Ser	Leu	Val	Glu	Tyr	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Phe	Asp	Asn
	370					375					380				
Arg	Pro	Leu	Thr	Tyr	Glu	Glu	Ala	Arg	Arg	Tyr	Phe	His	Arg	Val	Ile
385					390					395					400
Tyr	Val	Ser	Ala	Thr	Pro	Gly	Asp	Leu	Glu	Ile	Gln	Glu	Ser	Arg	Gly
				405					410					415	
His	Ile	Ile	Glu	Gln	Ile	Ile	Arg	Pro	Thr	Gly	Ile	Pro	Asp	Leu	Leu
			420					425					430		
Pro	Glu	Ile	Arg	Pro	Ala	Lys	Gly	Gln	Ile	Asp	Asp	Leu	Leu	Glu	Glu
		435					440					445			
Ile	Arg	Gln	Arg	Leu	Arg	Lys	Asp	Gln	Glu	Lys	Ile	Leu	Val	Ile	Ser
	450					455					460				
Val	Thr	Lys	Lys	Leu	Ala	Glu	Asp	Ile	Ala	Ala	Phe	Leu	Ala	Glu	Leu
465					470					475					480
Gly	Ile	Ala	Ala	Ala	Tyr	Leu	His	Ser	Gly	Ile	Glu	Thr	Ala	Glu	Arg
				485					490					495	
Thr	Gln	Ile	Leu	Thr	Asp	Leu	Arg	Leu	Gly	Asn	Ile	Asp	Val	Leu	Ile

(2) INFORMATION POUR LA SEQ ID NO: 871:

(A) LONGUEUR: 379 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(853700..854836)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 871:

Gly 1	Leu	Ile	Phe	Arg 5	Lys	Asn	Pro	Glu	Met 10	Ser	Cys	Ile	Asp	Lys 15	Leu
Arg	Ile	Lys	Glu 20	Lys	Ala	Arg	Ser	Glu 25	Val	Phe	Ser	Pro	Arg 30	Glu	Ser
Thr	Met	Lys	Lys	Lys	Arg	Val	Leu 40	Thr	Gly	Asp	Arg	Pro 45	Thr	Gly	Lys
Leu	His 50	Leu	Gly	His	Trp	Ile 55	Gly	Ser	Ile	Met	Asn 60	Arg	Leu	Gln	Leu
Gln 65	Asn	Asp	Ser	Arg	Tyr 70	Asp	Cys	Phe	Phe	Ile 75	Ile	Ala	Asp	Leu 80	His
Thr	Leu	Thr	Thr	Lys 85	Thr	Arg	Lys	Glu	Glu 90	Val	Leu	Gln	Ile 95	Asp	Asn
His	Ile	Tyr	Asp 100	Val	Leu	Ala	Asp 105	Trp	Leu	Ser	Val	Gly 110	Ile	Asn	Pro
Glu	Lys	Ser	Ala	Ile	Tyr	Leu 120	Gln	Ser	Ala	Ile	Pro 125	Glu	Ile	Tyr	Glu
Leu	Asn 130	Leu	Ile	Phe	Ser	Met 135	Leu	Thr	Pro	Leu	Asn 140	His	Ile	Met	Gly
Ile 145	Pro	Ser	Ile	Lys	Glu 150	Met	Ala	Ser	Asn	Ala 155	Ser	Leu	Asn	Glu 160	Glu

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Ser Leu Ser His Gly Leu Ile Gly Tyr Pro Val Leu Gln Ser Ala Asp
      165                      170                      175
Ile Leu Leu Ala Lys Ala His Leu Val Pro Val Gly Lys Asp Asn Glu
      180                      185                      190
Ala His Val Glu Leu Thr Arg Asp Ile Ala Lys Thr Phe Asn Arg Leu
      195                      200                      205
Tyr Gly Glu Val Phe Pro Glu Pro Asp Ile Leu Gln Gly Glu Leu Thr
      210                      215                      220
Ala Leu Val Gly Thr Asn Gly Gln Gly Lys Met Ser Lys Ser Ala Asn
225                      230                      235                      240
Asn Ala Ile Tyr Leu Ser Asp Asp Ala Lys Thr Val Gln Glu Lys Ile
      245                      250                      255
Arg Lys Leu Tyr Thr Asp Pro Asn Arg Ile His Ala Thr Thr Pro Gly
      260                      265                      270
Arg Val Glu Gly Asn Pro Leu Phe Ile Tyr His Asp Leu Phe Asn Pro
      275                      280                      285
His Lys Glu Glu Val Glu Glu Phe Lys Thr Arg Tyr Arg Gln Gly Cys
      290                      295                      300
Ile Lys Asp Val Glu Val Lys Ala Arg Leu Ala Glu Glu Ile Asn Leu
305                      310                      315                      320
Phe Leu Asn Pro Phe Arg Glu Lys Arg Ser Glu Leu Val Ala Gln Pro
      325                      330                      335
Lys Phe Leu Glu Glu Ala Leu Gln Gln Gly Thr Glu Lys Met Arg Thr
      340                      345                      350
Val Ala Arg Glu Thr Met Glu Glu Val His Asp His Leu Gly Leu Ser
      355                      360                      365
Arg Lys Trp Arg Thr Ile Leu Ala Ser Ser Lys
      370                      375

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(2) INFORMATIONS POUR LA SEQ ID NO: 872:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 202 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(854920..855525)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 872:

```

Leu Lys Ser Tyr Lys Lys Leu Gln Leu Thr Phe Phe Leu Thr Leu Arg
1      5      10      15
Tyr Pro Val Met Thr Thr Lys Pro Lys Thr Leu Glu Ile Asp Asn Asn
      20      25      30
Thr Phe Leu Leu Glu Gly Asn Leu Lys Arg Ile Phe Ala Thr Pro
      35      40      45
Ile Gly Tyr Thr Thr Phe Arg Glu Phe Gln Asn Val Val Phe Asn Cys
50      55      60
Ala Gln Gly Gln Gln Glu Leu Ala Asn Phe Leu Phe Glu Met Leu Ile
65      70      75      80
Asn Gly Lys Leu Leu Gln Glu Leu Pro Ala Gly Gln Lys Gln Ser Ala
      85      90      95
Gln Ser Leu Ile Val Gln Phe Met Met Pro Ile Arg Val Ala Lys Asp
      100      105      110
Ile His Glu Arg Gly Glu Phe Ile Asn Phe Ile Thr Ser Asp Met Leu

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(2) INFORMATION POUR LA SEQ ID NO: 873:

(A) LONGUEUR: 268 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(855437..856240)

Val 1	Thr	Cys	Asn 5	Val	Met	Gly	Asn	Ile	Lys 10	Thr	Leu	Leu	Glu 15	Ile	Arg
Phe	Lys	Lys	Pro 20	Thr	Pro	Xaa	Lys	Met 25	Glu	Ser	Leu	Xaa	Lys 30	Lys	Arg
Leu	Glu	Gly 35	Glu	Leu	Ser	Pro	Xaa 40	Xaa	Asn	Gly	Phe	Thr 45	Thr	Pro	Lys
Leu	Cys 50	Ser	Gln	Glu	Glu	Ala 55	Arg	Phe	Arg	Gln	Leu 60	Leu	Glu	Glu	Tyr
Ser 65	Phe	Ser	Lys	Glu	Ile 70	Ser	His	Asn	Asp	Leu 75	Gln	Gln	Leu	Cys	His 80
Leu	Ser	Ala	Gln	Val 85	Lys	Gln	Ile	His 90	His	Gln	Ala	Val	Leu 95	Leu	His
Gly	Glu	Arg	Ile 100	Lys	Lys	Val	Arg	Glu 105	Leu	Leu	Lys	Thr 110	Tyr	Arg	Glu
Gly	Ala 115	Phe	Ser	Ala	Trp	Leu	Leu 120	Leu	Thr	Tyr	Gly	Asn 125	Arg	Gln	Thr
Pro	Tyr 130	Asn	Phe	Leu	Val	Tyr 135	Tyr	Glu	Leu	Phe	Ser 140	Ala	Leu	Pro	Asp
Thr 145	Leu	Lys	Leu	Glu	Leu 150	Glu	Arg	Leu	Pro	Arg 155	Gln	Ala	Val	Tyr	Thr 160
Leu	Ala	Ser	Arg	Glu 165	Gly	Ser	Gln	Glu	Lys 170	Lys	Glu	Glu	Ile 175	Ile	Arg
Asn	Tyr	Gln	Gly 180	Glu	Thr	Arg	Gly	Glu 185	Leu	Leu	Glu	Ile 190	Ile	Arg	Arg
Glu	Phe 195	Pro	Leu	Leu	Pro	Thr	Asp 200	Arg	Arg	Gln	Ser	Ser 205	Leu	Ala	Gln
Gln	Ala 210	Phe	Ser	Phe	Phe	Ala 215	Lys	Gly	Thr	Lys	Leu 220	Leu	Gln	Arg	Cys
Thr 225	Asp	Ile	Ser	Gln	Glu 230	Glu	Leu	Leu	Ser	Leu 235	Glu	Lys	Leu	Ile	Lys 240
Lys	Leu	Gln	Lys	Val 245	Thr	Thr	Asn	Leu	Leu 250	Ser	Asn	Thr	Lys	Val 255	Ser

Arg Asn Asp Asp Glu Thr Gln Asn Ser Arg Asn Arg  
260 265

(2) INFORMATIONS POUR LA SEQ ID NO: 874:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 317 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(856233..857183)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 874:

Thr	Phe	Leu	Pro	Glu	Asp	Thr	Val	Pro	Asn	Asn	Ile	Glu	Lys	Arg	Tyr
1				5					10					15	
Leu	Glu	Ser	Phe	Leu	Thr	Leu	Phe	Ile	Ser	Phe	Asn	Leu	Ile	Arg	Pro
			20					25					30		
Cys	Leu	Trp	Thr	Asn	Gln	Tyr	Lys	Gly	Ile	Lys	Ala	Thr	Lys	Lys	Glu
		35					40					45			
Arg	Gly	Phe	Leu	Pro	Leu	Gln	Gly	Leu	His	Leu	Val	Ile	Asn	Met	Lys
	50					55					60				
Thr	Ile	Ala	Val	Asn	Ser	Phe	Lys	Gly	Gly	Thr	Ala	Lys	Thr	Ser	Thr
65					70					75				80	
Thr	Leu	His	Leu	Gly	Ala	Ala	Leu	Ala	Gln	Tyr	His	Lys	Ala	Arg	Val
				85					90					95	
Leu	Leu	Ile	Asp	Phe	Asp	Ala	Gln	Ala	Asn	Leu	Thr	Ala	Gly	Leu	Gly
			100					105					110		
Leu	Asp	Pro	Asp	Cys	Tyr	Asp	Ser	Leu	Ala	Val	Val	Leu	Gln	Gly	Glu
		115					120					125			
Lys	Asn	Ile	Glu	Glu	Val	Ile	Arg	Pro	Ile	Asp	Ser	Ser	Gly	Leu	Asp
	130					135					140				
Leu	Ile	Pro	Ala	Asp	Thr	Trp	Leu	Glu	Arg	Val	Glu	Val	Ser	Gly	Ser
145					150					155					160
Leu	Ala	Ala	Asp	Arg	Tyr	Ser	His	Glu	Arg	Leu	Lys	Ile	Ile	Leu	Ser
				165					170					175	
Lys	Ile	Glu	His	Arg	Tyr	Asp	Tyr	Val	Ile	Ile	Asp	Thr	Pro	Pro	Ser
			180					185					190		
Leu	Cys	Trp	Leu	Thr	Glu	Ser	Ala	Leu	Ile	Ala	Ala	Gln	His	Ala	Leu
		195					200					205			
Ile	Cys	Ala	Thr	Pro	Glu	Phe	Tyr	Ser	Val	Lys	Gly	Leu	Glu	Arg	Leu
	210					215					220				
Ala	Thr	Phe	Ile	Gln	Gly	Ile	Ser	Ser	Arg	His	Pro	Leu	Asn	Ile	Leu
225					230					235					240
Gly	Val	Thr	Leu	Ser	Phe	Trp	Asn	Tyr	Arg	Gly	Lys	Asn	Asn	Ala	Ala
				245					250					255	
Phe	Thr	Glu	Leu	Ile	Gln	Lys	Thr	Phe	Pro	Gly	Lys	Leu	Leu	Asn	Thr
			260					265					270		
Arg	Ile	Arg	Arg	Asp	Ile	Thr	Ile	Ser	Glu	Ala	Ala	Ile	His	Gly	Lys
		275				280						285			
Pro	Val	Phe	Ser	Thr	Ala	Pro	Ser	Ala	Arg	Ala	Ser	Glu	Asp	Tyr	Leu
	290					295					300				
Lys	Leu	Thr	Glu	Glu	Leu	Leu	Phe	Leu	Leu	Ser	Asp	Met			
305					310					315					

(2) INFORMATIONS POUR LA SEQ ID NO: 875:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 663 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(857451..859439)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 875:

Asn	Ala	Thr	Met	Ala	Asn	Thr	Pro	Arg	Lys	Lys	Arg	Arg	Phe	Phe	Ala	1	5	10	15
Ala	Val	Cys	Ser	Lys	Phe	Phe	Ile	Tyr	Gly	Glu	Gly	Met	Ile	His	Val	20	25	30	
Thr	Cys	Asn	Gln	Glu	Ala	Phe	Glu	Leu	Pro	Glu	Gly	Ala	Ser	Ala	Met	35	40	45	
Asp	Leu	Ala	Asn	Lys	Met	Lys	Gln	Ser	His	Cys	Phe	Val	Gly	Ala	Leu	50	55	60	
Ile	Asn	Asp	Gln	Glu	Lys	Asp	Leu	Ser	Thr	Thr	Leu	Gln	Asp	Gly	Asp	65	70	75	80
Thr	Val	Leu	Phe	Leu	Thr	Trp	Asp	Asp	Pro	Lys	Gly	Arg	Glu	Ile	Phe	85	90	95	
Leu	His	Thr	Ser	Ala	His	Ile	Leu	Ala	Gln	Ala	Val	Leu	Arg	Leu	Trp	100	105	110	
Pro	Ser	Ala	Gln	Pro	Thr	Ile	Gly	Pro	Val	Ile	Asp	Gln	Gly	Phe	Tyr	115	120	125	
Tyr	Asp	Phe	Ala	Asn	Leu	Ser	Ile	Ser	Glu	Glu	Asp	Phe	Pro	Ala	Ile	130	135	140	
Glu	Ala	Met	Ala	Lys	Thr	Ile	Ala	Glu	Glu	Lys	Phe	Pro	Ile	Ser	Arg	145	150	155	160
Gln	Val	Phe	Pro	Asp	Lys	Glu	Ala	Ala	Leu	Ala	Tyr	Phe	Ser	Gln	Asn	165	170	175	
Pro	Phe	Lys	Ala	Glu	Leu	Ile	Ala	Glu	Leu	Pro	Glu	Glu	Val	Glu	Ile	180	185	190	
Ser	Ala	Tyr	Thr	Gln	Gly	Glu	Phe	Leu	Asp	Leu	Cys	Arg	Gly	Pro	His	195	200	205	
Leu	Pro	Ser	Thr	Ala	Pro	Val	Lys	Ala	Phe	Lys	Leu	Arg	Thr	Ser		210	215	220	
Ser	Ala	Tyr	Trp	Lys	Gly	Asp	Pro	Ser	Arg	Glu	Ser	Leu	Ile	Arg	Ile	225	230	235	240
Tyr	Gly	Val	Ser	Phe	Pro	Thr	Thr	Lys	Glu	Leu	Lys	Glu	His	Leu	His	245	250	255	
Gln	Leu	Glu	Glu	Ala	Lys	Lys	Arg	Asp	His	Arg	Val	Leu	Gly	Thr	Lys	260	265	270	
Leu	Asp	Leu	Phe	Ser	Gln	Gln	Thr	Cys	Ser	Ala	Gly	Met	Pro	Phe	Phe	275	280	285	
His	Pro	Arg	Gly	Met	Val	Val	Trp	Asn	Ala	Leu	Val	Asp	Tyr	Trp	Lys	290	295	300	
Arg	Leu	His	Gln	Arg	Ala	Gly	Tyr	Gln	Gln	Ile	Gln	Thr	Pro	Gln	Leu	305	310	315	320
Met	Asn	Arg	Glu	Leu	Trp	Glu	Ile	Ser	Gly	His	Trp	Glu	Asn	Tyr	Lys	325	330	335	
Glu	Asn	Met	Tyr	Thr	Leu	Thr	Val	Asp	Glu	Glu	Asp	Tyr	Ala	Ile	Lys	340	345	350	

Pro Met Asn Cys Pro Gly Cys Met Leu Tyr Tyr Lys Thr Gln Leu His  
 355 360 365  
 Ser Tyr Arg Glu Phe Pro Leu Arg Ile Ala Glu Ile Gly His Val His  
 370 375 380  
 Arg His Glu Leu Ser Gly Ala Leu Ser Gly Leu Met Arg Val Arg Thr  
 385 390 395 400  
 Phe His Gln Asp Asp Ala His Val Phe Leu Thr Pro Glu Gln Val Glu  
 405 410 415  
 Glu Glu Thr Leu Asn Ile Leu Asn Leu Val Ser Glu Leu Tyr Gly Thr  
 420 425 430  
 Phe Gly Leu Glu Tyr His Leu Glu Leu Ser Thr Arg Pro Glu Gln Gly  
 435 440 445  
 Thr Ile Gly Ser Asp Asp Leu Trp Glu Leu Ala Thr Glu Ala Leu Lys  
 450 455 460  
 Arg Ala Leu Val Lys Ser Gln Lys Pro Phe Ile Ile Ser Pro Gly Glu  
 465 470 475 480  
 Gly Ala Phe Tyr Gly Pro Lys Ile Asp Ile His Val Lys Asp Ala Ile  
 485 490 495  
 Asn Arg Thr Trp Gln Cys Gly Thr Ile Gln Leu Asp Met Phe Leu Pro  
 500 505 510  
 Glu Arg Phe Asp Leu Lys Tyr Thr Asn Ala Gln Gly Glu Lys Ser Thr  
 515 520 525  
 Pro Ile Met Leu His Arg Ala Leu Phe Gly Ser Ile Glu Arg Phe Leu  
 530 535 540  
 Gly Ile Leu Ile Glu His Phe Lys Gly Arg Phe Pro Leu Trp Leu Ser  
 545 550 555 560  
 Pro Glu His Val Arg Ile Ile Thr Val Ala Asp Arg His Glu Ala Arg  
 565 570 575  
 Ala Gln Glu Leu Ala Lys His Phe Ser Gln Met Gly Ile Ile Val Ser  
 580 585 590  
 Val Asp Ser Ser Asn Glu Ser Val Ser Lys Lys Ile Arg Asn Ala Gln  
 595 600 605  
 Asn Met Gln Val Asn Tyr Met Ile Thr Ile Gly Asp Lys Glu Leu Glu  
 610 615 620  
 Thr His Leu Leu Ala Val Arg Thr Arg Asp Asn Arg Val Leu Asn Asp  
 625 630 635 640  
 Ile Ala Val Glu Gln Phe Ser His Val Ile Leu Glu Glu Leu Arg Ser  
 645 650 655  
 Leu Ser Leu Thr Pro Ser Leu  
 660

## (2) INFORMATIONS POUR LA SEQ ID NO: 876:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 120 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(859587..859946)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 876:

Lys Pro Ile Thr Glu Ser Asn Thr Ile Gly Met Ile Ala Gly Arg Gly  
 1 5 10 15  
 Arg Arg Arg Asp Ser Arg Leu His Asn Ser Ser Pro Lys Arg Thr Thr

(2) INFORMATION POUR LA SEQ ID NO: 877:

(A) LONGUEUR: 333 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 859642..860640

Ile	Arg	Ala	Thr	Arg	Phe	Met	Val	Ala	Val	Lys	Ala	Leu	Leu	Phe	Ala
1				5					10					15	
Cys	Thr	Leu	Arg	Thr	Cys	Val	Phe	Lys	Pro	Cys	Cys	Asp	Met	Ala	Ile
			20					25					30		
Phe	Leu	Ile	Phe	Leu	Asn	Ala	Phe	Ile	Trp	Ser	Ser	Ser	Phe	Ala	Leu
		35					40					45			
Ser	Lys	Ser	Ala	Met	Glu	Ala	Ala	Ala	Pro	Leu	Phe	Val	Thr	Gly	Ser
	50					55					60				
Arg	Met	Val	Leu	Ala	Gly	Val	Val	Leu	Phe	Gly	Leu	Leu	Leu	Cys	Lys
65					70					75					80
Arg	Glu	Ser	Leu	Arg	Leu	Pro	Arg	Pro	Ala	Ile	Met	Pro	Ile	Val	Leu
				85					90					95	
Leu	Ser	Val	Ile	Gly	Phe	Tyr	Leu	Thr	Asn	Val	Leu	Glu	Phe	Ile	Gly
			100					105					110		
Leu	Gln	Arg	Leu	Ser	Ser	Ser	Thr	Ala	Cys	Phe	Ile	Tyr	Gly	Phe	Ser
		115					120				125				
Pro	Phe	Thr	Ala	Ala	Phe	Cys	Ser	Tyr	Val	Gln	Leu	Arg	Glu	Val	Val
	130					135					140				
Thr	Trp	Lys	Lys	Leu	Gly	Gly	Leu	Ser	Leu	Gly	Leu	Val	Ser	Tyr	Leu
145					150					155					160
Val	Tyr	Leu	Leu	Phe	Gly	Gly	Ser	Glu	Asp	Val	Ala	Glu	Trp	Gly	Trp
				165					170					175	
Gln	Leu	Gly	Leu	Pro	Glu	Leu	Leu	Leu	Ile	Ala	Ala	Thr	Cys	Leu	Ser
			180					185					190		
Ser	Tyr	Gly	Trp	Thr	Leu	Leu	Arg	Lys	Leu	Gly	Arg	Arg	Cys	Glu	Ser
		195					200				205				
Leu	Ser	Met	Thr	Ala	Ile	Asn	Ala	Tyr	Ala	Met	Val	Ile	Ala	Gly	Val
	210					215					220				
Leu	Ser	Leu	Ile	His	Ser	Ala	Val	Thr	Glu	Val	Trp	Asn	Pro	Val	Pro
225					230					235					240



Val	Glu	Asn	Pro	Leu	Leu	Phe	Leu	Gln	Ala	Ile	Gly	Ala	Leu	Val	Ile
				245					250					255	
Phe	Ser	Asn	Leu	Ile	Cys	Tyr	Asn	Leu	Phe	Ala	Lys	Leu	Leu	Arg	Ser
		260					265						270		
Phe	Ser	Ser	Thr	Phe	Leu	Ser	Phe	Cys	Asn	Leu	Val	Met	Pro	Leu	Phe
		275					280					285			
Ala	Ser	Phe	Phe	Gly	Trp	Leu	Leu	Leu	Gly	Glu	Ser	Phe	Pro	Pro	Gly
	290					295					300				
Leu	Leu	Phe	Ala	Val	Gly	Phe	Met	Val	Leu	Gly	Cys	Arg	Leu	Ile	Tyr
305					310					315					320
His	Glu	Glu	Phe	Arg	Gln	Gly	Tyr	Val	Leu	Thr	Ser	Glu			
				325					330						

(2) INFORMATIONS POUR LA SEQ ID NO: 878:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 292 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(860724..861599)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 878:

Pro	Thr	Arg	Ala	Ala	Ser	Ala	Lys	Ser	Trp	Ser	Ser	Ser	Phe	Gln	Gln
1				5					10					15	
Gln	Asn	Gln	Ala	Ile	Gln	Asn	Gln	Val	Ala	Met	Ala	Pro	Glu	Ile	Gly
			20				25						30		
Asn	Ala	Ile	Arg	Thr	Gln	Ala	Gly	His	Gln	Ala	Lys	Ala	Thr	Glu	Leu
		35					40					45			
Gln	Ala	Gln	Gln	Ser	Leu	Ile	Ser	Gly	Ile	Thr	Asn	Ile	Val	Gly	Phe
	50					55					60				
Ala	Val	Ser	Val	Gly	Gly	Gly	Ile	Leu	Ser	Ala	Ser	Lys	Ser	Leu	Gly
65				70					75					80	
Gly	Leu	Lys	Ser	Ala	Ala	Phe	Thr	Asn	Glu	Thr	Ala	Ser	Ala	Ala	Thr
				85					90					95	
Ser	Ala	Thr	Ser	Ser	Leu	Ala	Lys	Thr	Ala	Thr	Ser	Ala	Leu	Asp	Asp
			100					105					110		
Val	Ala	Gly	Thr	Ala	Thr	Ala	Val	Gly	Ala	Lys	Ala	Thr	Ser	Gly	Ala
		115					120					125			
Ala	Ser	Ala	Ala	Ser	Ser	Ala	Ala	Thr	Lys	Leu	Thr	Gln	Asn	Met	Ala
	130					135					140				
Glu	Ser	Ala	Ser	Lys	Thr	Leu	Ser	Gln	Thr	Ala	Ser	Lys	Ser	Ala	Gly
145				150					155					160	
Gly	Leu	Phe	Gly	Gln	Ala	Leu	Asn	Thr	Pro	Ser	Trp	Ser	Glu	Lys	Val
				165					170					175	
Ser	Arg	Gly	Met	Asn	Val	Val	Lys	Thr	Gln	Gly	Thr	Arg	Ala	Thr	Lys
			180					185					190		
Phe	Ala	Gly	Arg	Ala	Leu	Ser	Ser	Ala	Met	Asn	Ile	Ser	Gln	Met	Val
		195					200					205			
His	Gly	Leu	Thr	Ala	Gly	Ile	Asp	Gly	Ile	Val	Gly	Gly	Val	Ile	Gly
	210					215					220				
Ala	Gln	Val	Ala	Gln	Glu	Gln	Arg	Met	Ala	Gly	Met	Ala	Glu	Ala	Arg
225					230					235					240
Ala	Glu	Glu	Leu	Lys	Ser	Leu	Asn	Ser	Val	Gln	Ala	Gln	Tyr	Ala	Ser

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                245                250                255
Gln Ala Gln Gln Leu Gln Glu Gln Ser Gln Gln Ser Phe Asn Ser Ala
                260                265                270
Leu Gln Thr Leu Gln Ser Ile Ser Asp Ser Ala Leu Gln Thr Thr Ala
                275                280                285
Ser Met Phe Asn
                290

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(2) INFORMATIONS POUR LA SEQ ID NO: 879:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 158 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(861580..862053)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 879:

```

Trp Arg Ser Cys Val Met Thr Thr Gly Val Arg Gly Asp Asn Ala Pro
1          5          10          15
Asp Pro Ser Leu Leu Ala Gln Leu Thr Gln Asn Ala Asn Ser Ala Ser
          20          25          30
Ala Ala Ser Thr Gly Lys Asn Gly Gln Val Ala Gly Ala Lys Gln Glu
          35          40          45
Asn Val Asp Ala Ser Phe Glu Asp Leu Leu Gln Asp Ala Gln Gly Thr
          50          55          60
Gly Gly Ser Lys Lys Ala Thr Ala Asn Gln Thr Ser Lys Ser Arg Lys
65          70          75          80
Ser Glu Lys Ala Gln Ala Ser Ser Gly Thr Ser Thr Thr Thr Ser Val
          85          90          95
Ala Gln Ala Ser Gln Thr Ala Thr Ala Gln Ala Val His Gly Ala Arg
          100         105         110
Asp Ser Gly Phe Asn Ser Asp Gly Ser Ala Thr Leu Pro Ser Pro Thr
          115         120         125
Gly Thr Glu Val Asn Gly Val Val Leu Arg Lys Gly Met Gly Thr Leu
          130         135         140
Ala Leu Met Gly Leu Ile Met Thr Tyr Ser Arg Ser Lys Cys
145          150          155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 880:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 481 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(862098..863540)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 880:

Arg	Gly	Tyr	Met	Ser	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Ser	Asn	
1				5					10						15	
Leu	Lys	Asn	Val	Leu	Ser	Gln	Val	Ile	Ala	Ser	Thr	Pro	Gln	Gly	Val	
			20					25					30			
Pro	Asn	Ala	Asp	Lys	Leu	Thr	Asp	Asn	Gln	Val	Lys	Gln	Val	Gln	Gln	
		35					40					45				
Thr	Arg	Gln	Asn	Arg	Asp	Asp	Leu	Ser	Met	Glu	Ser	Asp	Val	Ala	Val	
	50				55						60					
Ala	Gly	Thr	Ala	Gly	Lys	Asp	Arg	Ala	Ala	Ser	Ala	Ser	Gln	Ile	Glu	
65					70					75					80	
Gly	Gln	Glu	Leu	Ile	Glu	Gln	Gln	Gly	Leu	Ala	Ala	Gly	Lys	Glu	Thr	
				85					90					95		
Ala	Ser	Ala	Asp	Ala	Thr	Ser	Leu	Thr	Gln	Ser	Ala	Ser	Lys	Gly	Ala	
			100					105					110			
Ser	Ser	Gln	Gln	Cys	Ile	Glu	Asp	Thr	Ser	Lys	Ser	Leu	Glu	Leu	Ser	
		115					120					125				
Ser	Leu	Ser	Ser	Leu	Ser	Ser	Val	Asp	Ala	Thr	His	Leu	Gln	Glu	Ile	
	130					135					140					
Gln	Ser	Ile	Val	Ser	Ser	Ala	Met	Gly	Ala	Thr	Asn	Glu	Leu	Ser	Leu	
145					150					155					160	
Thr	Asn	Leu	Glu	Thr	Pro	Gly	Leu	Pro	Lys	Pro	Ser	Thr	Thr	Pro	Arg	
				165					170					175		
Gln	Glu	Val	Met	Glu	Ile	Ser	Leu	Ala	Leu	Ala	Lys	Ala	Ile	Thr	Ala	
			180					185					190			
Leu	Gly	Glu	Ser	Thr	Gln	Ala	Ala	Leu	Glu	Asn	Phe	Gln	Ser	Thr	Gln	
		195					200					205				
Ser	Gln	Ser	Ala	Asn	Met	Asn	Lys	Met	Ser	Leu	Glu	Ser	Gln	Gly	Leu	
	210					215					220					
Lys	Ile	Asp	Lys	Glu	Arg	Glu	Glu	Phe	Lys	Lys	Met	Gln	Glu	Ile	Gln	
225					230					235					240	
Gln	Lys	Ser	Gly	Thr	Asn	Ser	Thr	Met	Asp	Thr	Val	Asn	Lys	Val	Met	
				245					250					255		
Ile	Gly	Val	Thr	Val	Ala	Ile	Thr	Val	Ile	Ser	Val	Val	Ser	Ala	Leu	
			260					265					270			
Phe	Thr	Cys	Gly	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Ala	Ala	Gly	Ala	Thr	
		275					280					285				
Ala	Ala	Thr	Ala	Gly	Ala	Thr	Ala	Ala	Ala	Thr	Thr	Ala	Thr	Ser	Val	
	290					295					300					
Thr	Thr	Thr	Val	Ala	Thr	Gln	Val	Thr	Met	Gln	Ala	Val	Val	Gln	Val	
305					310					315					320	
Val	Lys	Gln	Ala	Ile	Gln	Ala	Val	Lys	Arg	Ala	Ile	Val	Gln	Ala		
				325				330					335			
Ile	Lys	Gln	Gly	Ile	Lys	Gln	Gly	Ile	Lys	Gln	Ala	Ile	Lys	Gln	Ala	
		340					345					350				
Val	Lys	Ala	Ser	Val	Lys	Thr	Leu	Ala	Lys	Asn	Val	Gly	Lys	Ile	Phe	
		355					360					365				
Ser	Ala	Gly	Lys	Asn	Ala	Val	Ser	Lys	Ser	Phe	Pro	Lys	Leu	Ser	Lys	
	370					375					380					
Val	Ile	Asn	Thr	Leu	Gly	Ser	Lys	Trp	Val	Thr	Leu	Gly	Val	Gly	Ala	
385					390					395					400	
Leu	Thr	Ala	Val	Pro	Gln	Leu	Val	Ser	Gly	Ile	Thr	Ser	Leu	Gln	Leu	
				405					410					415		
Ser	Asp	Met	Gln	Lys	Glu	Leu	Ala	Gln	Ile	Gln	Lys	Glu	Val	Gly	Ala	
			420				425					430				
Leu	Thr	Ala	Gln	Ser	Glu	Met	Met	Lys	Ala	Phe	Thr	Leu	Phe	Trp	Gln	
		435					440					445				
Gln	Ala	Ser	Lys	Ile	Ala	Ala	Lys	Gln	Thr	Glu	Ser	Pro	Ser	Glu	Thr	
	450					455					460					
Gln	Gln	Gln	Ala	Ala	Lys	Thr	Gly	Ala	Gln	Ile	Ala	Lys	Xaa	Cys	Pro	

465  
Gln

470

475

480

(2) INFORMATIONS POUR LA SEQ ID NO: 881:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 120 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(863571..863930)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 881:

Thr	Met	Ser	Lys	Lys	His	Lys	His	Lys	Gln	Ala	His	Thr	Ser	Ser	Lys
1				5					10					15	
Pro	Lys	Val	Xaa	Pro	Ala	Tyr	Val	Ser	Lys	Lys	Glu	Ser	Pro	Ala	Leu
			20					25					30		
Gln	Glu	Leu	Gln	Asn	Ala	Met	Ile	Ser	Phe	Ser	Gln	Asp	Leu	Pro	Leu
		35					40					45			
Ala	Gln	Met	Phe	Ser	Glu	Ile	Gln	Asp	Glu	Lys	Gln	Leu	Ala	Lys	Met
	50					55					60				
Met	Ala	Ala	Leu	Ser	Gly	Met	Leu	Asp	Ser	Leu	Pro	Val	Glu	Thr	Leu
65					70					75					80
Thr	Lys	Gly	Val	Phe	Asp	Asn	Pro	Lys	Glu	Glu	Ala	Gln	Leu	Ser	Gln
				85					90					95	
Glu	Ile	Ser	Ser	Ile	Phe	Leu	Gly	Leu	Lys	His	Leu	Thr	Glu	Thr	Val
			100					105					110		
Asn	Lys	His	Ile	Ala	Asp	Glu	Lys								
			115				120								

(2) INFORMATIONS POUR LA SEQ ID NO: 882:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(863996..864697)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 882:

Asn	Leu	Ile	Leu	Leu	Val	Val	Ile	Cys	Tyr	Phe	Ile	Phe	Leu	Gly	Ile
1				5					10					15	
Ile	Ala	Met	Ser	Thr	Pro	Ser	Ser	Asn	Asn	Ser	Lys	Lys	Pro	Ser	Ala
			20					25					30		
Ser	Phe	Asn	Lys	Lys	Ser	Arg	Ser	Arg	Leu	Ala	Glu	Ile	Ala	Ala	Gln
		35					40					45			
Lys	Lys	Ala	Lys	Ala	Glu	Asp	Leu	Glu	Gln	Lys	Tyr	Pro	Val	Pro	Thr
	50					55					60				

Glu	Glu	Glu	Thr	Lys	Gln	Val	Leu	Met	Asp	Ile	Leu	Gln	Gly	Leu	Ser	65	70	75	80
Asn	Gly	Leu	Thr	Leu	Gln	Gln	Ile	Leu	Gly	Leu	Ser	Asp	Val	Leu	Leu	85	90	95	
Glu	Glu	Ile	Tyr	Thr	Val	Ala	Tyr	Thr	Phe	Tyr	Ser	Gln	Gly	Lys	Tyr	100	105	110	
Arg	Glu	Ala	Ile	Gly	Leu	Phe	Gln	Ile	Leu	Thr	Ala	Ser	Lys	Pro	Gln	115	120	125	
Cys	Tyr	Lys	Tyr	Ile	Leu	Gly	Leu	Ser	Ser	Cys	Tyr	His	Gln	Leu	Lys	130	135	140	
Met	Tyr	Asp	Glu	Ala	Ala	Phe	Gly	Phe	Phe	Leu	Ala	Phe	Asp	Ala	Gln	145	150	155	160
Pro	Glu	Asn	Pro	Ile	Pro	Pro	Tyr	Tyr	Ile	Ala	Asp	Ser	Leu	Met	Lys	165	170	175	
Leu	Asn	Gln	Pro	Glu	Glu	Ser	Gln	Asp	Phe	Leu	Asp	Ile	Thr	Ile	Asp	180	185	190	
Met	Cys	Lys	Asn	Lys	Pro	Glu	Tyr	Lys	Val	Leu	Lys	Asp	Arg	Cys	Ser	195	200	205	
Ile	Met	Lys	Gln	Ser	Leu	Asp	Ala	Val	Leu	Lys	Lys	Glu	Lys	Ser	Ala	210	215	220	
Lys	Gly	Ser	Glu	Thr	Gln	Ala	Ser	Val	Ser							225	230		

## (2) INFORMATIONS POUR LA SEQ ID NO: 883:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 437 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 864938..866248

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 883:

Ser	Arg	Ile	Arg	Leu	Leu	Asp	Ser	Val	Thr	Val	Asn	Gln	Ile	Ser	Ala	1	5	10	15
Gly	Glu	Val	Ile	Glu	Asn	Ala	Ala	Ser	Val	Val	Lys	Glu	Leu	Ile	Glu	20	25	30	
Asn	Ser	Leu	Asp	Ala	Gly	Ala	Asp	Glu	Ile	His	Ile	Glu	Thr	Leu	Gly	35	40	45	
Gly	Gly	Arg	Gly	Gln	Ile	Val	Val	Arg	Asp	Asn	Gly	Val	Gly	Met	Asp	50	55	60	
Pro	Glu	Glu	Val	Pro	Val	Ala	Leu	Gln	Arg	His	Ala	Thr	Ser	Lys	Ile	65	70	75	80
Ala	His	Phe	Ala	Asp	Ile	Phe	Ser	Leu	Ala	Ser	Tyr	Gly	Phe	Arg	Gly	85	90	95	
Glu	Ala	Leu	Pro	Ser	Ile	Ala	Ser	Ile	Ser	Lys	Met	Glu	Ile	His	Thr	100	105	110	
Ala	Arg	Ala	Gly	Gly	Leu	Gly	Ser	Lys	Thr	Leu	Ile	Glu	Lys	Gly	Glu	115	120	125	
Pro	Val	Cys	Cys	Glu	Pro	Ala	Pro	Arg	Gln	Gln	Gly	Thr	Thr	Ile	Ala	130	135	140	
Val	His	Ser	Leu	Phe	Tyr	Asn	Val	Pro	Met	Arg	Gln	Ser	Phe	Gln	Lys	145	150	155	160
Ser	Pro	Gln	Met	Asp	Arg	Leu	Ala	Ile	Arg	Arg	Leu	Leu	Glu	Asn	Ser				

Val	Leu	Ser	Ser	165	Glu	Gly	Ile	Gly	Trp	170	Thr	Trp	Ile	Ser	Glu	Arg	Arg	175
			180						185						190			
Gln	Glu	Leu	His	Val	Ala	Lys	Lys	Gln	Gly	Phe	Ile	Glu	Arg	Val	Ala			
		195					200					205						
Leu	Val	Leu	Gly	Glu	Ser	Phe	Val	Gln	Glu	Ala	Phe	Phe	Ile	Asp	Lys			
		210				215					220							
Gln	Gln	Gly	Asp	Leu	Arg	Val	Leu	Gly	Phe	Leu	Gly	Ser	Pro	Asn	Gln			
225					230					235					240			
His	Arg	Ser	Thr	Arg	Gln	Gly	Gln	Arg	Leu	Phe	Ile	Asn	Asn	Arg	Ala			
				245					250					255				
Val	Glu	Ser	Ser	Phe	Ile	Ser	Lys	Lys	Val	Ala	Glu	Ala	Tyr	Ala	Trp			
			260					265					270					
Met	Ile	Pro	Ala	Gln	Arg	Tyr	Pro	Ile	Phe	Val	Leu	Lys	Leu	Phe	Leu			
		275					280					285						
Pro	Pro	Met	Trp	Cys	Asp	Phe	Asn	Val	His	Pro	Gln	Lys	Thr	Glu	Val			
		290				295					300							
Arg	Leu	Leu	Gln	Glu	Gly	Gln	Ile	Ser	Asn	Leu	Leu	Val	Glu	Ala	Ile			
305					310					315					320			
Ser	Glu	Ala	Leu	Leu	Arg	Arg	Ser	Ser	Ser	Leu	Glu	Glu	Ile	Val	Leu			
				325					330				335					
Lys	Val	Pro	Thr	Glu	Lys	Ile	Pro	Ile	Glu	Asn	Glu	Gly	Ile	Ser	Val			
			340					345					350					
Pro	Ser	Ile	Arg	Pro	Ala	Ile	Val	Ser	Ala	Pro	Leu	Ser	Cys	Pro	Thr			
		355				360					365							
Phe	Ser	Gln	Gln	Pro	Tyr	Leu	Lys	Thr	Glu	Met	Ala	Thr	Ile	Val	Ser			
		370				375				380								
Arg	Asp	Ser	Ala	Ser	Ser	Ser	Leu	Ser	Val	Val	Glu	Lys	Val	Arg	Phe			
385					390					395					400			
Leu	Thr	Ser	Leu	Gly	Lys	Val	Leu	Leu	Val	Glu	Asp	Ser	Glu	Gly	Val			
				405					410					415				
His	Val	Val	Phe	Val	Gln	Leu	Arg	Val	Asn	Ile	Cys	Phe	Met	Phe	Leu			
			420					425					430					
Tyr	Tyr	Pro	Ser	Val														
				435														

(2) INFORMATIONS POUR LA SEQ ID NO: 884:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 866303..866605

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 884:

Leu	Ser	Trp	Lys	Gln	Thr	Phe	Tyr	Arg	Cys	Gly	Leu	Glu	Ala	Leu	Thr
1			5					10					15		
Ala	Leu	Gly	Ile	Glu	Leu	Ser	Arg	Ile	Ser	Pro	Asp	Ser	Phe	Ala	Ile
			20				25						30		
Glu	Ser	Ala	Pro	Pro	Phe	Ile	Gln	Glu	Glu	Glu	Leu	Lys	Glu	Trp	Ile
		35				40					45				
Val	Ala	Leu	Ala	Gln	Glu	Gly	Ala	Leu	His	Val	Gly	Glu	Ser	Phe	Glu
		50				55					60				

Gln Leu Val Glu Asn Thr Val Gln Lys Leu Val Phe Ser Arg Asn Ala  
 65 70 75 80  
 Arg Ala Phe Asp Tyr Ala Trp Leu Asp Ile Leu Trp Lys Leu Gly Lys  
 85 90 95  
 Pro Glu Lys Ser Val  
 100

(2) INFORMATIONS POUR LA SEQ ID NO: 885:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 356 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 866665..867732

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 885:

Met Asn Gln Asn Pro Ile Lys Arg Leu Gln Asp Ser Leu Val Glu Arg  
 1 5 10 15  
 Ala Leu Asp Ala Phe Leu Ile Glu Lys Asp Glu Asp Ile Ser Tyr Phe  
 20 25 30  
 Leu Gln Asp Gln Ala Arg Ser Gly Val Leu Leu Ile Thr Arg Asp Glu  
 35 40 45  
 Ala Val Leu Phe Val Ser Pro Leu Asp Lys Asp Leu Tyr Ala Arg Ile  
 50 55 60  
 Gln Asp Val Val Leu Val Ser Tyr Ser Lys Ser Val Asp Gln Glu Leu  
 65 70 75 80  
 Gly Ser Tyr Ile Glu Asn Thr Gly Leu Lys Thr Ile Gly Phe Asp Ser  
 85 90 95  
 Glu Tyr Thr Pro Tyr Gly Ile Ala Gln Lys Arg Met Asn Ser Gly Tyr  
 100 105 110  
 Ala Phe Ser Pro Gln Ser Leu Val Ala Glu Lys Leu Arg Cys Val Lys  
 115 120 125  
 Ser Thr Glu Glu Ile Gln Lys Met Thr Arg Ala Ala Glu Ile Gly Ser  
 130 135 140  
 Ala Gly Tyr Asp Phe Val Leu Ala Ala Leu Arg Pro Gly Ile Thr Glu  
 145 150 155 160  
 Lys Glu Leu Val Arg Met Leu His Val Phe Trp Ala Asn Leu Gly Ile  
 165 170 175  
 Glu Lys Val Ser Phe Pro Pro Ile Ile Ala Phe Gly Glu Asn Ala Ala  
 180 185 190  
 Phe Pro His Ala Ile Pro Thr Asn Arg Ser Leu Lys Lys Gly Asp Val  
 195 200 205  
 Val Leu Ile Asp Ile Gly Val Cys Tyr Glu Gly Tyr Cys Ser Asp Met  
 210 215 220  
 Thr Arg Thr Val Ala Phe Gly Ala Ala Pro Glu Gln Gln Leu Leu Asp  
 225 230 235 240  
 Gly Tyr Val Ala Val Ala Glu Ala Gln Arg Ala Ala Ile Glu Phe Cys  
 245 250 255  
 Arg Ala Gly Val Pro Cys Arg Asp Val His Lys Glu Ala Val Arg Ile  
 260 265 270  
 Leu Arg Ala His Gly Met Glu Lys Ala Phe Ile His Gly Leu Gly His  
 275 280 285  
 Gly Val Gly Arg Glu Val His Glu Tyr Pro Arg Leu Ser Pro Phe Ser

290	295	300
Asp Ala Thr Leu Gln Leu Asn Met Ala Val Thr Val Glu Pro Gly Val		
305	310	315
Tyr Phe Pro Gly Val Gly Gly Ile Arg Ile Glu Asp Thr Ile Val Ile		
	325	330
Gly Val Asn Glu Asn Leu Asn Leu Thr Asn Arg Lys Val Ser Ser Glu		
	340	345
Ile Ile Ile Ile		350
355		

(2) INFORMATIONS POUR LA SEQ ID NO: 886:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 427 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 867810..869090

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 886:

Phe Phe Phe Ser Asn Gln Leu Leu Tyr Thr Ile Leu Phe Cys Phe Ser	
1 5 10 15	
Val Val Met Arg Gln Leu His Phe Phe Phe Tyr Gln Trp Ile Arg Gly	
20 25 30	
Ala Ala Leu Ile Gly Ala Ile Ala Gly Val Cys Ser Pro Leu Thr Ala	
35 40 45	
Glu Glu Lys Gln Pro Ala Cys Ser Gly Ala Trp Ala Leu Gln Asp Phe	
50 55 60	
Ser Ile Glu Glu Glu Leu Pro Asp Leu Arg Asn Gln Phe Val Phe Leu	
65 70 75 80	
Gly Cys Asn Lys Arg Pro Asp Ala Arg Ser Gly Lys Phe Phe Leu Glu	
85 90 95	
Leu Ala Thr Thr Asn Ala Ile Gln Glu Val Ser Leu Gly Glu Lys Val	
100 105 110	
Phe Leu Arg Gln Gly Pro Asp Glu Thr Leu Val Phe Ser Ala Glu	
115 120 125	
Pro Thr Pro Leu Trp Leu Glu Cys Arg Pro Ser Ser Asp Gly Arg Ser	
130 135 140	
Leu Asp Val Val Val Arg Met Lys Gly Ala Leu Gly Gly Ala Val Ser	
145 150 155 160	
Ser Pro Lys Glu Arg Ala His Phe Ser Leu Ser Met Ala Pro Arg Cys	
165 170 175	
Ser Gln Thr Trp Glu Ile Gly Gly Met Arg Val Glu Pro Ser Ile Ala	
180 185 190	
Val Lys Gln Arg Ile Arg Cys Val Gly Gly Asp Lys Phe Leu Leu Met	
195 200 205	
His Gly Gly Ala Asp Tyr Val Ile Gln Ala Ala Lys Glu Arg Val Asp	
210 215 220	
Phe Glu Ser Leu Ser Gly Glu Ala Tyr Ser Gln Tyr Leu Ala Val Gly	
225 230 235 240	
Asp Val Leu Leu Trp Asp Gln Asp Arg Trp Val Pro Tyr Lys Thr Phe	
245 250 255	
Gln Gly Asp Gly Thr Arg Val Pro Leu Leu Glu Val Lys Arg Leu Asp	
260 265 270	



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Asp Arg Met Met Val Ile Glu Leu Trp Ser Ile Asp Gly Leu Met Ser
      275                      280                285
Gln Gln Ile Thr Leu Val Lys Gln Val Ser Ser Pro Ile Glu Ile Ala
      290                      295                300
Glu Leu Val Lys Glu Phe Ser Phe Val Gly Met Arg Thr Trp Ser Arg
305                      310                315                320
Pro Ile Ile Thr Ala Gly Lys Asp Arg Leu Val Leu Ser Ala Asp Asp
      325                      330                335
Trp Val Ile His Thr Gly Glu Arg Trp Glu Arg Val Thr Ser Lys Arg
      340                      345                350
Gln Leu Glu Asp Tyr Leu Ser Gly Lys Leu Arg Ser Pro Leu Leu Val
      355                      360                365
Phe Glu Arg Ile Asp Lys Glu Asp Gly Glu Phe Val Phe Lys Gly His
      370                      375                380
Val Phe Asn Thr Gln Arg Thr Val Val Glu Thr Ile Ser Leu Pro Leu
385                      390                395                400
Lys Gln Val Leu Glu Thr Val Ala Gln Ser His Leu Gly Gln Glu Ser
      405                      410                415
Gly Thr Lys Asn Ser Arg Ile Gly Gly Gly Ser
      420                      425

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(2) INFORMATIONS POUR LA SEQ ID NO: 887:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 869094..869357

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 887:

```

Val Lys Asn Ile Leu Gly Tyr Gly Phe Leu Gly Thr Phe Cys Leu Gly
1      5                      10                15
Ser Leu Thr Val Pro Ser Phe Ser Ile Thr Ile Thr Glu Lys Leu Ala
      20                      25                30
Ser Leu Glu Gly Lys Thr Glu Ser Leu Ala Pro Phe Ser His Ile Ser
      35                      40                45
Ser Phe Asn Ala Glu Leu Lys Glu Ala Asn Asp Val Leu Lys Ser Leu
      50                      55                60
Tyr Glu Glu Ala Leu Ser Leu Arg Ser Arg Gly Glu Thr Ser Gln Ala
65      70                      75                80
Val Trp Asp Glu Leu Arg Thr Asp
      85

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(2) INFORMATIONS POUR LA SEQ ID NO: 888:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 701 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 869270..871372

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 888:

Cys	Ser	Gln	Ile	Phe	Ile	Arg	Arg	Ser	Phe	Val	Ser	Pro	Phe	Ser	Arg
1				5					10					15	
Arg	Asp	Phe	Ala	Gly	Gly	Met	Gly	Arg	Val	Ala	Asn	Arg	Leu	Ile	Gly
			20					25					30		
Ala	Lys	Gln	Arg	Ile	Arg	Ser	Leu	Glu	Asp	Leu	Trp	Ser	Val	Glu	Val
		35					40					45			
Ala	Glu	Arg	Gly	Gly	Asp	Pro	Glu	Asp	Tyr	Ala	Leu	Trp	Asn	His	Pro
	50					55					60				
Glu	Thr	Thr	Ile	Tyr	Asn	Leu	Val	Ser	Asp	Tyr	Gly	Asp	Glu	Gln	Ser
65				70						75					80
Ile	Tyr	Val	Ile	Pro	Gln	Asn	Val	Gly	Ala	Met	Arg	Ile	Thr	Ala	Met
				85					90					95	
Ser	Lys	Leu	Val	Val	Pro	Lys	Glu	Gly	Phe	Glu	Glu	Cys	Leu	Ser	Leu
			100					105					110		
Leu	Leu	Met	Arg	Leu	Gly	Ile	Gly	Ile	Arg	Gln	Val	Ser	Pro	Trp	Ile
		115					120					125			
Lys	Glu	Leu	Tyr	Leu	Thr	Asn	Arg	Glu	Glu	Ser	Gly	Val	Leu	Gly	Ile
	130					135					140				
Phe	Gly	Ser	Arg	Gln	Glu	Leu	Asp	Ser	Leu	Pro	Met	Thr	Ala	His	Ile
145				150						155					160
Ala	Phe	Val	Leu	Ser	Ser	Lys	Asn	Leu	Asp	Ala	Arg	Ala	Asp	Val	Gln
				165					170					175	
Ala	Leu	Arg	Lys	Phe	Ala	Asn	Ser	Asp	Thr	Met	Leu	Ile	Asp	Phe	Ile
			180					185					190		
Gly	Gly	Lys	Val	Trp	Leu	Phe	Gly	Ala	Val	Ser	Glu	Ile	Thr	Glu	Leu
		195					200					205			
Leu	Lys	Ile	Tyr	Glu	Phe	Leu	Gln	Ser	His	Asn	Ile	Arg	Glu	Glu	His
	210					215					220				
Xaa	Ile	Val	Ser	Leu	Ser	Lys	Ile	Glu	Pro	Ser	Glu	Met	Leu	Xaa	Ile
225				230						235					240
Leu	Lys	Ala	Ala	Phe	Arg	Glu	Asp	Leu	Ala	Lys	Glu	Gly	Glu	Asp	Ser
				245					250					255	
Ser	Gly	Val	Gly	Leu	Lys	Val	Val	Pro	Leu	Gln	Asn	His	Gly	Arg	Ser
			260					265					270		
Leu	Phe	Leu	Ser	Gly	Ala	Leu	Pro	Ile	Val	Gln	Lys	Ala	Ile	Asp	Leu
		275					280					285			
Ile	Arg	Glu	Leu	Glu	Glu	Gly	Ile	Glu	Ser	Pro	Thr	Asp	Lys	Thr	Val
	290					295					300				
Phe	Trp	Tyr	His	Val	Lys	His	Ser	Asp	Pro	Gln	Glu	Leu	Ala	Ala	Leu
305				310						315					320
Leu	Ser	Gln	Val	His	Asp	Ile	Phe	Ser	Asn	Gly	Ala	Ser	Gly	Ala	Ser
				325					330					335	
Ser	Ser	Cys	Asp	Thr	Gly	Val	Val	Ser	Ser	Lys	Ala	Gly	Ser	Ser	Ser
			340					345					350		
Asn	Gly	Leu	Gly	Val	His	Ile	Asp	Thr	Ser	Leu	Arg	Ser	Ser	Val	Lys
		355					360					365			
Glu	Gly	Ser	Ala	Lys	Tyr	Gly	Ser	Phe	Ile	Ala	Asp	Ser	Lys	Thr	Gly
	370					375					380				
Thr	Leu	Ile	Met	Val	Ile	Glu	Lys	Glu	Ala	Leu	Pro	Lys	Ile	Lys	Met
385				390						395					400
Leu	Leu	Lys	Lys	Leu	Asp	Val	Pro	Lys	Lys	Met	Val	Arg	Ile	Glu	Val
				405					410					415	
Leu	Leu	Phe	Glu	Arg	Lys	Leu	Ser	Asn	Gln	Arg	Lys	Ser	Gly	Leu	Asn
			420					425					430		

Leu Leu Arg Leu Gly Glu Glu Val Cys Lys Gln Gly Thr Gln Ala Val  
 435 440 445  
 Ser Trp Ala Ser Gly Gly Ile Leu Glu Phe Leu Phe Lys Gly Gly Ala  
 450 455 460  
 Lys Gly Ile Val Pro Ser Tyr Asp Phe Ala Tyr Gln Phe Leu Met Ala  
 465 470 475 480  
 Gln Glu Asp Val Arg Ile Asn Ala Ser Pro Ser Val Val Thr Met Asn  
 485 490 495  
 Gln Thr Pro Ala Arg Ile Ala Ile Val Glu Glu Met Ser Ile Val Val  
 500 505 510  
 Ser Ser Asp Lys Asp Lys Ala Gln Tyr Asn Arg Ala Gln Tyr Gly Ile  
 515 520 525  
 Met Ile Lys Ile Leu Pro Val Ile Asn Ile Gly Glu Glu Asp Gly Lys  
 530 535 540  
 Ser Phe Ile Thr Leu Glu Thr Asp Ile Thr Phe Asp Ser Thr Gly Arg  
 545 550 555 560  
 Asn His Ala Asp Arg Pro Asp Val Thr Arg Arg Asn Ile Thr Asn Lys  
 565 570 575  
 Val Arg Ile Gln Asp Gly Glu Thr Val Ile Ile Gly Gly Leu Arg Cys  
 580 585 590  
 Asn Gln Thr Met Asp Ser Arg Asp Gly Ile Pro Phe Leu Gly Glu Leu  
 595 600 605  
 Pro Gly Ile Gly Lys Leu Phe Gly Met Asp Ser Ala Ser Asp Ser Gln  
 610 615 620  
 Thr Glu Met Phe Met Phe Ile Thr Pro Lys Ile Leu Asp Asn Pro Ser  
 625 630 635 640  
 Glu Thr Glu Glu Lys Leu Glu Cys Ala Phe Leu Ala Ala Arg Pro Gly  
 645 650 655  
 Glu Asn Asp Asp Phe Leu Arg Ala Leu Val Ala Gly Gln Gln Ala Ala  
 660 665 670  
 Lys Gln Ala Ile Glu Arg Lys Glu Ser Thr Val Trp Gly Glu Glu Ser  
 675 680 685  
 Ser Gly Ser Arg Gly Arg Val Glu Tyr Asp Gly Arg Glu  
 690 695 700

(2) INFORMATIONS POUR LA SEQ ID NO: 889:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 428 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 871299..872582

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 889:

Lys Glu Lys Ser Leu Pro Tyr Gly Glu Lys Asn Pro Pro Ala Leu Glu  
 1 5 10 15  
 Glu Gly Trp Ser Met Met Asp Gly Asn Lys Gly Thr Met Gln Asp Leu  
 20 25 30  
 Leu Asp Arg Leu Pro Tyr Ser Phe Leu Lys Lys Asn Tyr Leu Leu Pro  
 35 40 45  
 Val Glu Asp Leu Gly Asp Lys Ile Val Phe Ala Arg His Leu Lys Lys  
 50 55 60  
 Thr Pro Leu Glu Ala Leu Asp Glu Val Arg Leu Ile Thr Gln Lys Pro

65					70					75					80
Leu	Ser	Leu	Val	Ser	Lys	Glu	Glu	Ala	Glu	Ile	Ile	His	Gly	Leu	Gln
				85					90					95	
Lys	Leu	Tyr	Ser	Asp	Lys	Asp	Gly	Lys	Ala	Ser	Glu	Met	Leu	Gln	Ser
			100					105					110		
Met	Gln	Glu	Ala	Val	Val	Pro	Glu	Ser	Glu	Ser	Asp	Thr	Thr	Glu	Leu
		115					120					125			
Leu	Glu	Asn	Gln	Glu	Asn	Ser	Ala	Pro	Val	Val	Arg	Leu	Leu	Asn	Leu
	130					135					140				
Ile	Leu	Lys	Glu	Ala	Ile	Glu	Glu	Arg	Ala	Ser	Asp	Ile	His	Phe	Asp
145					150					155					160
Pro	Val	Glu	Asp	Leu	Leu	Arg	Ile	Arg	Tyr	Arg	Ile	Asp	Gly	Val	Leu
			165						170					175	
His	Asp	Arg	His	Ala	Pro	Pro	Asn	His	Leu	Arg	Ala	Ala	Leu	Ile	Thr
			180					185					190		
Arg	Ile	Lys	Val	Leu	Thr	Lys	Leu	Asp	Ile	Ala	Glu	His	Arg	Leu	Pro
		195					200					205			
Gln	Asp	Gly	Arg	Ile	Lys	Leu	Gln	Leu	Gly	Gly	Gln	Glu	Ile	Asp	Met
	210					215					220				
Arg	Val	Ser	Thr	Val	Pro	Val	Ile	His	Gly	Glu	Arg	Val	Val	Leu	Arg
225					230					235					240
Ile	Leu	Asp	Lys	Arg	Asn	Val	Ile	Leu	Asp	Ile	Arg	Gly	Leu	Cys	Met
			245						250					255	
Pro	Pro	Lys	Met	Glu	Thr	Ser	Phe	Arg	Lys	Ala	Ile	Gly	Val	Pro	Glu
			260				265						270		
Gly	Ile	Leu	Leu	Val	Thr	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Thr
	275					280						285			
Leu	Tyr	Ser	Val	Ile	Gln	His	Leu	Ser	Gly	Pro	Phe	Thr	Asn	Ile	Met
	290					295				300					
Thr	Ile	Glu	Asp	Pro	Pro	Glu	Tyr	Lys	Leu	Pro	Gly	Val	Ala	Gln	Ile
305					310					315					320
Ala	Val	Lys	Pro	Lys	Ile	Gly	Leu	Thr	Phe	Ser	Lys	Gly	Leu	Arg	His
			325						330					335	
Leu	Leu	Arg	Gln	Asp	Pro	Asp	Val	Leu	Met	Val	Gly	Glu	Ile	Arg	Asp
		340					345						350		
Gln	Glu	Thr	Ala	Glu	Ile	Ala	Ile	Gln	Ala	Ala	Leu	Thr	Gly	His	Leu
	355					360						365			
Val	Val	Ser	Thr	Leu	His	Thr	Asn	Asp	Ala	Val	Ser	Ala	Ile	Pro	Arg
	370					375					380				
Leu	Leu	Asp	Met	Gly	Val	Glu	Pro	Tyr	Leu	Leu	Ser	Ala	Thr	Met	Ile
385					390				395						400
Gly	Leu	Ser	Leu	Asn	Asp	Ser	Ser	Val	Glu	Phe	Val	Arg	Ile	Ala	Lys
			405					410					415		
Asn	Ser	Val	Trp	Pro	Met	Cys	Lys	Asn	Arg	Leu	Tyr				
		420						425							

(2) INFORMATIONS POUR LA SEQ ID NO: 890:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 144 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 872429..872860

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 890:

Cys	Cys	Phe	Cys	Asn	Pro	Ala	Ser	Phe	Arg	His	Gly	Ser	Arg	Ala	Leu
1				5					10					15	
Phe	Ile	Ile	Arg	Asn	Asn	Asp	Arg	Ala	Val	Ala	Gln	Arg	Leu	Val	Arg
			20					25					30		
Arg	Ile	Cys	Thr	His	Cys	Lys	Glu	Phe	Cys	Val	Ala	Asp	Val	Gln	Glu
		35					40					45			
Gln	Ala	Leu	Leu	Arg	Ala	Leu	Gly	Lys	Asp	Pro	Phe	Ala	Pro	Leu	Cys
	50					55					60				
Lys	Gly	Arg	Gly	Cys	Ser	Gln	Cys	Phe	Arg	Ser	Gly	Tyr	Lys	Gly	Arg
65					70					75					80
Gln	Gly	Ile	Tyr	Glu	Phe	Val	Asp	Val	Thr	Thr	Thr	Leu	Arg	Ser	Glu
				85					90					95	
Ile	Ala	Leu	Gly	Arg	Pro	Tyr	His	Ile	Leu	Arg	Gly	Val	Ala	Glu	Arg
			100					105					110		
Glu	Gly	Tyr	Cys	Pro	Leu	Leu	Glu	His	Gly	Val	Glu	Leu	Ala	Leu	Ala
		115					120					125			
Gly	Glu	Thr	Thr	Leu	Ser	Glu	Val	Leu	Arg	Val	Ala	Lys	Arg	Ser	Glu
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 891:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 347 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 872875..873915

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 891:

Met	Ala	Arg	Phe	Leu	Cys	Thr	Tyr	Leu	Asp	Gln	Ser	Glu	Lys	Lys	Arg
1				5					10					15	
Arg	Ser	Phe	Val	Glu	Ala	Phe	His	Gln	Arg	Glu	Ala	Arg	Glu	Leu	Leu
			20					25					30		
Ala	Ala	Gln	Gly	Ala	Arg	Ile	Leu	Asp	Ile	Arg	Lys	Val	Arg	Glu	Arg
		35					40					45			
Asn	Tyr	Arg	Val	Thr	Thr	Thr	Glu	Leu	Val	Ile	Phe	Thr	Lys	Gln	Leu
	50					55					60				
Ala	Leu	Leu	Leu	Arg	Ser	Gly	Ile	Ser	Leu	Tyr	Asp	Ala	Leu	Thr	Ser
65					70					75					80
Leu	Arg	Asp	Gln	Tyr	Gln	Gly	His	Ala	Leu	Ala	Gly	Val	Leu	Thr	Ser
			85					90					95		
Leu	Met	Glu	Ala	Leu	Arg	Ser	Gly	Gly	Val	Phe	Ser	Glu	Ala	Leu	Ala
		100						105					110		
Arg	Leu	Pro	His	Ile	Phe	Asp	Ser	Phe	Tyr	Gln	Asn	Ser	Val	Arg	Ser
		115					120					125			
Gly	Glu	Ser	Ile	Gly	Asn	Leu	Glu	Gly	Ala	Leu	Met	Asn	Ile	Ile	Lys
	130					135					140				
Val	Leu	Glu	Glu	Lys	Glu	Lys	Leu	Ser	Lys	Ser	Leu	Ala	Ala	Ala	Leu
145					150					155					160
Ser	Tyr	Pro	Ala	Ile	Leu	Leu	Val	Phe	Ser	Cys	Ala	Val	Val	Val	Phe
			165						170					175	
Phe	Leu	Ile	Gly	Val	Ile	Pro	Thr	Leu	Lys	Glu	Thr	Phe	Glu	Asp	Met



## (2) INFORMATIONS POUR LA SEQ ID NO: 893:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 874028..874438

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 893:

Gln	Ala	Val	Phe	Lys	Arg	Phe	Asn	Tyr	Arg	Arg	Glu	Thr	Val	Lys	Lys
1				5					10					15	
Thr	Lys	Lys	Arg	Lys	Gln	Ser	Ile	Thr	Leu	Val	Glu	Met	Met	Val	Val
			20					25						30	
Ile	Thr	Leu	Ile	Gly	Ile	Ile	Gly	Gly	Ala	Leu	Ala	Phe	Asn	Met	Arg
		35					40					45			
Gly	Ser	Leu	Gln	Lys	Gly	Lys	Ile	Phe	Gln	Thr	Glu	Gln	Asn	Cys	Ala
	50					55					60				
Arg	Val	Tyr	Asp	Val	Leu	Met	Met	Glu	Tyr	Ala	Ser	Gly	Asn	Leu	Ser
65					70					75				80	
Leu	Lys	Glu	Val	Ile	Ala	Asn	Lys	Glu	Ala	Ile	Leu	Glu	Asp	Ser	Ala
				85					90					95	
Trp	Cys	Lys	Glu	Ile	Lys	Lys	Leu	Leu	Lys	Asp	Ala	Trp	Gly	Glu	Asp
			100					105					110		
Leu	Leu	Val	Lys	Met	Asn	Asp	Lys	Gly	Asp	Asp	Ile	Val	Val	Phe	Ser
		115					120					125			
Lys	Lys	Val	Arg	Asn	Glu	Gln	Arg	Gly							
		130					135								

## (2) INFORMATIONS POUR LA SEQ ID NO: 894:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 874778..875386

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 894:

Arg	Arg	Arg	Gln	Ala	Phe	Met	Phe	Gly	Arg	Arg	Tyr	Gly	Gly	Leu	Ile
1				5					10					15	
Pro	Trp	Pro	Glu	Lys	Gly	Ser	Arg	Cys	Thr	Glu	Val	Phe	Met	Phe	Arg
			20					25					30		
Lys	Ile	Lys	Lys	Lys	Arg	Ala	Phe	Leu	Leu	Ser	Glu	Leu	Leu	Ile	Ala
		35					40					45			
Cys	Val	Leu	Ile	Ser	Leu	Leu	Leu	Gly	Ser	Leu	Gly	Tyr	Trp	Thr	Arg
	50					55					60				
Arg	Ile	Trp	Ile	Ser	His	Lys	Glu	Lys	Glu	His	Val	Tyr	Arg	Ile	Phe
65					70					75				80	
Leu	Asn	Glu	Ser	Lys	Thr	Tyr	Arg	Phe	Leu	Arg	Gly	Thr	Phe	Leu	Ser

				85					90				95		
Thr	Ile	Ala	Met	Glu	Ala	Gln	Glu	Glu	Leu	Val	Phe	Ser	Phe	Asp	Arg
			100					105					110		
Gly	Val	Tyr	Val	Asp	Pro	His	Leu	Ala	Gly	Val	Val	Gln	Gly	Thr	Leu
		115					120					125			
His	Tyr	Asp	Pro	Ile	Thr	Gln	Glu	Ile	Ser	Leu	Ile	Val	Ala	Ser	Glu
	130					135					140				
Arg	Glu	Glu	Ala	Arg	Gln	Glu	Lys	Ile	Ser	Leu	Trp	Thr	His	Val	Leu
145				150						155					160
Ser	Met	Glu	Trp	Lys	Val	Leu	Arg	Tyr	Gln	Gly	Leu	Gly	Glu	Gly	Pro
			165					170						175	
Asp	Arg	Val	Tyr	Leu	Thr	Leu	Val	Arg	Lys	Val	Gly	Ala	Leu	Pro	Pro
		180					185						190		
Arg	Thr	Leu	Ser	Tyr	Ile	Phe	Ala	Val	Gly	Arg					
		195				200									

(2) INFORMATION POUR LA SEQ ID NO: 895:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 875774..876382

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 895:

Val	Ala	Thr	Arg	Thr	Val	Cys	Ala	Val	Arg	Ala	His	Ser	Ser	Arg	Cys
1				5					10					15	
Gly	Val	Pro	Gly	Lys	Lys	Ala	Leu	Pro	Ala	Gln	Lys	Glu	Glu	Asn	Asn
			20					25					30		
Ser	Pro	Thr	Pro	Lys	Pro	Gly	Ser	Glu	Trp	Pro	Glu	Asn	Gly	Ser	Pro
		35				40						45			
Pro	Glu	Lys	Glu	Thr	Arg	Trp	Val	Glu	Lys	Lys	Pro	Lys	Ser	Asn	Lys
	50					55					60				
Thr	Thr	Arg	Ser	Leu	Leu	His	Phe	Leu	Asn	Tyr	Glu	Glu	Lys	Asn	Thr
65				70						75				80	
Asn	Gln	Gly	Arg	Leu	Asn	Leu	Leu	Phe	Thr	Asp	Pro	Val	Ile	Leu	Gln
				85					90					95	
Ala	Phe	Ile	Asn	Asn	Ser	Lys	Ala	Tyr	Ser	Glu	Leu	Glu	Arg	Val	Arg
			100					105					110		
Gln	Glu	Val	Trp	Glu	Ser	Ala	Arg	Gln	Gln	Glu	Leu	Ala	Ile	Lys	Ala
		115					120					125			
Tyr	Gly	Gln	Ala	Ala	Ala	Leu	Glu	Ile	Phe	Lys	Thr	Arg	Thr	Asp	Phe
	130					135					140				
Arg	Thr	Glu	Leu	Gln	Asp	Lys	Thr	Gln	Val	Ile	Leu	His	Arg	Tyr	Asp
145					150					155				160	
Leu	Leu	Ser	Leu	Leu	Asn	Lys	Lys	Val	Phe	Asp	Tyr	Thr	Leu	Gly	Thr
				165					170					175	
Ala	Gly	Asp	Tyr	Ile	Phe	Val	Val	Asp	Pro	Glu	Asn	Glu	Gly	Val	Asn
			180					185					190		
Arg	Ser	Arg	Cys	Val	Ser	Arg	Arg	Lys	Thr	Asn					
		195					200								



(2) INFORMATIONS POUR LA SEQ ID NO: 896:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 270 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(877000..877809)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 896:

Phe	Gln	Lys	Pro	Ala	Asp	Tyr	Val	Trp	Thr	Val	Phe	Leu	Leu	Leu	Ala	1	5	10	15
Ala	Arg	Ile	Leu	Ser	Met	Leu	Ser	Ile	Ile	Pro	Phe	Leu	Gly	Ala	Lys	20	25	30	
Leu	Phe	Pro	Ser	Pro	Ile	Lys	Ile	Gly	Ile	Ala	Leu	Ser	Trp	Met	Gly	35	40	45	
Leu	Leu	Leu	Pro	Gln	Val	Ile	Gln	Asp	Ser	Thr	Ile	Val	His	Tyr	Gln	50	55	60	
Asp	Leu	Asp	Ile	Phe	Tyr	Ile	Leu	Leu	Ile	Lys	Glu	Ile	Leu	Ile	Gly	65	70	75	80
Val	Leu	Ile	Gly	Phe	Leu	Phe	Ser	Phe	Pro	Phe	Tyr	Ala	Ala	Gln	Ser	85	90	95	
Ala	Gly	Ser	Phe	Ile	Thr	Asn	Gln	Gln	Gly	Ile	Gln	Gly	Leu	Glu	Gly	100	105	110	
Ala	Thr	Ser	Leu	Val	Ser	Ile	Glu	Gln	Thr	Ser	Pro	His	Gly	Ile	Phe	115	120	125	
Tyr	His	Tyr	Phe	Val	Thr	Ile	Val	Phe	Trp	Leu	Ala	Gly	Gly	His	Arg	130	135	140	
Ile	Ile	Leu	Ser	Val	Leu	Leu	Gln	Ser	Leu	Glu	Ile	Ile	Pro	Leu	His	145	150	155	160
Ala	Val	Phe	Pro	Glu	Ser	Met	Met	Ser	Leu	Arg	Ala	Pro	Met	Trp	Ile	165	170	175	
Ala	Ile	Leu	Lys	Met	Cys	Gln	Leu	Cys	Leu	Ile	Met	Thr	Ile	Gln	Leu	180	185	190	
Ser	Ala	Pro	Ala	Ala	Val	Ala	Met	Leu	Met	Ser	Asp	Leu	Phe	Leu	Gly	195	200	205	
Ile	Ile	Asn	Arg	Met	Ala	Pro	Gln	Val	Gln	Val	Ile	Tyr	Leu	Leu	Ser	210	215	220	
Ala	Leu	Lys	Ala	Phe	Met	Gly	Leu	Leu	Phe	Leu	Thr	Leu	Ala	Trp	Trp	225	230	235	240
Phe	Ile	Val	Lys	Gln	Ile	Asp	Tyr	Phe	Thr	Leu	Ala	Trp	Phe	Lys	Glu	245	250	255	
Ile	Pro	Thr	Met	Leu	Phe	Gly	Ala	His	Pro	Pro	Lys	Val	Leu			260	265	270	

(2) INFORMATIONS POUR LA SEQ ID NO: 897:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(877876..878151)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 897:

Met	Leu	Ala	Thr	Ser	Phe	Lys	Ser	Ile	Leu	Phe	Glu	Tyr	Ser	Tyr	Glu
1				5					10					15	
Ala	Leu	Leu	Leu	Ile	Leu	Ile	Ile	Ser	Ala	Pro	Pro	Ile	Ile	Leu	Ala
			20					25					30		
Ser	Val	Val	Gly	Ile	Met	Val	Ala	Ile	Phe	Gln	Ala	Ala	Thr	Gln	Ile
		35					40					45			
Gln	Glu	Gln	Thr	Phe	Ala	Phe	Ala	Ile	Lys	Leu	Val	Val	Ile	Phe	Gly
	50					55					60				
Thr	Leu	Met	Ile	Thr	Gly	Gly	Trp	Leu	Cys	Ser	Met	Ile	Leu	Arg	Phe
65					70					75					80
Ala	Ala	Gln	Ile	Phe	Gln	Asn	Phe	Tyr	Lys	Trp	Lys				
					85					90					

(2) INFORMATIONS POUR LA SEQ ID NO: 898:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 225 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(878172..878846)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 898:

Ser	Glu	Thr	Tyr	Pro	Asp	Leu	Thr	Thr	Gln	Ala	Val	Ile	Leu	Leu	Phe
1				5					10					15	
Leu	Ala	Leu	Ser	Pro	Phe	Leu	Val	Met	Leu	Leu	Thr	Ser	Tyr	Leu	Lys
			20					25				30			
Ile	Ile	Ile	Thr	Leu	Val	Leu	Leu	Arg	Asn	Ala	Leu	Gly	Val	Gln	Gln
		35					40					45			
Thr	Pro	Pro	Ser	Gln	Val	Leu	Asn	Gly	Ile	Ala	Leu	Ile	Leu	Ser	Ile
	50					55					60				
Tyr	Val	Met	Phe	Pro	Thr	Gly	Val	Ala	Met	Tyr	His	Asp	Ala	Lys	Lys
65					70					75					80
Gly	Ile	Glu	Ser	Ser	Ala	Val	Pro	Arg	Asp	Leu	Phe	Ser	Ala	Glu	Gly
				85					90					95	
Ala	Glu	Thr	Val	Phe	Val	Ala	Leu	Asn	Lys	Ser	Lys	Glu	Pro	Leu	Arg
			100					105					110		
Ser	Phe	Leu	Ile	Lys	Asn	Thr	Pro	Lys	Pro	Gln	Ile	Gln	Ser	Phe	Tyr
		115					120					125			
Lys	Ile	Ser	Gln	Lys	Thr	Phe	Pro	Pro	Glu	Leu	Arg	Gln	Gln	Leu	Thr
	130					135					140				
Pro	Ser	Asp	Phe	Met	Ile	Ile	Pro	Ala	Phe	Ile	Met	Gly	Gln	Ile	
145					150				155					160	
Lys	Asn	Ala	Phe	Glu	Ile	Gly	Val	Leu	Ile	Tyr	Leu	Pro	Phe	Phe	Val
			165						170					175	
Ile	Asp	Leu	Val	Thr	Ala	Asn	Val	Leu	Val	Ala	Met	Gln	Met	Met	Met
			180					185				190			
Leu	Ser	Pro	Leu	Ser	Ile	Ser	Leu	Pro	Leu	Lys	Leu	Leu	Leu	Val	Val
		195					200					205			

Met Val Asp Gly Trp Thr Leu Leu Leu Glu Gly Leu Met Ile Ser Phe  
 210 215 220  
 Lys  
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 899:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 93 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 878883..879161

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 899:

Gln Val Leu Ser Phe Tyr Arg Trp Ser Ile Arg Trp Thr Thr Lys Arg  
 1 5 10 15  
 Leu Phe Ser Phe Phe Trp Arg Cys Trp Lys Phe Leu Leu Arg Ser Gly  
 20 25 30  
 Arg Ala Arg Lys Ala Arg Arg Gly Ala Leu Cys Cys Gly Thr Ser Thr  
 35 40 45  
 Gly Glu Ala Ile Gly Ser Ala Lys Asn Ala Glu Lys Glu Glu Asn Ser  
 50 55 60  
 Asn Asn Gln Ser His Lys Ile Gln Tyr Leu Val Phe Leu Ala Leu Arg  
 65 70 75 80  
 Leu Ile Cys Cys Arg Ser Val Arg Arg Phe Phe Met Phe  
 85 90

(2) INFORMATIONS POUR LA SEQ ID NO: 900:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 223 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(879105..879773)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 900:

Met Lys Phe Phe Ser Leu Ile Tyr Lys Asp Gln Glu Val Val Pro Asn  
 1 5 10 15  
 Lys Lys Val Leu Ser Pro Asp Ala Tyr Thr Ala Val Leu Thr Ala Gln  
 20 25 30  
 Glu Leu Leu Glu Lys Thr Gln Glu Asp Cys Glu Ala Tyr Thr Gln Asn  
 35 40 45  
 Thr His Glu Glu Cys Ala Lys Leu Arg Glu Glu Ala Lys Asn Gln Gly  
 50 55 60  
 Phe Gln Glu Gly Ser Lys Ala Trp Ser Lys Gln Leu Ala Phe Leu Ile  
 65 70 75 80  
 Thr Glu Thr Gln Ala Met Arg Glu Gln Ile Lys Ala Ser Leu Val Pro

				85					90					95					
Leu	Ala	Ile	Ala	Ser	Val	Lys	Lys	Ile	Ile	Gly	Lys	Glu	Leu	Glu	Thr				
			100					105					110						
Lys	Pro	Glu	Thr	Val	Val	Ser	Ile	Ile	Ser	Glu	Ser	Leu	Lys	Asp	Leu				
		115					120					125							
Thr	Gln	Asn	Lys	Arg	Ile	Val	Ile	His	Ile	Asn	Pro	Gln	Asp	Leu	Ala				
		130				135				140									
Ile	Val	Glu	Gln	His	Arg	Pro	Glu	Leu	Lys	Lys	Leu	Val	Glu	Tyr	Ala				
145					150					155					160				
Asp	Val	Leu	Leu	Leu	Ser	Pro	Lys	Ala	Ser	Val	Ser	Pro	Gly	Gly	Cys				
			165						170						175				
Ile	Ile	Glu	Thr	Glu	Thr	Gly	Ile	Val	Asn	Ala	Gln	Leu	Asp	Val	Gln				
			180					185					190						
Leu	Ala	Ala	Leu	Glu	Gln	Ala	Phe	Ser	Ala	Ile	Leu	Lys	His	Lys	Lys				
		195				200						205							
Pro	Ala	Asp	Ala	Ser	Thr	Thr	Asp	Gln	Pro	Gln	Ser	Lys	Lys	Asp					
		210				215						220							

(2) INFORMATIONS POUR LA SEQ ID NO: 901:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(880052..880885)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 901:

Val	Thr	Ala	Asn	Thr	Phe	Gly	Ile	Leu	Asn	Ile	Leu	Met	Lys	Gln	Ala				
1				5				10						15					
Lys	Ala	Asp	Asp	Leu	Ala	Gln	Phe	Leu	Pro	Glu	His	Leu	Leu	Leu	Asp				
		20						25					30						
Ser	Pro	His	His	Gln	Asp	Ile	Pro	Leu	Gln	Ser	Leu	Ser	Phe	Asn	Met				
		35				40						45							
Arg	Trp	Leu	Ala	Thr	Ile	His	Pro	Ser	Trp	Ile	Ser	Val	Ala	Met	Lys				
	50				55					60									
Glu	Phe	Pro	Pro	Val	Val	Gln	Ser	Gln	Leu	Leu	Ala	Trp	Leu	Pro	Leu				
65				70					75					80					
Pro	Leu	Thr	Gln	Glu	Leu	Leu	Pro	Leu	Leu	Asp	Ser	Gly	Val	Thr	Pro				
			85					90					95						
Ala	Thr	Lys	Arg	Cys	Leu	Asp	Phe	Gly	Ala	Phe	Tyr	Leu	Leu	Asp	Leu				
		100						105					110						
Leu	Ser	Lys	Lys	Val	Arg	Pro	Pro	Gly	Ile	Thr	Glu	Glu	Ile	Phe	Leu				
		115				120						125							
Pro	Ala	Ser	Pro	Phe	Asn	Ala	Met	Leu	Tyr	Tyr	Val	Gly	Pro	Thr	Lys				
	130				135						140								
Met	Ala	Leu	Ile	Asn	Cys	Leu	Gly	Leu	Tyr	Thr	Leu	Ala	Gln	Glu	Met				
145				150					155					160					
Arg	Asn	Val	Val	Asp	Arg	Val	Val	Ile	Asp	Arg	Val	Gln	Arg	Val	Leu				
			165					170					175						
Ser	Glu	Thr	Glu	Arg	Met	Phe	Leu	Asn	Tyr	Cys	Lys	Thr	His	Pro	Met				
		180						185					190						
Lys	His	Leu	Glu	Pro	Thr	Ala	Phe	Leu	Ala	Ser	Trp	Glu	Glu	Asp	Gln				
		195				200						205							

```

Ala Leu Arg His Phe Ile His Val Gln Gly Leu Arg Phe Leu Ala Arg
 210                      215                      220
Ala Leu Ala Lys Glu Asp Ser Ser Phe Leu Trp Tyr Phe Ile Arg Arg
225                      230                      235                      240
Leu Asp Val Gly Arg Gly Tyr Ile Phe Glu Lys Ala Leu Gln Ser Ser
                      245                      250                      255
Ile Asp Ser Pro His Asn Glu Tyr Phe Arg Glu Arg Leu Glu His Cys
                      260                      265                      270
Ile Ser Ile Leu Val Gln
                      275

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 902:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 314 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(880889..881830)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 902:

```

Phe Ile Leu Ala Leu Phe Phe Cys Ser Ala Cys Asp Ser Arg Ser Met
 1                      5                      10                      15
Ile Thr His Gly Leu Ser Gly Arg Asp Ala Asn Glu Ile Val Val Leu
                      20                      25                      30
Leu Val Ser Lys Gly Val Ala Ala Gln Lys Val Pro Gln Ala Ala Ser
                      35                      40                      45
Ser Thr Gly Gly Ser Gly Glu Gln Leu Trp Asp Ile Ser Val Pro Ala
 50                      55                      60
Ala Gln Ile Thr Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro
65                      70                      75                      80
Arg Met Lys Gly Thr Ser Leu Leu Asp Leu Phe Ser Lys Gln Gly Leu
                      85                      90                      95
Val Pro Ser Glu Met Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser
                      100                      105                      110
Glu Gln Met Ala Thr Thr Ile Arg Lys Met Asp Gly Ile Val Asp Ala
                      115                      120                      125
Ser Val Gln Ile Ser Phe Ser Pro Glu Glu Asp Gln Arg Pro Leu Thr
 130                      135                      140
Ala Ser Val Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser
145                      150                      155                      160
Ile Met Val Ser Lys Ile Lys Arg Leu Val Ala Ser Ala Val Pro Gly
                      165                      170                      175
Leu Tyr Pro Glu Asn Val Ser Val Val Ser Asp Arg Ala Ser Tyr Ser
                      180                      185                      190
Asp Ile Thr Ile Asn Gly Pro Trp Gly Leu Ser Asp Glu Met Asp Tyr
 195                      200                      205
Val Ser Val Trp Gly Ile Ile Leu Ala Lys His Ser Leu Thr Lys Phe
 210                      215                      220
Arg Leu Val Phe Tyr Phe Leu Ile Leu Leu Leu Phe Ile Leu Ser Cys
225                      230                      235                      240
Gly Leu Leu Trp Val Ile Trp Lys Thr His Thr Leu Ile Ser Ala Leu
                      245                      250                      255
Gly Gly Thr Lys Gly Phe Phe Asp Pro Ala Pro Tyr Ser Gln Leu Ser

```

```

                260                265                270
Phe Thr Gln Asn Lys Pro Ala Pro Lys Glu Thr Pro Gly Ala Ala Glu
      275                280                285
Gly Ala Glu Ala Gln Thr Ala Ser Glu Gln Pro Pro Lys Glu Asn Ala
      290                295                300
Glu Lys Gln Glu Glu Asn Asn Glu Asp Ala
305                310

```

(2) INFORMATIONS POUR LA SEQ ID NO: 903:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 319 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(881948..882904)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 903:

```

Lys Met Thr Asp Ser Glu Ser Pro Thr Pro Lys Lys Ser Ile Pro Ala
1      5      10      15
Arg Phe Pro Lys Trp Leu Arg Gln Lys Leu Pro Leu Gly Arg Val Phe
      20      25      30
Ala Gln Thr Asp Asn Thr Ile Lys Asn Lys Gly Leu Pro Thr Val Cys
      35      40      45
Glu Glu Ala Ser Cys Pro Asn Arg Thr His Cys Trp Ser Arg His Thr
      50      55      60
Ala Thr Tyr Leu Ala Leu Gly Asp Ala Cys Thr Arg Arg Cys Gly Phe
      65      70      75      80
Cys Asp Ile Asp Phe Thr Arg Asn Pro Leu Pro Pro Asp Pro Glu Glu
      85      90      95
Gly Ala Lys Ile Ala Glu Ser Ala Lys Ala Leu Gly Leu Lys His Ile
      100     105     110
Val Ile Thr Met Val Ser Arg Asp Asp Leu Glu Asp Gly Gly Ala Ser
      115     120     125
Ala Leu Val His Ile Ile Glu Thr Leu His Thr Glu Leu Pro Thr Ala
      130     135     140
Thr Ile Glu Val Leu Ala Ser Asp Phe Glu Gly Asn Ile Ala Ala Leu
      145     150     155     160
His His Leu Leu Asp Thr His Ile Ala Ile Tyr Asn His Asn Val Glu
      165     170     175
Thr Val Glu Arg Leu Thr Pro Phe Val Arg His Lys Ala Thr Tyr Arg
      180     185     190
Arg Ser Leu Met Met Leu Glu Asn Ala Ala Lys Tyr Leu Pro Asn Leu
      195     200     205
Met Thr Lys Ser Gly Ile Met Val Gly Leu Gly Glu Gln Glu Ser Glu
      210     215     220
Val Lys Gln Thr Leu Lys Asp Leu Ala Asp His Gly Val Lys Ile Val
      225     230     235     240
Thr Ile Gly Gln Tyr Leu Arg Pro Ser Arg Arg His Ile Pro Val Lys
      245     250     255
Ser Tyr Val Ser Pro Glu Thr Phe Asp Tyr Tyr Arg Ser Val Gly Glu
      260     265     270
Ser Leu Gly Leu Phe Ile Tyr Ala Gly Pro Phe Val Arg Ser Ser Phe
      275     280     285

```

```

Asn Ala Asp Ser Val Phe Glu Ala Met Arg Gln Gly Lys Pro Gln Pro
 290                295                300
Leu Arg Tyr Phe Arg Thr Lys Ile Ser His Ile Thr Cys Ser Phe
305                310                315

```

(2) INFORMATIONS POUR LA SEQ ID NO: 904:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(882901..883794)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 904:

```

Thr Ser Lys Lys Ser Leu Lys Lys Trp Pro Leu Leu Ala Glu Gly Val
 1          5          10          15
Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val
          20          25          30
Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Asn Pro Asp
          35          40          45
Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe
 50          55          60
Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val
 65          70          75          80
Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val
          85          90          95
Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala
          100          105          110
Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met
          115          120          125
Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys
 130          135          140
Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg
 145          150          155          160
Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser
          165          170          175
Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr
          180          185          190
Ala Ala Gln Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe
          195          200          205
Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala
 210          215          220
Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val
 225          230          235          240
Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val
          245          250          255
Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His
          260          265          270
Pro Thr Leu Ala Glu Val Trp Ala Glu Ser Ala Leu Leu Ala Val Asp
          275          280          285
Thr Pro Leu His Met Pro Pro Ala Lys Lys
 290                295

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 905:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 212 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(883661..884296)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 905:

```

Met Asn Glu Ala Phe Asp Cys Val Val Ile Gly Ala Gly Pro Gly Gly
1      5      10      15
Tyr Val Ala Ala Ile Thr Ala Ala Gln Ala Gly Leu Lys Thr Ala Leu
      20      25      30
Ile Glu Lys Arg Glu Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
      35      40      45
Pro Ser Lys Ala Leu Leu Ala Gly Ala Glu Val Val Thr Gln Ile Arg
      50      55      60
His Ala Asp Gln Phe Gly Ile His Val Glu Gly Phe Ser Ile Asn Tyr
65      70      75      80
Pro Ala Met Val Gln Arg Lys Asp Ser Val Val Arg Ser Ile Arg Asp
      85      90      95
Gly Leu Asn Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Phe Ser Gly
      100     105     110
Xaa Gly Ser Leu Ile Ser Ser Thr Glu Val Lys Ile Leu Gly Glu Asn
      115     120     125
Pro Ser Val Ile Lys Ala His Ser Ile Ile Leu Ala Thr Gly Ser Glu
      130     135     140
Pro Arg Ala Phe Pro Gly Ile Pro Phe Ser Ala Glu Ser Pro Arg Ile
145     150     155     160
Leu Cys Ser Thr Gly Val Leu Asn Leu Lys Glu Ile Pro Gln Lys Met
      165     170     175
Ala Ile Ile Gly Gly Arg Cys Asp Arg Leu Arg Ile Arg Phe Leu Ile
      180     185     190
Pro Tyr Val Arg Leu Arg Ser Phe Cys Asp Arg Ser Lys Leu Ser Asn
      195     200     205
Pro Cys Phe Glu
      210

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 906:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 163 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(884508..884996)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 906:



Arg	Xaa	Asp	Leu	Met	Pro	Phe	Ala	Lys	Glu	Ala	Asp	Leu	Gln	Arg	Thr
1				5					10					15	
Cys	Trp	Lys	Cys	Glu	Gly	Ser	Val	Ser	Ala	Cys	Met	Pro	Gln	Cys	Pro
			20					25					30		
Tyr	Cys	Ser	Ala	Phe	Leu	Gln	Asp	Pro	Pro	Val	Thr	Ser	Lys	Gly	Phe
		35					40					45			
Ser	Ser	Cys	His	Ile	Thr	Phe	Pro	Ser	Glu	Ala	Ser	Lys	Lys	Asn	Gly
	50					55					60				
Asp	Ser	Asp	Leu	Phe	Ala	Val	Ser	Ser	Glu	Asp	Trp	Glu	Ala	Val	Leu
65					70					75					80
Asn	Ser	Gln	Asn	Thr	Phe	Glu	Glu	Pro	Val	Gln	Glu	Pro	Ala	Pro	Ser
				85					90					95	
Gln	Trp	Asp	Trp	Leu	Gln	Tyr	Trp	Pro	Thr	Ala	Ala	Leu	Phe	Leu	Gly
			100					105					110		
Cys	Gly	Phe	Leu	Thr	Phe	Ser	Leu	Met	Ile	Leu	Leu	Phe	Ser	Thr	Asp
		115					120					125			
Ser	Gly	Leu	Val	Leu	Ser	Trp	Pro	Lys	Asn	Arg	Ser	Tyr	Ile	Tyr	Ala
	130					135					140				
Leu	Val	Gly	Ile	Leu	Leu	Ala	Tyr	Arg	Gly	Tyr	Arg	Ser	Leu	Pro	Glu
145					150					155					160
His	Ser	Lys													

(2) INFORMATIONS POUR LA SEQ ID NO: 907:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(885166..888777)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 907:

Gln	Arg	Leu	Ile	Leu	Met	Ile	Leu	Asn	Ser	Leu	Ser	Met	Phe	Arg	His
1				5					10					15	
Gln	Ala	Thr	Arg	Phe	Leu	Gln	Asp	Asn	Arg	Asp	Ser	Ile	Ala	Val	Ser
			20					25					30		
Phe	Ser	Lys	Asn	Thr	Tyr	Lys	Ile	Thr	Ile	Pro	Asp	Glu	Asp	Ser	Pro
		35					40					45			
Asp	Gly	Glu	Trp	Ile	Ser	Thr	Leu	Ser	Phe	Asn	Asp	Glu	Glu	Arg	Leu
	50					55					60				
Ser	Phe	Ala	Ala	Cys	Ser	Cys	Pro	Asp	Gly	Asp	Cys	Cys	Glu	His	Leu
65					70					75					80
Leu	Thr	Ala	Thr	Leu	Ala	Ala	Tyr	Asp	Pro	Thr	Glu	Gly	Ala	Leu	Leu
				85					90					95	
His	Val	Lys	Phe	Glu	Ser	Ser	Phe	Trp	Trp	Gly	Leu	Phe	Tyr	Gln	Leu
			100					105					110		
Phe	Leu	Ser	Lys	Ala	Pro	Leu	His	Ala	Pro	Gly	Asp	Lys	Val	Tyr	Thr
		115					120					125			
Ile	Gln	Ser	Gln	Gln	Leu	Ser	Val	Ser	Leu	Gln	Cys	Leu	Ser	Ala	Glu
	130					135					140				
Ala	Leu	Thr	Tyr	Trp	Leu	Pro	Ile	Val	His	Thr	Ser	Pro	Glu	Pro	Gln
145					150					155					160
Thr	Ile	Ser	Lys	Glu	Thr	Phe	Ser	Gln	Ser	Ala	Leu	Tyr	Arg	Ile	Ala

				165					170					175	
Arg	Glu	Leu	Phe	Met	Phe	Ser	Gln	Lys	Gly	Ala	Ser	Leu	Val	Ile	Gln
			180					185					190		
Glu	Asn	Pro	Gln	Gly	Phe	Pro	Ser	Leu	Phe	Ser	Leu	Gln	Trp	Glu	Gly
		195					200					205			
Ile	Ala	Leu	Ser	Ile	Glu	Val	Leu	Asp	Val	Asp	Thr	Leu	Lys	Ala	Leu
	210				215						220				
Phe	Pro	Leu	Leu	Glu	Phe	Ser	Gln	Thr	Ser	Leu	Tyr	Ser	Gly	Glu	Pro
225				230						235					240
Tyr	Leu	Leu	His	Asn	Val	His	Val	Val	Pro	Glu	Gln	Ala	Arg	Ile	Tyr
			245						250					255	
Phe	Thr	Lys	Glu	Tyr	Pro	Pro	Leu	Pro	Lys	Ser	Ile	Lys	Glu	Tyr	Gln
		260						265					270		
Glu	Thr	Val	Leu	Gly	Pro	Ile	Lys	Tyr	Phe	Ala	Glu	Ala	Lys	Lys	Cys
		275					280					285			
Thr	Ser	Ile	Pro	Lys	Thr	Leu	Ser	Leu	Pro	Ile	His	Ile	Ile	Pro	Ala
	290				295						300				
Leu	Asp	Arg	Ser	Phe	Arg	Glu	His	Leu	Leu	Ser	Gln	Leu	Cys	Tyr	Glu
305				310						315					320
Thr	Glu	Glu	Arg	Pro	Ile	His	Tyr	Ala	Ile	His	Phe	Leu	Arg	Asp	Ala
			325					330						335	
Ser	Leu	Ser	Phe	Ser	Ala	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	Leu	Ser	Glu
			340					345					350		
Gly	His	Ile	Ile	Tyr	Pro	Glu	Phe	Cys	Tyr	Ile	Pro	Asn	Lys	Gly	Leu
	355					360					365				
Leu	Ala	Val	Ser	Gly	Leu	Leu	Ser	Pro	Glu	Ser	Ser	Phe	Thr	Ile	Arg
	370				375						380				
Ser	Asp	His	Ile	Glu	Asn	Phe	Leu	Asp	Glu	Tyr	Gly	Pro	Phe	Ile	Lys
385				390						395					400
Glu	Pro	Gly	Phe	Glu	Thr	Phe	Ser	Asn	Gln	Ser	Pro	Val	Gly	Ser	Leu
			405					410						415	
Ser	Tyr	Asn	Val	Thr	Glu	Gln	Gly	Val	Leu	Leu	Phe	His	Tyr	Asp	Thr
		420					425						430		
Gly	Asn	Ala	Ala	Asp	Ile	Glu	Leu	Arg	Phe	Gly	Lys	Trp	Thr	Tyr	Tyr
	435				440							445			
Ser	Arg	Gln	Gly	Phe	Phe	Leu	Asn	Ser	Arg	Leu	Asp	Leu	Ala	Leu	Gln
	450				455						460				
Asp	Gly	Leu	Thr	Ile	Glu	Ala	Pro	Gln	Val	Ala	Asp	Phe	Ile	Leu	Thr
465				470						475					480
His	Glu	Val	Ala	Leu	Lys	Ser	Ile	Pro	Asn	Phe	Phe	Ala	Ala	Gln	Pro
			485						490					495	
Pro	Leu	Lys	Ser	Ile	Arg	Phe	Glu	Val	His	Lys	Glu	Lys	Lys	Gly	Ser
		500					505						510		
Gly	Ile	Tyr	Leu	Gln	Pro	Ile	Phe	Glu	Gly	Leu	Glu	His	Glu	Ser	Cys
	515														

Phe	Leu	Asn	Leu	Asp	Asn	Cys	Leu	Phe	Val	Phe	Leu	Lys	Gln	Phe	Leu		
				645					650					655			
Ser	Ser	Gln	Arg	Tyr	Asp	Ile	Gln	Glu	Asn	Thr	Leu	Ile	Thr	Met	Val		
		660						665					670				
Thr	Asp	Ile	Phe	Lys	Leu	Asp	Ala	Leu	Ala	Pro	Met	Ile	Thr	Asp	Pro		
		675					680					685					
Asn	Ile	Gln	Ala	Ser	Glu	Glu	Asp	Leu	Ala	Tyr	Phe	Ser	Gln	Leu	Lys		
	690					695					700						
Ser	Ala	Cys	Leu	Pro	Pro	Ile	Pro	Val	Asn	Leu	Phe	Ser	Thr	Asp	His		
705					710					715					720		
Lys	Leu	Arg	Pro	Tyr	Gln	Asn	Ser	Gly	Leu	Leu	Trp	Leu	Trp	Phe	Leu		
			725						730					735			
Tyr	Asn	His	Arg	Leu	Ser	Gly	Leu	Leu	Cys	Asp	Glu	Met	Gly	Leu	Gly		
			740				745						750				
Lys	Thr	His	Gln	Ala	Thr	Ala	Leu	Leu	Asp	Ile	Val	Ala	Gln	Thr	Ala		
		755					760					765					
Lys	Asn	Pro	Lys	Phe	Leu	Val	Val	Cys	Pro	Thr	Ser	Val	Leu	Pro	His		
	770					775					780						
Trp	Glu	His	Val	Leu	Ala	Ser	His	Leu	Pro	Gln	Ala	Ser	Leu	Phe	Ser		
785					790					795					800		
Phe	His	Gly	Pro	His	Lys	Pro	Lys	Thr	Leu	Pro	Asp	Cys	Asp	Ile	Leu		
			805						810					815			
Ile	Thr	Ser	Tyr	Gly	Thr	Leu	Arg	Gln	Asn	Tyr	Ala	Leu	Phe	Tyr	Lys		
			820				825						830				
Val	Ser	Phe	Thr	Val	Ala	Val	Phe	Asp	Glu	Ile	His	Thr	Ala	Lys	Asn		
		835					840					845					
Lys	Ser	Ser	Gln	Ile	His	Lys	Ile	Leu	Cys	Arg	Leu	Asp	Ala	Gln	Met		
	850					855					860						
Lys	Leu	Gly	Leu	Thr	Gly	Thr	Pro	Val	Glu	Asn	Leu	Ile	Glu	Phe			
865					870					875				880			
Lys	Gly	Leu	Leu	Asp	Ile	Ile	Leu	Pro	Asn	Tyr	Leu	Pro	Ser	Asp	Ala		
			885						890					895			
Leu	Phe	Lys	Arg	Leu	Phe	Thr	His	Lys	Asn	Ala	Ser	Glu	Thr	Asp	Glu		
			900				905						910				
Asp	Ile	Ile	Ser	Ser	Lys	Asp	Leu	Leu	Leu	Lys	Leu	Thr	Arg	Pro	Phe		
		915					920					925					
Ile	Leu	Arg	Arg	Thr	Lys	Lys	Leu	Val	Leu	Pro	Glu	Leu	Pro	Glu	Lys		
	930					935					940						
Val	Glu	Ser	Leu	Ile	Pro	Cys	Arg	Leu	Ser	Pro	Glu	Gln	Ser	Gln	Leu		
945					950					955					960		
Tyr	Ser	Ser	Thr	Leu	Glu	Lys	Glu	Lys	Cys	Gln	Ile	Gln	Gln	Leu	Glu		
			965						970					975			
Lys	Glu	Glu	Asp	Pro	Ala	Ser	Val	Asn	Tyr	Leu	His	Val	Phe	Ala	Leu		
			980				985						990				
Leu	Asn	Gln	Leu	Lys	Gln	Ile	Cys	Asp	His	Pro	Ala	Val	Tyr	Phe	Lys		
		995					1000					1005					
Asp	Pro	Glu	Ser	Tyr	Lys	Asn	His	Ser	Ser	Gly	Lys	Trp	Ala	Ala	Phe		
	1010					1015					1020						
Val	Lys	Leu	Leu	Asn	Asp	Ser	Leu	Ala	Ser	Gly	Tyr	Lys	Val	Val	Val		
1025					1030					1035					1040		
Phe	Ser	Gln	Tyr	Ile	Gln	Met	Ile	Arg	Ile	Ile	Ala	Leu	Tyr	Leu	Glu		
			1045						1050					1055			
Glu	His	Ala	Ile	Glu	Tyr	Ala	Leu	Val	Gln	Gly	Lys	Ser	Gln	Asn	Arg		
		1060					1065						1070				
Lys	Glu	Glu	Ile	Asp	Arg	Phe	Ser	Asn	Asp	Pro	Asn	Cys	Arg	Val	Phe		
		1075					1080					1085					
Ile	Gly	Ser	Leu	Leu	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Leu	Thr	Ala	Gly		
	1090					1095					1100						
Asn	Val	Val	Ile	Met	Tyr	Asp	Arg	Trp	Trp	Asn	Pro	Ala	Lys	Glu	Asn		

1105		1110		1115		1120									
Gln	Ala	Leu	Asp	Arg	Val	His	Arg	Ile	Gly	Gln	Lys	Asn	Thr	Val	Phe
		1125		1130		1135									
Ile	Tyr	Lys	Leu	Val	Thr	Glu	Asp	Thr	Leu	Glu	Glu	His	Ile	His	Tyr
		1140		1145		1150									
Leu	Ile	Glu	Lys	Lys	Met	Arg	Leu	Leu	Asn	Gln	Val	Thr	Thr	Thr	Gln
		1155		1160		1165									
Asp	Ser	Asn	Ile	Leu	His	Val	Leu	Asn	Arg	Glu	Asp	Leu	Ile	Thr	Ile
		1170		1175		1180									
Leu	Ser	Tyr	Lys	Asp	Glu	His	Met	Leu	Ser	Glu	Glu	Val	Gln	Glu	Asp
1185				1190		1195								1200	
Ser	Gly	Asp	Ser												

(2) INFORMATIONS POUR LA SEQ ID NO: 908:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 403 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(888940..890148)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 908:

Ser	His	Lys	Gly	Leu	Ser	Ile	Trp	Ser	Ile	Gly	Gly	Ser	Ile	Phe	Ala
1			5					10						15	
Met	Phe	Phe	Gly	Ala	Gly	Asn	Val	Val	Phe	Pro	Leu	Ala	Leu	Gly	His
			20					25					30		
His	Phe	Tyr	Tyr	His	Ile	Ser	Tyr	Ala	Cys	Leu	Gly	Met	Ile	Leu	Thr
		35				40						45			
Ala	Val	Leu	Thr	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Met	Met	Leu	Tyr	Ser
		50				55					60				
Gly	Asn	Tyr	Arg	Ser	Phe	Phe	Ala	Ser	Ile	Gly	Arg	Met	Pro	Gly	Met
65				70						75				80	
Val	Leu	Met	Val	Ala	Ile	Leu	Cys	Ile	Ile	Gly	Pro	Phe	Gly	Gly	Ile
			85					90					95		
Pro	Arg	Thr	Ile	Ala	Val	Ser	Tyr	Asp	Thr	Leu	Ala	Ser	Leu	Gly	Asp
			100					105					110		
Lys	His	Pro	Thr	Leu	Leu	Pro	Ser	Leu	Pro	Trp	Phe	Ser	Val	Phe	Phe
		115				120						125			
Cys	Val	Leu	Val	Tyr	Leu	Phe	Val	Cys	Lys	Leu	Ser	Lys	Leu	Ile	Gln
		130				135					140				
Trp	Leu	Gly	Ser	Val	Phe	Phe	Pro	Val	Met	Leu	Gly	Thr	Leu	Ala	Trp
145				150						155				160	
Leu	Ile	Ile	Lys	Gly	Leu	Leu	Leu	Pro	Ala	His	Ala	Leu	Pro	Ser	Glu
			165					170					175		
Ser	Val	Thr	Phe	Ser	Lys	Gln	Gln	Ala	Phe	Val	Thr	Gly	Leu	Ser	Glu
			180					185					190		
Gly	Phe	Asn	Thr	Met	Asp	Leu	Leu	Gly	Ala	Phe	Phe	Phe	Cys	Ser	Ile
		195				200						205			
Val	Leu	Val	Ser	Ile	Gln	Gln	Leu	Met	Val	Gln	Gln	Lys	His	Glu	Ser
		210				215						220			
Ser	Glu	Glu	Lys	Pro	Leu	Glu	Phe	His	His	Ile	Gly	Lys	Thr	Glu	Lys
225				230						235				240	

```

Tyr Lys Leu Ala Met Ser Phe Leu Leu Ala Ala Ala Leu Leu Ser Leu
                245                250                255
Val Tyr Leu Gly Phe Ala Phe Cys Ala Ala Arg His Ala Gly Ala Leu
                260                265                270
Ile Asp Val Gln Arg Gly Gln Ile Leu Gly Arg Ile Ser Ala Leu Val
                275                280                285
Val Gly Pro Asn Ser Phe Leu Thr Gly Leu Ser Val Phe Leu Ala Cys
                290                295                300
Leu Thr Thr Ala Ile Ala Val Thr Gly Ile Phe Ala Asp Phe Ile Ala
305                310                315                320
Arg Val Val Ser Ser Gln Lys Met Ser Tyr Ser Asn Ala Leu Ile Val
                325                330                335
Thr Leu Val Pro Thr Tyr Leu Val Ser Ile Leu Ser Phe Glu Asn Ile
                340                345                350
Ser Lys Ile Leu Ile Pro Ile Leu Glu Met Ser Tyr Pro Ala Leu Ile
                355                360                365
Ala Leu Thr Cys Gly Val Ile Ala Lys Lys Leu Trp Asp Phe Arg His
370                375                380
Val Lys Thr Leu Phe Tyr Leu Val Phe Ala Leu Thr Ile Leu Tyr Lys
385                390                395                400
Leu Ser Val

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 909:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 280 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: complement(890325..891164)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 909:

```

Ala Ile Ser Thr Pro Ala Leu Ala Cys Ser Leu Leu His Ile Asp Asp
1                5                10                15
Leu Ala Glu Cys Leu Thr Thr Asp Tyr Gly Glu Glu Glu Ala Ile Arg
                20                25                30
Leu Ala Lys Ile Phe Leu Glu Glu Ala Pro Cys Ser Ile Arg Val Asn
                35                40                45
Thr Arg Arg Ile Ser Val Asp Lys Leu Gln Lys Val Leu Pro Phe Pro
50                55                60
Cys Gln Arg Gly Ala Ala Pro Ser Ser Leu Arg Phe Glu Lys Arg Tyr
65                70                75                80
Pro Leu Gln His Thr Arg Ala Phe Arg Arg Gly Leu Phe Glu Ile Gln
                85                90                95
Asp Glu Ser Ser Gln Ile Ile Thr Asn Ala Ile Leu Ile Lys Asp Ser
                100                105                110
Asp Thr Val Leu Asp Phe Cys Ala Gly Ala Gly Gly Lys Ser Leu Ile
                115                120                125
Phe Ala Gln Arg Ala Arg His Val Thr Leu His Asp Ser Arg Pro Gln
130                135                140
Ala Leu Glu Glu Ala Arg His Arg Ser Pro Arg Ser Gly Ile Lys Asn
145                150                155                160
Phe Thr Ile Pro Ser Gln Pro Leu Lys Lys His Ser Phe Ser Leu Val

```

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 911:

Met	Arg	Thr	Phe	Phe	Leu	Leu	Cys	Arg	Phe	Phe	Ile	Cys	Leu	Ala	Pro
1				5					10					15	
Phe	Phe	Leu	Ser	Phe	Pro	Leu	Tyr	Ala	Asp	Pro	His	Thr	Val	Leu	Thr
			20					25					30		
Lys	Gly	Ile	Ala	Ala	Ala	Val	Val	His	Ala	Asp	Ser	Gly	Ala	Ile	Leu
			35				40					45			
Lys	Glu	Lys	Asn	Leu	Asp	His	Lys	Ile	Phe	Pro	Ala	Ser	Met	Thr	Lys
	50					55					60				
Ile	Ala	Thr	Ala	Leu	Leu	Ile	Leu	Arg	Gln	Tyr	Pro	Asp	Val	Leu	Thr
65					70					75					80
Arg	Phe	Ile	Thr	Thr	Arg	Arg	Glu	Pro	Leu	Thr	Ser	Ile	Thr	Pro	Gln
				85					90					95	
Ala	Lys	Gln	Gln	Ser	Gly	Tyr	Arg	Ser	Pro	Pro	His	Trp	Leu	Glu	Thr
			100					105					110		
Asp	Gly	Met	Thr	Ile	Gln	Leu	Lys	Val	Lys	Glu	Glu	Val	Ser	Gly	Trp
			115				120					125			
Asp	Leu	Phe	His	Ala	Leu	Leu	Ile	Ser	Ser	Ala	Asn	Asp	Ala	Ala	Asn
	130					135					140				
Val	Leu	Ala	Asp	Ala	Cys	Cys	Gln	Ser	Val	Ser	Ala	Phe	Met	Arg	Gln
145					150					155					160
Leu	Asn	Glu	Phe	Leu	Arg	Glu	Leu	Gly	Cys	Gln	Asn	Thr	His	Phe	Asn
				165					170					175	
Ser	Pro	His	Gly	Leu	His	His	Pro	Asp	His	Tyr	Thr	Thr	Ala	Arg	Asp
			180					185					190		
Leu	Ser	Leu	Ile	Met	Lys	Glu	Ala	Leu	Lys	Glu	Pro	Leu	Phe	Arg	Gln
			195				200					205			
Val	Ile	His	Thr	Ala	Ser	Tyr	Thr	Met	Glu	Ala	Thr	Asn	Leu	Ser	Pro
	210					215					220				
Glu	Arg	Val	Leu	Ser	Ser	Thr	Asn	Lys	Leu	Leu	Ser	Ser	Ser	Ser	Thr
225					230					235					240
Tyr	Phe	Tyr	Pro	Pro	Cys	Leu	Gly	Gly	Lys	Thr	Gly	Thr	Thr	Lys	Ser
				245					250					255	
Ala	Gly	Lys	Asn	Ile	Ile	Phe	Ala	Ala	Glu	Lys	Asn	Asn	Arg	Ser	Ile
			260					265					270		
Ile	Val	Val	Ala	Ala	Gly	Tyr	Phe	Gly	Pro	Ala	Ala	Gln	Leu	Tyr	Gln
			275				280					285			
Asp	Ala	Ile	Ala	Leu	Cys	Glu	Asp	Leu	Phe	Asn	Glu	Gln	Leu	Leu	Arg
	290					295					300				
Cys	Phe	Leu	Ile	Pro	Pro	Ala	Ser	His	Tyr	Pro	Val	Pro	Thr	Arg	Phe
305					310					315					320
Gly	Thr	Val	Thr	Ala	Pro	Val	Ala	Gln	Gly	Ile	Tyr	Tyr	Asp	Phe	Tyr
				325					330					335	
Pro	Ser	Glu	Gly	Asp	Pro	Leu	Leu	Thr	Leu	Ser	Leu	Glu	Pro	Asn	Lys
			340					345					350		
Ile	Ser	Phe	Pro	Ile											

435

(2) INFORMATIONS POUR LA SEQ ID NO: 912:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 151 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 893356..893808

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 912:

```

Gln Ile Thr Leu Glu Lys Gly Glu Thr Ala Val Ser Leu Asp Phe Leu
1      5      10      15
Glu Asp Phe Phe Arg Arg Ser Ile Thr Asn His Asn Thr Ala Phe Pro
20      25      30
Glu Gly Phe Leu Asp Ile Ser Asp Val Leu Ala Arg Ser Ala Leu Asp
35      40      45
Phe Lys Ala Glu Glu Leu Ala Asp Ser Ala Val Asn Asp Phe Ile Val
50      55      60
Ser Glu Ser Ser Asp Lys Leu Thr Leu Phe Asn Thr Asn Phe Ala Val
65      70      75      80
Trp Leu Val Pro Thr Leu Val Asp Gly Glu Ala Ile Thr Arg Gly Tyr
85      90      95
Ile Ala Leu Asn Gln Gly Glu Glu Phe Ser Pro Glu Leu Thr Phe Glu
100     105     110
Ala Ser Gly Lys Tyr Asn Asn Ser Ser Leu Ile Leu Glu Ala Leu Arg
115     120     125
Arg Tyr Leu Cys Asp Ile Gln Asp Thr Glu Lys Glu Leu Arg Ala Leu
130     135     140
Arg Pro Pro Ser Ile Asp Gly
145     150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 913:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 89 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(893643..893909)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 913:

```

Gln Asn Thr Arg Trp Met Phe Leu Ile Met Arg Glu Leu Thr Thr Gln
1      5      10      15
Met Leu Ser Leu Ser Leu Tyr Thr Gln Asn Leu Thr Thr His Ser Leu
20      25      30
Ile Tyr Pro Ser Ile Glu Gly Gly Arg Lys Ala Arg Asn Ser Phe Ser
35      40      45

```



Val Ser Trp Ile Ser His Lys Tyr Leu Arg Asn Ala Ser Lys Ile Lys  
 50 55 60  
 Leu Glu Leu Leu Tyr Phe Pro Asp Ala Ser Lys Val Asn Ser Gly Glu  
 65 70 75 80  
 Asn Ser Ser Pro Trp Phe Lys Ala Met  
 85

(2) INFORMATIONS POUR LA SEQ ID NO: 914:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(893821..894258)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 914:

Met Thr Phe Ser Glu Gly Glu Gln Val Phe Pro Ala Thr Leu Gln Asp  
 1 5 10 15  
 Leu Tyr Pro Met Leu Asp Phe Val Lys Arg Ala Gly Val His Cys Asn  
 20 25 30  
 Cys Thr Gln Lys Lys Leu Ser Lys Leu Glu Leu Ala Cys Glu Glu Leu  
 35 40 45  
 Leu Leu Asn Ile Ile Thr His Ala Tyr Lys Gly Leu Pro Ser Thr Gly  
 50 55 60  
 Trp Ile Arg Ile Leu Cys Thr Glu Thr Pro Asp Ala Leu Leu Val Arg  
 65 70 75 80  
 Ile Thr Asp His Gly Pro Ala Phe Asn Pro Ile Thr Ala Ser Pro Asp  
 85 90 95  
 Ile Met Arg Leu Asp Leu Pro Ile Glu Gln Arg Arg Ile Gly Gly Leu  
 100 105 110  
 Gly Ile Phe Leu Ala Lys Tyr Ser Val Asp Val Phe Asp Tyr Glu Arg  
 115 120 125  
 Val Asn Asp Thr Asn Val Val Thr Leu Thr Leu Tyr Thr Lys Pro His  
 130 135 140  
 Asn Ser  
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 915:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(894248..894778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 915:

Ser Ala Cys Gly Tyr Thr Val Leu Ser Pro His Tyr Val Glu Lys Lys

1				5					10					15					
Phe	Ser	Leu	Ser	Glu	Gly	Ile	Tyr	Val	Cys	Pro	Ile	Glu	Gly	Asp	Ser				
			20					25					30						
Leu	Gly	Asp	Leu	Val	Ser	Ser	Leu	Ser	Tyr	Glu	Leu	Glu	Lys	Arg	Gly				
		35					40					45							
Leu	His	Thr	Arg	Ser	Gln	Gly	Thr	Ser	Ser	Gly	Tyr	Val	Leu	Lys	Val				
	50					55				60									
Ser	Leu	Phe	Asn	Glu	Thr	Tyr	Glu	Asn	Ile	Gly	Phe	Ala	Tyr	Thr	Pro				
65				70				75						80					
Gln	Lys	Pro	Asp	Glu	Lys	Pro	Val	Lys	His	Phe	Ile	Val	Ser	Asn	Glu				
			85					90						95					
Gly	Arg	Leu	Ala	Leu	Ser	Ala	Lys	Val	Gln	Leu	Ile	Lys	Asn	Arg	Thr				
			100					105					110						
Gln	Glu	Ile	Leu	Val	Glu	Lys	Cys	Leu	Arg	Lys	Ser	Val	Thr	Phe	Asp				
		115				120						125							
Phe	Gln	Pro	Asp	Leu	Gly	Thr	Ala	Asn	Ala	His	Gln	Leu	Ala	Leu	Gly				
	130					135					140								
Gln	Phe	Glu	Met	His	Asn	Glu	Ala	Ile	Lys	Ser	Ala	Ser	Arg	Ile	Leu				
145				150				155						160					
Tyr	Ser	Gln	Leu	Ala	Glu	Thr	Ile	Val	Gln	Gln	Val	Tyr	Tyr	Asp	Leu				
			165					170						175					
Phe																			

(2) INFORMATIONS POUR LA SEQ ID NO: 916:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 281 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(895050..895892)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 916:

Thr	Lys	Ala	Ile	Arg	Asp	Leu	Thr	Asn	Ser	Leu	Phe	Leu	Phe	Tyr	Asp				
1			5					10					15						
Asp	Ala	Leu	Leu	Leu	Ser	Leu	Arg	Leu	Ala	Met	Lys	Val	Ile	Leu					
		20					25					30							
Arg	Ala	Leu	Cys	Leu	Phe	Leu	Val	Leu	Pro	Cys	Gly	Cys	Tyr	Ala	Arg				
		35				40					45								
Val	Pro	Ser	Phe	Glu	Pro	Phe	Arg	Gly	Ala	Ile	Ala	Pro	Asn	Arg	Tyr				
	50					55				60									
Ile	Pro	Lys	His	Ser	Pro	Glu	Leu	Tyr	Phe	Glu	Met	Gly	Asp	Lys	Tyr				
65				70				75						80					
Phe	Gln	Ala	Lys	Lys	Phe	Lys	Gln	Ala	Leu	Leu	Cys	Phe	Gly	Met	Ile				
			85					90						95					
Thr	His	His	Phe	Pro	Glu	His	Ala	Leu	His	Pro	Lys	Ala	Gln	Phe	Leu				
			100					105					110						
Val	Gly	Leu	Cys	Tyr	Leu	Glu	Met	Gly	His	Pro	Asp	Leu	Ala	Asp	Lys				
		115					120					125							
Ala	Leu	Thr	Gln	Tyr	Gln	Glu	Leu	Ala	Asp	Thr	Glu	Tyr	Ser	Glu	Gln				
	130					135					140								
Leu	Phe	Ala	Ile	Lys	Tyr	Ser	Ile	Ala	Gln	Ser	Phe	Ala	Asn	Gly	Lys				
145				150				155						160					

Arg	Lys	Asn	Ile	Val	Pro	Leu	Glu	Gly	Phe	Pro	Lys	Leu	Leu	Lys	Ala
			165						170					175	
Asp	Thr	Asp	Ala	Leu	Arg	Ile	Phe	Glu	Glu	Ile	Val	Thr	Ala	Ser	Ser
			180					185					190		
Asp	Ala	Asp	Leu	Lys	Ala	Ser	Ala	Leu	Tyr	Ala	Lys	Gly	Ala	Leu	Leu
			195				200					205			
Phe	Asp	Arg	Lys	Glu	Tyr	Ser	Glu	Ala	Ile	Lys	Thr	Leu	Lys	Lys	Val
	210					215					220				
Ser	Leu	Gln	Phe	Pro	Ser	His	Ser	Leu	Ser	Pro	Glu	Ser	Phe	Thr	Leu
225					230					235					240
Ile	Ala	Lys	Ile	His	Cys	Leu	Gln	Ala	Leu	Gln	Glu	Pro	Tyr	Asn	Glu
			245						250					255	
Gln	Tyr	Leu	Gln	Asp	Ala	Arg	Met	Lys	Gln	Gln	Leu	Tyr	Val	Asn	Asn
			260					265					270		
Thr	Leu	Ile	Ile	Leu	Ala	Ile	Gln	Lys							
		275					280								

(2) INFORMATIONS POUR LA SEQ ID NO: 917:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 293 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 895951..896829

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 917:

Lys	Gly	Trp	Val	Met	Lys	Lys	Val	Val	Phe	Ile	Ala	Ala	Ile	Phe	Ser
1				5					10					15	
Ser	Ile	Val	Phe	Trp	Asp	Lys	Ile	Pro	Tyr	Ser	His	Arg	Ile	Lys	Gln
			20					25					30		
Phe	Ala	Met	Asp	Tyr	Gly	Ile	Glu	Leu	Val	Glu	Lys	Ser	Ser	Gln	Leu
		35					40					45			
Val	Arg	Lys	Ile	Ser	Gly	Asn	Glu	Arg	Leu	Cys	Val	Phe	Glu	Arg	Arg
	50					55					60				
Val	Ser	Glu	Glu	Gln	Val	Leu	Ala	Met	Phe	Ala	Lys	Asp	Lys	Ala	Ser
65				70						75					80
Ala	Glu	Leu	Leu	Phe	Val	Pro	His	Val	Leu	Met	Arg	Val	Arg	Phe	Ser
				85					90					95	
Gly	Glu	Glu	Asp	Lys	Arg	Ala	Gly	Ser	His	Glu	Gly	Ala	Met	Leu	Trp
			100					105					110		
Ser	Leu	Ser	Asn	Gly	Glu	Met	Val	Leu	Asn	Thr	Gly	Ser	Trp	Thr	Tyr
		115					120						125		
Ser	Lys	Gly	Phe	Arg	Glu	Cys	Leu	Met	Leu	Lys	Ala	Gly	Lys	Gln	Asp
	130					135					140				
Val	Gln	Leu	Met	Gln	Val	Leu	Ala	Gly	Met	Gly	Gly	Ser	Ala	Ser	Arg
145				150						155					160
Glu	Val	Leu	Ser	Gln	Ala	Leu	Ser	Met	Arg	Asn	Val	Arg	Ala	Asp	Arg
				165					170					175	
Val	Ile	Arg	Ala	Cys	Gln	Lys	Lys	Lys	Leu	Ile	Phe	Thr	His	Asp	Asn
			180					185					190		
Leu	Ile	Tyr	Ser	His	Phe	Gln	Gln	Pro	Gln	Pro	Ile	Lys	Gly	Cys	Met
		195					200					205			
Thr	Val	Phe	Asn	Ser	Ser	Pro	Val	Trp	Leu	Ala	Lys	Pro	Lys	Gly	Ser

(2) INFORMATION POUR LA SEQ ID NO: 918:

(A) LONGUEUR: 1240 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(897064..900783)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 918:

Arg 1	Ala	Val	Leu	Thr 5	Trp	Ile	Pro	Leu	His 10	Cys	His	Ser	Gln	Tyr 15	Ser
Ile	Leu	Asp	Ala 20	Thr	Cys	Ser	Ile	Lys 25	Lys	Phe	Val	Ala	Lys 30	Ala	Val
Glu	Tyr	Gln	Ile 35	Pro	Ala	Leu	Ala 40	Leu	Thr	Asp	His	Gly 45	Asn	Leu	Phe
Gly	Ala	Val	Glu 50	Phe	Tyr	Lys 55	Thr	Cys	Lys	Gln	Asn 60	Ala	Ile	Lys	Pro
Ile 65	Ile	Gly	Cys	Glu	Leu 70	Tyr	Val	Ala	Pro	Ser	Ser 75	Arg	Phe	Asp	Lys 80
Lys	Lys	Glu	Arg 85	Lys	Ser	Arg	Val	Ala 90	Asn	His	Leu	Ile	Leu 95	Leu	Cys
Lys	Asp	Glu	Glu 100	Gly	Tyr	Arg	Asn 105	Leu	Cys	Leu	Leu	Ser	Ser 110	Leu	Ala
Tyr	Thr	Glu	Gly 115	Phe	Tyr	Tyr	Val 120	Pro	Arg	Ile	Asp 125	Arg	Asp	Leu	Leu
Ser	Gln	His	Ser 130	Lys	Gly	Leu 135	Ile	Cys	Leu	Ser	Ala 140	Cys	Leu	Ser	Gly
Ser 145	Val	Ala	Gln	Ala 150	Ala	Leu	Glu	Ser	Glu	Glu	Asp 155	Leu	Glu	Lys	Asp 160
Leu	Leu	Trp	Tyr 165	Gln	Asp	Leu	Phe	Gln 170	Glu	Asp	Phe	Phe	Ser 175	Glu	Val
Gln	Leu	His	Lys 180	Ser	Ser	Glu	Glu 185	Lys	Val	Ala	Leu	Phe	Glu 190	Glu	Ala
Trp	Leu	Lys	Gln 195	Asn	Tyr	Tyr	Gln 200	Phe	Ile	Glu	Lys 205	Gln	Leu	Lys	Val
Asn	Glu	Ala	Val 210	Leu	Ala 215	Thr	Ser	Lys	Arg	Leu	Gly 220	Ile	Pro	Ser	Val
Ala 225	Thr	Asn	Asp	Ile 230	His	Tyr	Leu	Asn	Pro	Asp	Asp 235	Trp	Leu	Ala	His 240
Glu	Val	Leu	Leu 245	Asn	Val	Gln	Ser	Arg	Glu 250	Pro	Ile	Arg	Thr 255	Ala	Lys

Gln	Asn	Thr	Tyr	Ile	Pro	Asn	Pro	Lys	Arg	Lys	Thr	Tyr	Pro	Ser	Arg		
			260					265					270				
Glu	Phe	Tyr	Phe	Lys	Ser	Pro	Gln	Glu	Met	Ala	Glu	Leu	Phe	Ala	Ala		
		275					280					285					
His	Pro	Glu	Thr	Ile	Thr	Asn	Thr	Cys	Ile	Val	Ala	Glu	Arg	Cys	His		
	290					295					300						
Leu	Glu	Leu	Asp	Phe	Glu	Thr	Lys	His	Tyr	Pro	Ile	Tyr	Val	Pro	Glu		
305					310					315					320		
Ala	Leu	Gln	Lys	Lys	Gly	Ser	Tyr	Thr	Glu	Glu	Glu	Arg	Tyr	Lys	Ala		
			325						330					335			
Ser	Ser	Ala	Phe	Leu	Glu	Glu	Leu	Cys	Glu	Gln	Gly	Leu	Thr	Ser	Lys		
		340						345					350				
Tyr	Thr	Pro	Glu	Leu	Leu	Gly	His	Ile	Ala	Lys	Lys	Phe	Pro	Gly	Glu		
		355					360					365					
Asp	Pro	Leu	Thr	Leu	Val	Lys	Glu	Arg	Leu	Lys	Leu	Glu	Ser	Ser	Ile		
	370					375					380						
Ile	Ile	Ser	Lys	Gly	Met	Cys	Asp	Tyr	Leu	Leu	Ile	Val	Trp	Asp	Ile		
385					390					395					400		
Ile	Asn	Trp	Ala	Lys	Asp	His	Gly	Ile	Pro	Val	Gly	Pro	Gly	Arg	Gly		
			405						410					415			
Ser	Gly	Ala	Gly	Ser	Val	Met	Leu	Phe	Leu	Leu	Gly	Ile	Thr	Glu	Ile		
		420						425					430				
Glu	Pro	Ile	Arg	Phe	Asp	Leu	Phe	Phe	Glu	Arg	Phe	Ile	Asn	Pro	Glu		
		435					440					445					
Arg	Ile	Ser	Tyr	Pro	Asp	Ile	Asp	Ile	Asp	Ile	Cys	Met	Ile	Gly	Arg		
	450				455						460						
Glu	Arg	Val	Ile	Asn	Tyr	Ala	Ile	Glu	Arg	His	Gly	Lys	Asp	Asn	Val		
465					470					475					480		
Ala	Gln	Ile	Ile	Thr	Phe	Gly	Thr	Met	Lys	Ala	Lys	Met	Xaa	Ile	Lys		
			485						490					495			
Asp	Val	Gly	Arg	Thr	Leu	Asp	Thr	Pro	Leu	Ala	Lys	Val	Asn	Phe	Ile		
		500						505					510				
Ala	Lys	His	Ile	Pro	Asp	Leu	Asn	Ala	Thr	Ile	Thr	Ser	Ala	Leu	Glu		
		515					520					525					
Ala	Asp	Pro	Glu	Leu	Lys	Gln	Leu	Tyr	Val	Asp	Asp	Ala	Glu	Ala	Ala		
	530					535					540						
Glu	Val	Ile	Asp	Met	Ala	Lys	Lys	Leu	Glu	Gly	Ser	Ile	Arg	Asn	Thr		
545					550					555					560		
Gly	Val	His	Ala	Ala	Gly	Val	Ile	Ile	Cys	Gly	Asp	Pro	Leu	Thr	Asn		
			565						570					575			
His	Ile	Pro	Ile	Cys	Val	Pro	Lys	Asp	Ser	Ser	Met	Ile	Ser	Thr	Gln		
		580						585					590				
Tyr	Ser	Met	Lys	Pro	Val	Glu	Ser	Val	Gly	Met	Leu	Lys	Val	Asp	Phe		
		595					600					605					
Leu	Gly	Leu	Lys	Thr	Leu	Thr	Gly	Ile	His	Ile	Ala	Thr	Gln	Ala	Ile		
	610					615					620						
Tyr	Lys	Lys	Thr	Gly	Ile	Leu	Leu	Arg	Ala	Ala	Thr	Ile	Pro	Leu	Asp		
625					630					635					640		
Asp	Gln	Asn	Thr	Phe	Ser	Leu	Leu	His	Gln	Gly	Lys	Thr	Met	Gly	Ile		
			645						650					655			
Phe	Gln	Met	Glu	Ser	Arg	Gly	Met	Gln	Asp	Leu	Ala	Lys	Asn	Leu	Arg		
		660					665						670				
Pro	Asp	Ala	Phe	Glu	Glu	Ile	Ile	Ala	Ile	Gly	Ala	Leu	Tyr	Arg	Pro		
		675					680					685					
Gly	Pro	Met	Asp	Met	Ile	Pro	Ser	Phe	Ile	Asn	Arg	Lys	His	Gly	Lys		
	690					695					700						
Glu	Asn	Ile	Glu	Xaa	Asp	His	Pro	Leu	Met	Glu	Pro	Ile	Leu	Lys	Glu		
705					710					715					720		
Thr	Phe	Gly	Ile	Met	Val	Tyr	Gln	Glu	Gln	Val	Met	Gln	Ile	Ala	Gly		

				725					730					735					
Ser	Leu	Ala	Lys	Tyr	Ser	Leu	Gly	Glu	Gly	Asp	Val	Leu	Arg	Arg	Ala				
			740					745					750						
Met	Gly	Lys	Lys	Asp	His	Glu	Gln	Met	Val	Lys	Glu	Arg	Glu	Lys	Phe				
		755					760					765							
Cys	Ser	Arg	Ala	Ala	Ala	Asn	Gly	Ile	Asp	Pro	Ser	Ile	Ala	Thr	Thr				
	770					775					780								
Ile	Phe	Asp	Lys	Met	Glu	Lys	Phe	Ala	Ser	Tyr	Gly	Phe	Asn	Lys	Ser				
785					790					795					800				
His	Ala	Ala	Ala	Tyr	Gly	Leu	Ile	Thr	Tyr	Thr	Thr	Ala	Tyr	Leu	Lys				
				805					810					815					
Ala	Asn	Tyr	Pro	Lys	Glu	Trp	Leu	Ala	Ala	Leu	Leu	Thr	Cys	Asp	Tyr				
			820					825					830						
Asp	Asp	Ile	Glu	Lys	Val	Gly	Lys	Leu	Ile	Gln	Glu	Ala	His	Ser	Met				
		835				840					845								
Asn	Ile	Leu	Val	Leu	Pro	Pro	Asp	Ile	Asn	Glu	Ser	Gly	Gln	Asp	Phe				
	850					855				860									
Glu	Ala	Thr	Gln	Glu	Gly	Ile	Arg	Phe	Ser	Leu	Gly	Ala	Val	Lys	Gly				
865					870					875					880				
Val	Gly	Met	Ser	Ile	Val	Asp	Ser	Ile	Val	Glu	Glu	Arg	Glu	Lys	Asn				
			885						890					895					
Gly	Pro	Tyr	Lys	Ser	Leu	Gln	Asp	Phe	Val	Gln	Arg	Ala	Asp	Phe	Lys				
		900						905					910						
Lys	Val	Thr	Lys	Lys	Gln	Leu	Glu	Asn	Leu	Val	Asp	Ala	Gly	Thr	Phe				
	915						920					925							
Asp	Cys	Phe	Glu	Pro	Asn	Lys	Asp	Leu	Ala	Leu	Ala	Ile	Leu	Asn	Asp				
	930					935					940								
Leu	Tyr	Asp	Thr	Phe	Phe	Arg	Glu	Lys	Lys	Glu	Ala	Ala	Thr	Gly	Val				
945					950					955					960				
Leu	Thr	Phe	Phe	Ser	Leu	Asp	Ser	Met	Xaa	Arg	Asp	Pro	Val	Lys	Ile				
			965						970					975					
Thr	Val	Xaa	Pro	Glu	Asn	Val	Ile	Gln	Arg	Ser	Pro	Lys	Glu	Leu	Leu				
		980						985					990						
Lys	Arg	Glu	Lys	Glu	Leu	Leu	Xaa	Val	Tyr	Leu	Thr	Ala	His	Pro	Met				
	995						1000					1005							
Asp	Ala	Val	Glu	His	Met	Leu	Pro	Phe	Leu	Ser	Val	Val	Pro	Ala	Arg				
	1010																		

Asn Gln Arg Phe Ala Ser Ile Ser Pro Asp Ala Asp Phe Phe Val Thr  
                           1205                          1210                          1215  
 Asp Asp Ile Ser Ser Leu Leu Gln Glu Ile Glu Ala Thr Asn Ile Pro  
                           1220                          1225                          1230  
 Ala Arg Val Leu Ala Thr Thr Val  
                           1235                          1240

(2) INFORMATIONS POUR LA SEQ ID NO: 919:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 414 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(900791..902032)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 919:

Leu Phe Phe Tyr Phe Thr Arg Lys Ser Xaa Xaa Phe Ala Met Pro Thr  
 1                          5                          10                          15  
 Leu Ile Ala Asp Leu Gly Phe Asp Lys Ala Gln Leu Gly Ile Ile Gly  
                           20                          25                          30  
 Ser Thr Leu Tyr Ile Thr Tyr Gly Ile Ser Lys Phe Val Ser Gly Val  
                           35                          40                          45  
 Met Ser Asp Gln Ser Asn Pro Arg Tyr Phe Met Ala Ile Gly Leu Ile  
                           50                          55                          60  
 Ile Thr Gly Ile Ser Asn Ile Phe Phe Gly Leu Ser Ser Thr Ile Pro  
 65                          70                          75                          80  
 Leu Phe Val Leu Phe Trp Gly Ile Asn Gly Trp Phe Gln Gly Trp Gly  
                           85                          90                          95  
 Trp Pro Pro Cys Ala Arg Leu Leu Thr His Trp Tyr Ser Lys Ser Glu  
                           100                          105                          110  
 Arg Gly Thr Trp Trp Ser Val Trp Ser Thr Ser His Asn Ile Gly Gly  
                           115                          120                          125  
 Ala Leu Ile Pro Val Leu Thr Gly Val Ala Ile Asp Tyr Thr Gly Trp  
                           130                          135                          140  
 Arg Gly Val Met Phe Ile Pro Gly Ile Ile Cys Ile Ile Met Gly Phe  
 145                          150                          155                          160  
 Ile Leu Ile Asp Arg Leu Arg Asp Thr Pro Gln Ser Leu Gly Leu Pro  
                           165                          170                          175  
 Ala Ile Glu Lys Phe Arg Lys Glu Glu Asp Ala His Pro His Glu Glu  
                           180                          185                          190  
 Thr Thr Ala Asp Ile Leu Glu Glu Glu Ala Glu Arg Glu Leu Ser Thr  
                           195                          200                          205  
 Lys Glu Ile Leu Phe Thr Tyr Val Leu Ser Asn Lys Trp Leu Trp Phe  
                           210                          215                          220  
 Leu Ser Phe Ala Ser Phe Ile Tyr Val Val Arg Met Ala Val Asn  
 225                          230                          235                          240  
 Asp Trp Ser Ala Leu Tyr Leu Ile Glu Thr Lys Asp Tyr Ser Thr Val  
                           245                          250                          255  
 Lys Ala Asn Leu Cys Val Ser Leu Phe Glu Ile Gly Gly Leu Phe Gly  
                           260                          265                          270  
 Met Leu Leu Ala Gly Trp Leu Ser Asp Thr Ile Ser Lys Gly Lys Arg  
                           275                          280                          285  
 Gly Pro Met Asn Val Val Phe Ser Leu Gly Leu Leu Val Ser Ile Leu

290		295		300											
Gly	Leu	Trp	Gly	Thr	Arg	Asp	Tyr	Phe	Val	Trp	Trp	Ile	Asp	Gly	Thr
305					310					315					320
Phe	Leu	Phe	Ile	Ile	Gly	Phe	Phe	Leu	Phe	Gly	Pro	Gln	Met	Met	Ile
			325						330					335	
Gly	Leu	Ala	Ala	Ala	Glu	Leu	Ser	His	Lys	Lys	Ala	Ala	Gly	Thr	Ala
			340					345					350		
Ser	Gly	Phe	Thr	Gly	Trp	Phe	Ala	Tyr	Phe	Gly	Ala	Ala	Phe	Ala	Gly
		355					360					365			
Tyr	Pro	Leu	Gly	Lys	Val	Ala	Gln	Asp	Trp	Gly	Trp	His	Gly	Phe	Phe
	370					375					380				
Val	Ala	Leu	Leu	Ala	Cys	Ala	Leu	Ile	Ala	Leu	Ile	Leu	Phe	Leu	Pro
385					390					395					400
Thr	Trp	Asn	Ala	Ser	Glu	Gln	Ser	Leu	Arg	Lys	His	Ser	His		
			405						410						

(2) INFORMATIONS POUR LA SEQ ID NO: 920:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 902677..903876

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 920:

Trp	Lys	Arg	Val	Glu	His	Ala	Ala	His	Arg	Ile	Cys	Asn	Leu	Tyr	Gly
1			5					10					15		
Phe	Asp	Glu	Ile	Arg	Thr	Pro	Val	Phe	Glu	Lys	Thr	Glu	Thr	Phe	Leu
		20					25					30			
Arg	Val	Gly	Glu	His	Ser	Asp	Ile	Val	Lys	Lys	Glu	Val	Tyr	Thr	Xaa
	35					40					45				
Leu	Asp	Lys	Lys	Gly	Arg	Ser	Leu	Thr	Leu	Arg	Pro	Glu	Gly	Thr	Ala
	50				55				60						
Ala	Val	Val	Arg	Ala	Leu	Leu	Asp	His	Ser	Ala	Asp	Met	Arg	Lys	Asp
65			70				75						80		
Asn	Lys	Phe	Tyr	Tyr	Ile	Leu	Pro	Met	Phe	Arg	Tyr	Glu	Arg	Xaa	Gln
		85					90					95			
Ser	Gly	Arg	Tyr	Arg	Gln	His	His	Gln	Phe	Gly	Leu	Glu	Ala	Ile	Gly
	100					105						110			
Val	Arg	His	Pro	Leu	Arg	Asp	Ala	Glu	Val	Leu	Ser	Leu	Leu	Trp	Asp
	115					120					125				
Phe	Tyr	Ala	Ala	Val	Gly	Leu	Gln	His	Met	Gln	Ile	His	Val	Asn	Phe
	130				135					140					
Leu	Gly	Gly	Gln	Lys	Thr	Arg	Ala	Arg	Tyr	Asp	Glu	Ala	Leu	Arg	Glu
145			150						155					160	
Phe	Phe	Arg	Lys	Asp	Leu	Asp	Arg	Leu	Ser	Pro	Leu	Ser	Gln	Glu	Arg
		165					170						175		
Tyr	His	Ala	Asn	Leu	Leu	Arg	Ile	Leu	Asp	Ser	Lys	Glu	Pro	Glu	Asp
	180					185						190			
Gln	Glu	Phe	Ile	Glu	Lys	Ala	Pro	Ser	Ile	Leu	Asp	Tyr	Ile	Asp	Asp
	195				200						205				
Arg	Asp	Leu	Ser	Tyr	Phe	Asp	Ala	Val	Leu	Ala	Gln	Leu	Lys	Ala	Leu
	210					215					220				



Gly	Ile	Pro	Phe	Ala	Ile	Asn	Pro	Arg	Leu	Val	Arg	Gly	Leu	Asp	Tyr
225					230					235					240
Tyr	Thr	Asp	Leu	Val	Phe	Glu	Ala	Val	Thr	Val	Val	Gly	Glu	Arg	Ser
			245						250					255	
Tyr	Ala	Leu	Gly	Gly	Gly	Gly	Arg	Tyr	Asp	Glu	Leu	Val	Ala	Gln	Ser
		260						265					270		
Gly	Gly	Pro	Ser	Met	Pro	Ala	Phe	Gly	Phe	Gly	Val	Gly	Leu	Glu	Arg
		275					280					285			
Val	Ile	Gln	Thr	Leu	Leu	Glu	Gln	Gly	Asn	Ser	Leu	Ser	Thr	Ser	Thr
	290					295					300				
Arg	Arg	Leu	Arg	Leu	Ile	Pro	Met	Asp	Glu	Gln	Ala	Asp	Ala	Phe	Cys
305					310					315					320
Phe	Ser	Trp	Ala	Asn	Arg	Leu	Arg	Asn	Leu	Gly	Ile	Ala	Thr	Glu	Val
			325					330						335	
Asp	Trp	Ser	His	Lys	Lys	Pro	Lys	Leu	Ser	Leu	Lys	Asp	Ala	Ala	Asp
		340						345					350		
Gln	Gln	Val	Ser	Phe	Val	Cys	Leu	Leu	Gly	Glu	Gln	Glu	Leu	Ala	Thr
		355					360					365			
Lys	Gln	Phe	Ile	Val	Lys	Asp	Met	Ser	Leu	His	Gln	Ser	Phe	Ser	Gly
	370					375					380				
Ala	Gln	Gln	Asp	Val	Glu	Gln	Arg	Leu	Val	Tyr	Glu	Val	Gln	Asn	Ala
385					390					395					400

(2) INFORMATIONS POUR LA SEQ ID NO: 921:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 87 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(903471..903731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 921:

Ser	Ala	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Gly	Phe	Leu	Trp	Leu	Gln	Ser
1			5					10					15		
Thr	Ser	Val	Ala	Met	Pro	Arg	Leu	Arg	Lys	Arg	Phe	Ala	His	Glu	Lys
		20					25					30			
Gln	Asn	Ala	Ser	Ala	Cys	Ser	Ser	Ile	Gly	Ile	Asn	Arg	Asn	Arg	Arg
	35					40					45				
Val	Glu	Val	Asp	Lys	Glu	Phe	Pro	Cys	Ser	Asn	Ser	Val	Trp	Ile	Thr
	50				55					60					
Leu	Ser	Asn	Pro	Thr	Pro	Lys	Pro	Lys	Ala	Gly	Ile	Glu	Gly	Pro	Pro
65				70						75				80	
Asp	Cys	Ala	Thr	Asn	Ser	Ser									
			85												

(2) INFORMATIONS POUR LA SEQ ID NO: 922:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 582 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 903860..905605

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 922:

Met	Lys	Tyr	Arg	Thr	His	Lys	Cys	Asn	Glu	Leu	Ser	Leu	Asp	His	Val	1	5	10	15
Gly	Glu	His	Val	Arg	Leu	Ser	Gly	Trp	Val	His	Arg	Tyr	Arg	Asn	His	20	25	30	
Gly	Gly	Val	Val	Phe	Ile	Asp	Leu	Arg	Asp	Arg	Phe	Gly	Ile	Thr	Gln	35	40	45	
Ile	Val	Cys	Arg	Gln	Glu	Glu	Asn	Pro	Glu	Leu	His	Gln	Leu	Met	Asp	50	55	60	
Gln	Val	Arg	Ser	Glu	Trp	Val	Leu	Cys	Val	Glu	Gly	Leu	Val	Cys	Ala	65	70	75	80
Arg	Leu	Glu	Gly	Met	Glu	Asn	Pro	Asn	Leu	Val	Thr	Gly	Ser	Ile	Glu	85	90	95	
Val	Glu	Val	Ser	Ser	Leu	Glu	Val	Leu	Ser	Arg	Ala	Gln	Asn	Leu	Pro	100	105	110	
Phe	Ser	Ile	Ser	Asp	Glu	His	Ile	Asn	Val	Asn	Glu	Glu	Leu	Arg	Leu	115	120	125	
Thr	Tyr	Arg	Tyr	Leu	Asp	Met	Arg	Arg	Gly	Asp	Ile	Leu	Asp	Arg	Leu	130	135	140	
Met	Cys	Arg	His	Lys	Val	Met	Leu	Ala	Cys	Arg	Gln	Tyr	Leu	Asp	Glu	145	150	155	160
Gln	Gly	Phe	Thr	Glu	Val	Val	Thr	Pro	Ile	Leu	Gly	Lys	Ser	Thr	Pro	165	170	175	
Glu	Gly	Ala	Arg	Asp	Tyr	Leu	Val	Pro	Ser	Arg	Ile	Tyr	Pro	Gly	Asn	180	185	190	
Phe	Tyr	Ala	Leu	Pro	Gln	Ser	Pro	Gln	Leu	Phe	Lys	Gln	Ile	Leu	Met	195	200	205	
Val	Gly	Gly	Leu	Asp	Arg	Tyr	Phe	Gln	Ile	Ala	Thr	Cys	Phe	Arg	Asp	210	215	220	
Glu	Asp	Leu	Arg	Ala	Asp	Arg	Gln	Pro	Glu	Phe	Thr	Gln	Ile	Asp	Met	225	230	235	240
Glu	Met	Ser	Phe	Gly	Gly	Pro	Glu	Asp	Leu	Phe	Pro	Val	Val	Glu	Glu	245	250	255	
Leu	Val	Thr	Arg	Leu	Phe	Ala	Val	Lys	Gly	Ile	Glu	Leu	Lys	Ala	Pro	260	265	270	
Phe	Leu	Arg	Met	Thr	Tyr	Gln	Glu	Ala	Lys	Asp	Ser	Tyr	Gly	Thr	Asp	275	280	285	
Lys	Pro	Asp	Leu	Arg	Phe	Ala	Leu	Arg	Leu	Lys	Asn	Cys	Cys	Glu	Tyr	290	295	300	
Ala	Arg	Lys	Phe	Thr	Phe	Ser	Ile	Phe	Leu	Asp	Gln	Leu	Ala	His	Gly	305	310	315	320
Gly	Thr	Val	Lys	Gly	Phe	Cys	Val	Pro	Gly	Gly	Ala	Asp	Met	Ser	Arg	325	330	335	
Lys	Gln	Leu	Asp	Ile	Tyr	Thr	Asp	Phe	Val	Lys	Arg	Tyr	Gly	Ser	Met	340	345	350	
Gly	Leu	Val	Trp	Ile	Lys	Lys	Gln	Asp	Gly	Gly	Val	Ser	Ser	Asn	Val	355	360	365	
Ala	Lys	Phe	Ala	Ser	Glu	Asp	Val	Phe	Gln	Glu	Met	Phe	Glu	Ala	Phe	370	375	380	
Glu	Ala	Lys	Asp	Gln	Asp	Ile	Leu	Leu	Leu	Ile	Ala	Ala	Pro	Glu	Ala	385	390	395	400
Val	Ala	Asn	Gln	Ala	Leu	Asp	His	Leu	Arg	Arg	Leu	Ile	Ala	Lys	Glu	405	410	415	

```

Arg Gln Leu Tyr Asp Ser Thr Gln Tyr Asn Phe Val Trp Ile Thr Asp
      420      425      430
Phe Pro Leu Phe Ala Lys Glu Glu Gly Glu Leu Cys Pro Glu His His
      435      440      445
Pro Phe Thr Ala Pro Leu Asp Glu Asp Ile Ser Leu Leu Asp Ser Asp
      450      455      460
Pro Phe Ala Val Arg Ser Ser Ser Tyr Asp Leu Val Leu Asn Gly Tyr
465      470      475      480
Glu Ile Ala Ser Gly Ser Gln Arg Ile His Asn Pro Asp Leu Gln Asn
      485      490      495
Lys Ile Phe Ala Leu Leu Lys Leu Ser Gln Glu Ser Val Lys Glu Lys
      500      505      510
Phe Gly Phe Phe Ile Asp Ala Leu Ser Phe Gly Thr Pro Pro His Leu
      515      520      525
Gly Ile Ala Leu Gly Leu Asp Arg Ile Met Met Val Leu Thr Gly Ala
530      535      540
Glu Thr Ile Arg Glu Val Ile Ala Phe Pro Lys Thr Gln Lys Ala Gly
545      550      555      560
Asp Leu Met Met Ser Ala Pro Ser Glu Ile Leu Pro Ile Gln Leu Lys
      565      570      575
Glu Leu Gly Leu Lys Leu
      580

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 923:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 243 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: 905746..906474

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 923:

```

Met Lys Asn Ile Leu Ser Trp Met Leu Met Phe Ala Val Ala Leu Pro
1      5      10      15
Ile Val Gly Cys Asp Asn Gly Gly Gly Ser Gln Thr Ser Ala Thr Glu
      20      25      30
Lys Ser Met Val Glu Asp Ser Ala Leu Thr Asp Asn Gln Lys Leu Ser
      35      40      45
Arg Thr Phe Gly His Leu Leu Ala Arg Gln Leu Ser Arg Thr Glu Asp
50      55      60
Phe Ser Leu Asp Leu Val Glu Val Ile Lys Gly Met Gln Ser Glu Ile
65      70      75      80
Asp Gly Gln Ser Ala Pro Leu Thr Asp Thr Glu Tyr Glu Lys Gln Met
      85      90      95
Ala Glu Val Gln Lys Ala Ser Phe Glu Ala Lys Cys Ser Glu Asn Leu
      100      105      110
Ala Ser Ala Glu Glu Phe Leu Lys Glu Asn Lys Glu Lys Ala Gly Val
      115      120      125
Ile Glu Leu Glu Pro Asn Lys Leu Gln Tyr Arg Val Val Lys Glu Gly
130      135      140
Thr Gly Arg Ala Leu Ser Gly Lys Pro Thr Ala Leu Leu His Tyr Thr
145      150      155      160
Gly Ser Phe Ile Asp Gly Lys Asp Phe Asp Ser Ser Glu Lys Asn Lys

```

				165					170					175					
Ala	Ala	Ile	Leu	Leu	Pro	Leu	Thr	Lys	Val	Ile	Pro	Gly	Phe	Ser	Gln				
			180						185					190					
Gly	Met	Gln	Gly	Met	Lys	Glu	Gly	Glu	Val	Arg	Val	Leu	Tyr	Ile	His				
		195						200					205						
Pro	Asp	Leu	Ala	Tyr	Gly	Thr	Ala	Gly	Gln	Leu	Pro	Pro	Asn	Ser	Leu				
	210					215					220								
Leu	Ile	Phe	Glu	Val	Xaa	Leu	Ile	Glu	Ala	Asn	Asp	Asp	Asn	Val	Ser				
225					230					235					240				
Val	Thr	Glu																	

(2) INFORMATIONS POUR LA SEQ ID NO: 924:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 906589..906945

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 924:

Pro	Leu	Gly	Phe	Ser	Leu	Ala	Asp	Lys	Phe	Val	Lys	Arg	Ala	Gly	Met				
1				5					10					15					
Asp	Tyr	Trp	Glu	Arg	Leu	Ser	Leu	Ser	Val	Val	Asp	Ser	Leu	Glu	Glu				
		20						25					30						
Ala	Leu	Leu	Gly	Val	Pro	Lys	Glu	Arg	Ile	Phe	Cys	Leu	Thr	Thr	Lys				
		35					40					45							
Gly	Ser	Ser	Tyr	Tyr	Gly	Glu	Arg	Glu	Leu	Pro	Leu	Asp	Gly	Thr	Tyr				
	50					55					60								
Ile	Phe	Gly	Ala	Glu	Ser	Lys	Gly	Leu	Ser	Gln	Thr	Val	Leu	Asp	Ala				
65					70					75				80					
Tyr	Ser	Ser	Gln	Cys	Leu	Tyr	Ile	Pro	Met	Ile	Glu	Gly	Thr	Arg	Ser				
			85						90				95						
Leu	Asn	Leu	Ala	Thr	Ser	Val	Gly	Ile	Val	Met	Tyr	Glu	Val	Ala	Arg				
		100						105					110						
Gln	Asn	Tyr	Lys	Thr	Leu	Phe													
		115																	

(2) INFORMATIONS POUR LA SEQ ID NO: 925:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 102 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(907001..907306)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 925:

```

Met Val Gln Val Val Ser Gln Glu Asn Phe Ala Asp Ser Ile Ala Ser
1          5          10          15
Gly Leu Val Leu Ile Asp Phe Phe Ala Glu Trp Xaa Gly Pro Cys Lys
          20          25          30
Met Leu Thr Pro Val Leu Glu Ala Leu Ala Ala Glu Leu Pro His Val
          35          40          45
Thr Ile Leu Lys Val Asp Ile Asp Ser Ser Pro Arg Pro Ala Glu Gln
          50          55          60
Tyr Ser Val Ser Ser Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Lys
65          70          75          80
Glu Val Glu Arg Ser Val Gly Leu Lys Asp Lys Asp Ser Leu Ile Lys
          85          90          95
Leu Ile Ser Lys His Gln
          100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 926:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 908101..908742

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 926:

```

Gln Arg Thr Cys Phe Xaa Xaa Glu Gln Ser Leu Arg Leu Ser Pro Val
1          5          10          15
Val Phe Val Arg Asp Lys Ile Ile Phe Lys Ser Thr Glu Asp Ala Ile
          20          25          30
Gln Leu Leu Glu Ala Asp Lys Lys Ile Trp Arg Glu Thr Glu Ile Gln
          35          40          45
Ile Ser Ser Gly Lys Pro Glu Val Asn Glu Gln Thr Lys Arg Ile Tyr
          50          55          60
Ile Cys Pro Phe Thr Gly Lys Val Phe Ala Asp Asn Val Tyr Ala Asn
65          70          75          80
Pro Gln Asp Ala Ile Tyr Asp Trp Leu Ser Cys Pro Gln Asn Arg
          85          90          95
Glu Arg Gln Ser Gly Val Ala Val Lys Arg Phe Leu Val Ser Asp Asp
          100          105          110
Pro Glu Val Ile Arg Ala Tyr Ile Val Pro Pro Lys Glu Pro Ile Ile
          115          120          125
Lys Thr Val Tyr Ala Ser Ala Val Thr Gly Lys Leu Phe His Ser Leu
          130          135          140
Pro Thr Leu Leu Glu Asp Phe Lys Thr Ser Tyr Leu Arg Pro Met Thr
145          150          155          160
Leu Glu Glu Val Gln Asn Gln Asn Lys Phe Gln Leu Glu Ser Ser Phe
          165          170          175
Leu Thr Leu Leu Gln Asn Ala Leu Glu Glu Glu Lys Ile Ala Glu Phe
          180          185          190
Val Glu Ser Leu Ala Asp Asp Thr Ala Phe His Lys Tyr Ile Ser Gln
          195          200          205
Trp Val Asp Thr Glu Glu
          210

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 927:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 158 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 908721..909194

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 927:

```

Pro Met Gly Arg Tyr Arg Arg Val Thr His Ser Cys Glu Glu Thr Ile
1          5          10          15
Asp Leu Ala Thr Arg Val Gly Arg Asp Leu Thr Pro Gly Met Val Val
          20          25          30
Leu Leu Ser Gly Asp Tyr Gly Ser Gly Lys Thr Glu Phe Val Arg Gly
          35          40          45
Ile Val Gln Gly Phe Leu Gly Glu Ala Ala Val Asp Gln Val Ala Ser
          50          55          60
Pro Ser Phe Ala Leu Leu His Val Tyr Glu Ala Gly Gly Arg Arg Val
65          70          75          80
Cys His Tyr Asp Leu Tyr Arg Leu Glu Thr Met Asp Ile Arg Asn Gly
          85          90          95
Ala Asp Leu Phe Gln Asp Ala Glu Glu Glu Asp Leu Ile Cys Val Glu
          100          105          110
Trp Pro Glu Ala Val Asn Leu Leu Pro Gln Phe Arg Lys Ser Val Cys
          115          120          125
Val Gln Met Arg Ser Leu Thr Asp Ala Gln Arg Glu Val Ser Ile Gly
          130          135          140
Val Thr Asp Gly Cys Asp Leu Ser Phe Phe Met Glu Asn Asp
145          150          155

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 928:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 129 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 909198..909584

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 928:

```

Arg Val Val Leu Leu Lys Asp Val Glu Phe Val Cys Leu Asp Cys Glu
1          5          10          15
Thr Thr Gly Leu Asp Val Lys Lys Asp Arg Val Ile Glu Phe Ala Ala
          20          25          30
Ile Arg Phe Thr Phe Asp Glu Ile Ile Asp Ser Val Glu Phe Leu Ile
          35          40          45
His Pro Glu Arg Ala Val Ser Ala Glu Ser Gln Lys Ile His Lys Ile
50          55          60

```

Ser Asp Ala Met Leu Arg Asp Lys Pro Lys Phe Gly Glu Val Phe Ser  
 65 70 75 80  
 Arg Ile Lys Gly Phe Phe Lys Glu Arg Asp His Ile Val Gly His His  
 85 90 95  
 Val Gly Phe Asp Leu Gln Val Leu Ser Gln Glu Ser Glu Arg Leu Gly  
 100 105 110  
 Glu Thr Leu Leu Pro Lys His His Tyr Val Ile Asp Thr Leu Arg Leu  
 115 120 125  
 Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 929:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 909583..909951

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 929:

Leu Lys Glu Tyr Gly Asp Ser Pro Asn Asn Ser Leu Glu Ala Leu Ala  
 1 5 10 15  
 Arg His Phe Asn Val Pro His Gln Gly Asn His Arg Ala Met Lys Asp  
 20 25 30  
 Val Glu Met Asn Val Lys Val Phe Lys His Leu Thr Lys Arg Phe Arg  
 35 40 45  
 Thr Leu Ser Gln Val Thr His Ile Leu Ser Lys Pro Ile Lys Met Lys  
 50 55 60  
 Tyr Met Pro Leu Gly Lys Tyr Lys Gly Trp Leu Phe Thr Asp Ile Pro  
 65 70 75 80  
 Leu Glu Tyr Leu Leu Trp Ala Ser Lys Met Asp Phe Asp Gln Asp Leu  
 85 90 95  
 Leu Phe Ser Ile Arg Ser Glu Ile Lys Ser Arg Lys Lys Gly Thr Gly  
 100 105 110  
 Phe Ala Gln Ala Asn Asn Pro Phe Leu Gly Leu  
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 930:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 910081..910569

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 930:

Lys Gly Asp Val Arg Lys Asp Asn Lys Glu Asp Lys Arg Lys Lys Val

1				5					10					15				
Ser	Ala	Ser	Cys	Ile	Thr	Asp	His	Ile	Tyr	Lys	Ile	Phe	Pro	Asn	Asp			
			20					25					30					
Leu	Asn	Thr	Asn	Asn	Thr	Xaa	Phe	Gly	Gly	Leu	Leu	Met	Ser	Leu	Leu			
		35					40					45						
Asp	Arg	Leu	Ala	Leu	Val	Val	Ala	Glu	Arg	His	Cys	Glu	Ser	Ile	Cys			
	50					55					60							
Val	Thr	Ala	Phe	Val	Asp	Ala	Met	Arg	Phe	Tyr	Ala	Pro	Ala	Tyr	Met			
65					70					75					80			
Gly	Glu	Asn	Leu	Ile	Cys	Cys	Ala	Ser	Val	Asn	Arg	Ser	Trp	Arg	Thr			
			85					90						95				
Ser	Leu	Glu	Val	Gly	Val	Lys	Val	Trp	Ala	Glu	Asn	Ile	Tyr	Lys	Gln			
			100					105					110					
Glu	His	Arg	His	Ile	Thr	Ser	Ala	Tyr	Phe	Thr	Phe	Val	Ala	Val	Asp			
		115					120					125						
Lys	Asn	Asn	Ser	Pro	Val	Glu	Val	Pro	Glu	Leu	Ile	Pro	Glu	Ser	Gln			
	130					135					140							
Glu	Glu	Ile	Arg	Arg	Phe	Arg	Glu	Ala	Asp	Gln	Arg	Arg	Ala	Leu	Arg			
145					150					155					160			
Leu	Lys	Leu																

(2) INFORMATIONS POUR LA SEQ ID NO: 931:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 910615..910944

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 931:

Ala	Ser	Lys	Gly	Val	Pro	Leu	Val	Phe	Lys	Pro	Val	Ser	Tyr	Ile	Ile			
1				5				10					15					
Leu	Ser	Trp	Val	Leu	Val	Cys	Leu	Ala	Gln	Pro	Asp	Val	Ser	Val	Val			
		20					25					30						
Ala	Ser	Val	Val	Ser	Cys	Ile	Cys	Gly	Tyr	Ser	Leu	Leu	Trp	Ala	Gly			
		35				40					45							
Leu	Phe	Ala	Leu	Val	Glu	Gln	Leu	Ser	Trp	Lys	Lys	Val	Trp	Cys	Ile			
	50				55					60								
Ala	Phe	Ile	Trp	Thr	Trp	Thr	Val	Glu	Gly	Ala	His	Phe	Ser	Trp	Met			
65				70						75					80			
Leu	Glu	Asp	Leu	Tyr	Val	Gly	Thr	Ser	Ile	Tyr	Phe	Val	Trp	Gly	Ile			
			85				90						95					
Leu	Leu	Ser	Tyr	Leu	Ala	Thr	Leu	Phe	Ala	Ser	Phe	Ser	Cys					
		100					105						110					

(2) INFORMATIONS POUR LA SEQ ID NO: 932:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire



(viii) POSITION DANS LE GENOME: 910948..912261

Val 1	Val	Trp	Cys	Cys 5	Arg	Lys	Gln	Tyr	Arg 10	Gly	Ala	Leu	Val	Trp 15	Leu
Pro	Gly	Val	Trp 20	Val	Ala	Ile	Glu	Ala 25	Ile	Arg	Tyr	Tyr	Gly 30	Leu	Leu
Ser	Gly 35	Val	Ser	Phe	Asp	Phe	Ile 40	Gly	Trp	Pro	Leu	Thr 45	Ala	Thr	Ala
Tyr	Gly 50	Arg	Gln	Phe	Gly	Ser 55	Phe	Phe	Gly	Trp	Ala 60	Gly	Gln	Ser	Phe
Leu 65	Val	Ile	Ala	Ala	Asn 70	Ile	Cys	Cys	Phe	Ala 75	Ala	Cys	Leu	Leu	Lys 80
His	Ser	Phe	Ser	Lys 85	Gly	Leu	Trp	Leu	Thr 90	Leu	Cys	Ala	Phe	Pro 95	Tyr
Leu	Leu	Gly 100	Gly	Ala	His	Tyr	Glu	Tyr 105	Leu	Lys	Lys	His	Phe	Ser	Asp
Ser	Glu 115	Val	Leu	Arg	Val	Ala	Ile 120	Val	Gln	Pro	Gly	Tyr 125	Ser	Pro	His
Met	His 130	Ala	Gly	Arg	Met	Ala 135	Ser	Ala	Ile	Trp	Arg 140	Gly	Leu	Val	Ser
Leu 145	Cys	Gln	Thr	Ile	Gln 150	Thr	Pro	Val	Asp	Val 155	Ile	Val	Phe	Pro	Glu 160
Val	Ser	Val	Pro	Phe 165	Gly	Leu	His	Arg	Gln 170	Ala	Tyr	Thr	Leu	His 175	Glu
Asn	Gln	Pro	Val 180	Leu	Glu	Ser	Leu 185	Leu	Pro	Asn	Lys	Ser	Trp 190	Gly	Glu
Phe	Phe 195	Thr	Asn	Leu	Asp	Trp	Ile 200	Gln	Ala	Ile	Ala 205	Glu	Arg	Tyr	Gln
Cys	Thr 210	Val	Ile	Met	Gly	Met 215	Glu	Arg	Trp	Glu	Asn 220	Lys	Gly	Gly	Ile
Leu 225	His	Leu	Tyr	Asn	Ala 230	Ala	Glu	Cys	Val	Ser 235	Arg	Glu	Gly	Glu	Ile 240
Thr	Ser	Tyr	Asp	Lys 245	Arg	Ile	Leu	Val	Pro	Gly 250	Gly	Glu	Tyr	Ile	Pro
Gly	Gly 260	Lys	Ile	Gly	Phe	Ser	Leu 265	Cys	Gln	Thr	Phe 270	Phe	Pro	Glu	Phe
Ala	Leu 275	Pro	Phe	Gln	Arg	Leu 280	Pro	Gly	Glu	Phe	Ser 285	Gly	Val	Val	Asn
Ile	Thr 290	Glu	Arg	Ile	Lys	Ala 295	Gly	Ile	Ser	Ile	Cys 300	Tyr	Glu	Glu	Thr
Phe 305	Gly	Tyr	Ala	Ile	Arg 310	Pro	Tyr	Lys	Arg	Gln 315	Ala	Asp	Ile	Leu	320
Val	Asn	Leu	Thr	Asn 325	Asp	Gly	Trp	Tyr	Pro	Arg 330	Ser	Arg	Leu	Pro 335	Leu
Val	His 340	Phe	Tyr	His	Gly	Met	Leu 345	Arg	Asn	Gln	Glu	Leu	Gly 350	Ile	Pro
Cys	Ile 355	Arg	Ala	Cys	His	Thr	Gly 360	Val	Ser	Ala	Ala 365	Val	Asp	Ser	Leu
Gly	Arg 370	Ile	Val	Gly	Ile	Leu 375	Pro	Trp	Glu	Ser	Arg 380	Thr	Cys	Pro	Val
Ser 385	Thr	Gly	Val	Leu	Gln 390	Val	Ser	Val	Pro	Leu 395	Tyr	Ser	Tyr	His	Thr 400
Val	Tyr	Ala	Arg	Leu	Gly	Asp	Ala	Pro	Leu	Leu	Leu	Ile	Ala	Val	Cys

```

                405                410                415
Ser Val Ile Gly Ala Ile Ala Tyr Phe Tyr Arg Lys Lys Lys Glu Thr
                420                425                430
Pro Pro Gln Thr Phe Phe
                435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 933:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 77 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 912399..912629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 933:

```

Gly Met Leu Phe Arg Gly Gly Ser Ala Phe Trp Lys Ser Cys Asp Ala
1                5                10                15
Tyr Xaa Arg Ala Arg Arg Gly Lys Tyr Arg Arg Ile Phe Ser Arg His
                20                25                30
Ala Ala Ser Glu Gln Tyr Ile Pro Ala Arg Leu Ala Asn Val Cys Gly
                35                40                45
Thr Gly Arg Ser Thr Thr Leu Ser Leu Asp Gly Ser Val Ile Ser Thr
                50                55                60
Val Glu His Leu Leu Ala Ser Leu Leu Leu Arg Ser Gly
65                70                75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 934:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 208 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 912595..913218

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 934:

```

Asn Thr Cys Trp His Arg Ser Tyr Phe Gly Val Asp Asn Val Arg Ile
1                5                10                15
Tyr Cys Ser Glu Asp Glu Ile Pro Ile Gly Asp Gly Ser Ala Gln Val
                20                25                30
Phe Met Asp Leu Ile Asp Gln Ala Gly Ile Gln Glu Gln Gln Thr
                35                40                45
Val Gln Ile Ala Arg Leu Ala His Pro Val Tyr Tyr Gln Tyr Gln Asp
                50                55                60
Thr Ile Leu Ala Ala Phe Pro Ser Asp Glu Phe Lys Ile Ser Tyr Thr
65                70                75                80
Leu His Tyr Ser His Asn Ser Thr Ile Gly Thr Gln Tyr Arg Ser Leu
                85                90                95

```

Val	Ile	Ser	Glu	Glu	Ser	Phe	Arg	Lys	Glu	Ile	Ala	Pro	Cys	Arg	Thr
			100					105					110		
Phe	Ala	Leu	Tyr	Ser	Glu	Leu	Cys	Phe	Leu	Met	Glu	Lys	Gly	Leu	Ile
		115					120					125			
Gly	Gly	Gly	Cys	Val	Gly	Asn	Ala	Val	Leu	Ser	Lys	Xaa	Asp	Gly	Val
		130				135					140				
Ile	Ser	Leu	Gly	Lys	Leu	Arg	Phe	Pro	Asp	Glu	Pro	Val	Arg	His	Lys
145					150					155					160
Ile	Leu	Asp	Leu	Ile	Gly	Asp	Leu	Ser	Leu	Val	Gly	Thr	Pro	Phe	Leu
			165					170						175	
Ala	His	Val	Ile	Ala	Val	Gly	Ser	Gly	His	Ser	Ser	Asn	Ile	Ala	Leu
			180					185					190		
Gly	Asn	Arg	Ile	Leu	Glu	Ala	Leu	Gln	His	Glu	Gln	Glu	Leu	Val	Lys
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 935:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 158 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 913203..913676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 935:

Thr	Gly	Val	Ser	Gln	Met	Asn	Glu	Lys	Pro	Val	Leu	Gly	Ile	Gln	Asp
1				5					10					15	
Ile	Gln	Asn	Leu	Leu	Pro	His	Arg	Tyr	Pro	Phe	Leu	Leu	Val	Asp	Lys
			20					25					30		
Ile	Leu	Ser	Tyr	Asp	Leu	Asn	Thr	Arg	Ser	Val	Val	Ala	Gln	Lys	Asn
		35				40						45			
Val	Thr	Ile	Asn	Glu	Pro	Phe	Phe	Ala	Gly	His	Phe	Pro	Gly	Ala	Pro
	50					55					60				
Ile	Met	Pro	Gly	Val	Leu	Ile	Leu	Glu	Ala	Leu	Ala	Gln	Ala	Ala	Gly
65					70					75					80
Val	Leu	Leu	Gly	Ile	Ile	Leu	Glu	Asn	Asp	Arg	Asp	Lys	Lys	Ile	Ala
				85					90					95	
Leu	Phe	Leu	Gly	Ile	Gln	Lys	Ala	Lys	Phe	Arg	Gln	Pro	Val	Lys	Pro
			100					105					110		
Gly	Asp	Val	Leu	Thr	Leu	Lys	Ala	Glu	Phe	Ser	Leu	Ile	Ser	Ala	Lys
		115				120						125			
Gly	Gly	Lys	Ala	Phe	Ala	Gln	Ala	Phe	Val	Gly	Ser	Gln	Val	Val	Ala
	130					135					140				
Glu	Gly	Glu	Leu	Ser	Phe	Val	Leu	Val	Lys	Lys	Glu	Ser	Ile		
145					150					155					

(2) INFORMATIONS POUR LA SEQ ID NO: 936:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 265 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 913691..914485

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 936:

Met	Thr	Asn	Ile	His	Pro	Thr	Ala	Ile	Val	Glu	Asp	Gly	Ala	Arg	Ile
1				5					10					15	
Gly	Asn	Asn	Val	Thr	Ile	Glu	Pro	Tyr	Ala	Ile	Val	Lys	Lys	Ser	Val
			20					25					30		
Thr	Leu	Trp	Asn	Asp	Val	Val	Val	Lys	Ser	Tyr	Ala	Tyr	Ile	Asp	Gly
		35					40					45			
Phe	Thr	Thr	Ile	Gly	Arg	Xaa	Thr	Thr	Val	Trp	Pro	Ser	Ala	Met	Ile
	50					55				60					
Gly	Asn	Lys	Pro	Gln	Asp	Leu	Lys	Phe	Lys	Gly	Glu	Lys	Thr	Phe	Val
65					70					75					80
Glu	Ile	Gly	Glu	His	Cys	Glu	Ile	Arg	Glu	Phe	Ala	Met	Ile	Thr	Ser
				85					90					95	
Ser	Thr	Phe	Glu	Gly	Thr	Thr	Val	Ser	Ile	Gly	Asn	Asn	Cys	Leu	Ile
			100					105					110		
Met	Pro	Trp	Ala	His	Ile	Ala	His	Asn	Cys	Ser	Val	Gly	Asn	Asn	Val
		115				120						125			
Val	Phe	Ser	Thr	His	Val	Gln	Leu	Ala	Gly	His	Val	Gln	Val	Gly	Asp
	130					135					140				
Cys	Val	Thr	Ile	Gly	Ser	Met	Val	Gly	Val	His	Gln	Phe	Val	Arg	Ile
145					150					155					160
Gly	Ser	Tyr	Ser	Met	Val	Gly	Ala	Met	Ser	Gly	Ile	Arg	Arg	Asp	Ile
				165					170					175	
Pro	Pro	Phe	Thr	Ile	Gly	Thr	Gly	Asn	Pro	Tyr	Ala	Leu	Gly	Gly	Ile
			180					185					190		
Asn	Lys	Val	Gly	Leu	Gln	Arg	Arg	Gln	Val	Ser	Phe	Glu	Thr	Arg	Leu
		195				200						205			
Ala	Leu	Ile	Lys	Thr	Phe	Lys	Arg	Val	Phe	Arg	Ser	Asp	Glu	Ser	Phe
	210					215					220				
Gln	Ala	Ser	Leu	Glu	Ser	Val	Leu	Glu	Asp	Phe	Gly	Glu	Val	Pro	Glu
225					230					235					240
Val	Arg	His	Phe	Val	Glu	Phe	Cys	Arg	Gln	Pro	Ser	Lys	Arg	Gly	Ile
				245					250					255	
Glu	Arg	Gly	Val	Asp	Cys	Glu	Asp	Leu							
			260					265							

(2) INFORMATIONS POUR LA SEQ ID NO: 937:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 207 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 914516..915136

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 937:

Leu	Ser	Leu	Ser	Leu	Arg	Val	Val	Tyr	Leu	Gly	Thr	Pro	Gln	Phe	Ala
1				5				10						15	

Ala	Thr	Val	Leu	Lys	Thr	Leu	Leu	Asp	Ala	His	Thr	His	Ile	Val	Gly
		20						25					30		
Val	Val	Thr	Arg	Ala	Asp	Lys	Pro	Gln	Lys	Arg	Ser	Ser	Lys	Leu	Ile
		35					40					45			
Ser	Ser	Pro	Val	Lys	Gln	Leu	Ala	Leu	Ser	Lys	Asn	Ile	Pro	Leu	Leu
		50				55					60				
Gln	Pro	Ile	Lys	Thr	Thr	Asp	Pro	Ala	Phe	Leu	Ala	Gln	Leu	Arg	Glu
65				70					75						80
Trp	Gln	Ala	Asp	Val	Phe	Ile	Val	Val	Ala	Tyr	Gly	Val	Ile	Leu	Lys
			85						90					95	
Gln	Glu	Leu	Leu	Asp	Ile	Pro	Thr	Tyr	Gly	Cys	Tyr	Asn	Leu	His	Ala
			100					105					110		
Gly	Leu	Leu	Pro	Ala	Tyr	Arg	Gly	Ala	Ala	Pro	Ile	Gln	Arg	Cys	Ile
		115					120					125			
Met	Asp	Gly	Gly	Val	Leu	Ser	Gly	Asn	Thr	Val	Ile	Arg	Met	Asp	Ala
		130				135					140				
Gly	Met	Asp	Thr	Gly	Asp	Ile	Ala	Asn	Val	Asn	Tyr	Val	Ala	Ile	Gly
145				150					155						160
Glu	Asp	Met	Thr	Ala	Gly	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Ala	Ser	Gly
			165						170					175	
Gly	Glu	Leu	Leu	Lys	Thr	Leu	Gln	Glu	Ile	Glu	Ala	Gly	Thr	Val	
		180					185					190			
Arg	His	Val	Pro	Gln	Asn	Glu	Ala	Met	Leu	Arg	Trp	Leu	Leu	Asn	
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 938:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 108 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 915144..915467

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 938:

Gly	Arg	Gly	Arg	Asp	Ser	Leu	Gly	Cys	Ser	Ser	Phe	Ser	Ser	Ile	Arg
1				5					10					15	
Ala	Tyr	Pro	Gly	Ser	Leu	Ala	Cys	Ser	Gly	Arg	Leu	Asp	Ser	Leu	Ser
		20					25					30			
Ile	Pro	Arg	Glu	Arg	Gly	Xaa	Arg	Leu	Gly	Val	Leu	Ser	Ala	Arg	Met
		35				40					45				
Glu	Ser	Phe	Ser	Gly	Asn	Tyr	Gly	Asp	Pro	Gly	Glu	Val	Leu	Gly	Val
	50				55						60				
Ser	Gly	Glu	Asp	Leu	Leu	Ile	Ala	Cys	Arg	Gln	Gly	Ala	Leu	Arg	Leu
65				70					75						80
Arg	Met	Val	Gln	Pro	Glu	Gly	Lys	Ala	Ser	Met	Lys	Ala	Lys	Asp	Phe
			85						90					95	
Phe	Asn	Gly	Gln	Ser	Arg	Leu	Val	Ser	Lys	Leu	Phe				
		100						105							

(2) INFORMATIONS POUR LA SEQ ID NO: 939:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 335 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 915629..916633

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 939:

Val	Asn	Met	Ala	Ala	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	1	5	10	15
Ala	Leu	Lys	Ala	Phe	Phe	Thr	Gln	Pro	Ser	Asn	Lys	Met	Ala	Arg	Val	20	25	30	
Val	Asn	Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Val	Lys	Val	Ala	Lys	Ser	35	40	45	
Ala	Ala	Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	50	55	60	
Ser	Ser	Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	65	70	75	80
Ala	Arg	Thr	Val	Leu	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	85	90	95	
Gly	Thr	Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	Tyr	Met	Lys	Ala	Ala	100	105	110	
Ser	Gln	Lys	Pro	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Val	Ala	Asp	Leu	Cys	115	120	125	
Val	Ser	His	Lys	Arg	Arg	Ala	Ala	Ala	Val	Cys	Ser	Phe	Ile	Gly		130	135	140	
Gly	Ile	Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Ile	Leu	Phe	145	150	155	160
Val	Asn	Lys	Ile	Trp	Arg	Asn	Arg	Phe	Phe	Leu	Pro	Lys	Leu	Lys	Gln	165	170	175	
Ile	Trp	Asp	Leu	Leu	Leu	Ala	Ile	Leu	Trp	Arg	Leu	Thr	Met	Gln	Arg	180	185	190	
Leu	Trp	Trp	Val	Leu	Asp	Ser	Leu	Ser	Val	Arg	Lys	Glu	Gln	Ile	Ala	195	200	205	
Lys	Pro	Pro	Ala	Leu	Val	Leu	Arg	Glu	Lys	Ser	Arg	His	Ser	Asn	Cys	210	215	220	
Arg	Glu	Arg	Lys	Met	Leu	Ala	Arg	Gly	Glu	Ser	Leu	Glu	Arg	Lys	Pro	225	230	235	240
Arg	Arg	Ser	Arg	Ala	Ser	Ser	Met	His	Ser	Ser	Leu	Cys	Thr	Arg	Ser	245	250	255	
Phe	Trp	Asn	Ala	Leu	Pro	Thr	Phe	Ser	Asn	Trp	Cys	Arg	Cys	Leu	Leu	260	265	270	
Gln	Trp	Val	Phe	Val	Gln	Leu	Trp	Leu	Arg	Asp	Val	Arg	Ser	Leu	Pro	275	280	285	
Gln	Leu	Leu	Asp	Cys	Gly	Leu	Ser	Ala	Thr	Glu	Tyr	Xaa	Gly	Phe	Phe	290	295	300	
Lys	Phe	Leu	Lys	Lys	Lys	Ala	Val	Ser	Lys	Lys	Lys	Gln	Pro	Phe	Leu	305	310	315	320
Ser	Thr	Lys	Cys	Leu	Ala	Phe	Leu	Ile	Val	Lys	Ile	Val	Phe	Leu		325	330	335	

(2) INFORMATIONS POUR LA SEQ ID NO: 940:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 916051..916539

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 940:

Leu	His	Arg	Arg	Asn	Tyr	Leu	Pro	Arg	Asp	Ile	Arg	Ser	Tyr	Pro	Ser
1				5					10					15	
Asp	Ser	Val	Cys	Gln	Gln	Asn	Leu	Ala	Gln	Pro	Phe	Leu	Ser	Ser	Gln
		20						25					30		
Thr	Lys	Ala	Asn	Met	Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn
		35					40					45			
His	Ala	Ala	Phe	Val	Val	Gly	Ser	Gly	Leu	Ala	Ile	Ser	Ala	Glu	Arg
	50					55					60				
Ala	Asp	Cys	Glu	Ala	Pro	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Ser
65					70					75					80
Leu	Glu	Leu	Ser	Gly	Glu	Glu	Asn	Ala	Cys	Glu	Arg	Arg	Val	Ala	Gly
				85					90					95	
Glu	Lys	Ala	Lys	Thr	Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met
			100				105						110		
His	Glu	Lys	Phe	Leu	Glu	Cys	Val	Ala	Asp	Val	Phe	Lys	Leu	Val	Pro
		115					120					125			
Leu	Pro	Ile	Thr	Met	Gly	Ile	Arg	Ala	Ile	Val	Ala	Ala	Gly	Cys	Thr
	130					135					140				
Phe	Thr	Thr	Ala	Val	Ile	Gly	Leu	Trp	Thr	Phe	Cys	Asn	Arg	Val	Xaa
145					150					155					160
Gly	Ile	Phe													

(2) INFORMATIONS POUR LA SEQ ID NO: 941:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 221 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 916965..917627

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 941:

Met	Arg	Ser	Gln	Leu	Ser	Leu	Ile	Gly	Lys	Lys	Glu	Gly	Met	Met	His
1				5					10					15	
Val	Phe	Asp	Lys	Asn	Gly	Asn	Leu	Val	Ala	Cys	Ser	Val	Ile	Ser	Val
		20						25					30		
Asp	Ala	Asn	Val	Val	Ala	Gln	Leu	Lys	Thr	Ala	Ser	Ser	Asp	Gly	Tyr
		35					40					45			
Asn	Ala	Val	Gln	Ile	Gly	Ala	Asp	Val	Val	Gln	Ala	Pro	Glu	Lys	Thr
	50					55					60				
Ile	Glu	Lys	Arg	Phe	Ser	Lys	Ala	Leu	Leu	Gly	His	Phe	Lys	Lys	Ser
65					70					75					80
Gly	Gly	Arg	Ala	Cys	Arg	Val	Leu	Lys	Glu	Val	Val	Val	Ser	Glu	Glu

(2) INFORMATION POUR LA SEQ ID NO: 942:

(A) LONGUEUR: 222 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 917639..918304

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 942:

Met	Val	Leu	Leu	Ser	Lys	Phe	Asp	Phe	Ser	Gly	Lys	Glu	Leu	Gly	Lys
1				5					10					15	
Phe	Glu	Leu	Pro	Asp	Ala	Phe	Phe	Thr	Glu	Gly	Arg	Glu	Gln	Ser	Val
			20					25					30		
Lys	Asp	Tyr	Leu	Val	Ala	Ile	Gln	Ala	Asn	Lys	Arg	Gln	Trp	Ser	Ala
		35					40					45			
Cys	Thr	Arg	Gly	Arg	Ser	Glu	Val	Ser	His	Ser	Thr	Lys	Lys	Pro	Phe
	50					55					60				
Arg	Gln	Lys	Gly	Thr	Gly	Asn	Ala	Arg	Gln	Gly	Cys	Leu	Ala	Ala	Pro
65					70					75					80
Gln	Phe	Arg	Gly	Gly	Gly	Ile	Val	Phe	Gly	Pro	Lys	Pro	Lys	Phe	Asp
				85					90					95	
Gln	His	Ile	Arg	Ile	Asn	Lys	Lys	Glu	Arg	Arg	Ala	Ala	Ile	Arg	Leu
			100					105					110		
Leu	Leu	Ala	Gln	Lys	Ile	Gln	Thr	Gly	Lys	Leu	Ile	Val	Ala	Glu	Asn
		115					120					125			
Ser	Val	Phe	Val	Ser	Ser	Leu	Asp	Ala	Pro	Lys	Thr	Lys	Glu	Ala	Leu
	130					135					140				
Arg	Phe	Leu	Lys	Glu	Cys	Asn	Val	Glu	Cys	Arg	Gly	Val	Leu	Phe	Val
145					150					155					160
Asp	Ser	Leu	Ala	His	Val	Gly	Ser	Asn	Glu	Asn	Leu	Arg	Leu	Ser	Val
				165					170					175	
Arg	Asn	Leu	Ser	Ala	Val	Arg	Gly	Phe	Thr	Tyr	Gly	Glu	Asn	Ile	Ser
		180						185					190		
Gly	Tyr	Asp	Ile	Ala	Ala	Ala	Arg	Asn	Ile	Val	Val	Ser	Glu	Lys	Ala
		195					200					205			



Leu Glu Leu Leu Val Glu Ser Leu Val Ser Thr Thr Lys Asp  
 210 215 220

(2) INFORMATIONS POUR LA SEQ ID NO: 943:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 93 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 918377..918655

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 943:

Met	Leu	Glu	Gly	Leu	Ser	Leu	Gly	Asp	Gly	Glu	Gly	Lys	Lys	Lys	Gly
1			5					10					15		
Ser	Phe	Cys	Lys	Asp	Pro	Lys	Tyr	Thr	Phe	Ile	Val	Ala	Gly	Asp	Ala
		20					25					30			
Thr	Lys	Pro	Met	Ile	Ala	Glu	Ala	Ile	Glu	Ala	Ile	Tyr	Ser	Ala	Lys
		35				40					45				
Gly	Val	Lys	Val	Lys	Lys	Val	Asn	Thr	Met	Cys	Val	Lys	Pro	Gln	Pro
	50				55					60					
Thr	Arg	Ile	Phe	Arg	Gly	Arg	Arg	Lys	Gly	Arg	Thr	Ala	Gly	Phe	Lys
65				70					75					80	
Lys	Ala	Ile	Val	Thr	Phe	Val	Asp	Gly	His	Ser	Ile	Gly			
			85					90							

(2) INFORMATIONS POUR LA SEQ ID NO: 944:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 918682..919533

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 944:

Met	Phe	Lys	Lys	Phe	Lys	Pro	Val	Thr	Pro	Gly	Thr	Arg	Gln	Leu	Ile
1			5					10					15		
Leu	Pro	Ser	Phe	Asp	Glu	Leu	Thr	Thr	Gln	Gly	Glu	Leu	Lys	Gly	Ser
		20					25					30			
Ser	Ser	Arg	Arg	Ser	Val	Arg	Pro	Asn	Lys	Lys	Leu	Ser	Phe	Phe	Lys
		35				40					45				
Lys	Ser	Ser	Gly	Gly	Arg	Asp	Asn	Leu	Gly	His	Ile	Ser	Cys	Arg	His
	50				55					60					
Arg	Gly	Gly	Gly	Val	Arg	Arg	His	Tyr	Arg	Val	Ile	Asp	Phe	Lys	Arg
65				70					75					80	
Asn	Lys	Asp	Gly	Ile	Glu	Ala	Lys	Val	Ala	Ser	Val	Glu	Tyr	Asp	Pro
			85					90					95		
Asn	Arg	Ser	Ala	Tyr	Ile	Ala	Leu	Leu	Asn	Tyr	Val	Asp	Gly	Glu	Lys

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 919738..920157

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 946:

Trp	Leu	Asp	Thr	Ser	Trp	Glu	Ser	Ser	Leu	Gln	Gln	Glu	Cys	Leu	Arg
1				5					10					15	
Ala	Ile	Pro	Leu	Lys	Lys	Gly	Ile	Ile	Arg	Arg	Gln	Val	Met	Phe	Lys
			20					25					30		
Ala	Thr	Ala	Arg	Tyr	Ile	Arg	Val	Gln	Pro	Arg	Lys	Ala	Arg	Leu	Ala
		35				40						45			
Ala	Gly	Leu	Met	Arg	Asn	Arg	Ser	Val	Val	Glu	Ala	Gln	Gln	Gln	Leu
	50					55					60				
Ser	Phe	Ser	Gln	Met	Lys	Ala	Gly	Arg	Cys	Leu	Lys	Lys	Val	Leu	Asp
65					70				75					80	
Ser	Ala	Ile	Ala	Asn	Ala	Glu	Ser	Asn	Glu	Asn	Ile	Lys	Arg	Glu	Asn
				85					90					95	
Leu	Cys	Val	Leu	Glu	Val	Arg	Val	Asp	Ala	Gly	Pro	Met	Phe	Lys	Arg
			100					105					110		
Met	Lys	Ser	Lys	Ser	Arg	Gly	Gly	Arg	Ala	Pro	Ile	Leu	Lys	Arg	Thr
		115				120						125			
Ser	His	Leu	Thr	Val	Ile	Val	Gly	Glu	Arg	Gly	Gln				
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 947:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 219 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 920184..920840

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 947:

Met	Ser	Ser	Arg	Val	Xaa	Thr	Ala	Val	Thr	Lys	Lys	Trp	Arg	Ser	Leu
1				5		-			10					15	
Trp	Tyr	Gly	Asn	Asn	Gln	Glu	Phe	Ala	Lys	Phe	Leu	Ile	Glu	Asp	Val
			20					25					30		
Lys	Ile	Arg	Glu	Phe	Leu	Lys	Lys	Lys	Pro	Ser	Cys	Gln	Gly	Ala	Ala
		35				40						45			
Gly	Phe	Val	Val	Lys	Arg	Met	Ser	Gly	Lys	Ile	Glu	Val	Thr	Ile	His
	50					55					60				
Thr	Ala	Arg	Pro	Gly	Leu	Val	Ile	Gly	Lys	Lys	Gly	Ala	Glu	Val	Asp
65					70				75					80	
Ser	Leu	Lys	Ala	Glu	Leu	Lys	Lys	Leu	Thr	Gly	Lys	Asp	Val	Trp	Val
				85					90					95	
Glu	Ile	Ala	Glu	Val	Lys	Arg	Pro	Glu	Leu	Asn	Ala	Gln	Leu	Val	Ala
			100					105					110		
Asp	Gly	Ile	Ala	Lys	Gln	Ile	Glu	Arg	Arg	Val	Ser	Phe	Arg	Arg	Ala
		115				120						125			
Met	Lys	Lys	Ala	Leu	Gln	Ser	Val	Met	Asp	Ala	Gly	Ala	Leu	Gly	Val

```

      130                      135                      140
Lys Val Gln Val Ser Gly Arg Leu Ala Gly Ala Glu Ile Ala Arg Ser
145                      150                      155                      160
Glu Trp Tyr Lys Asn Gly Arg Val Pro Leu His Thr Leu Arg Ala Asp
      165                      170                      175
Ile Asp Tyr Ala Thr Ala Ser Ala Glu Thr Thr Tyr Gly Ile Ile Gly
      180                      185                      190
Ile Lys Val Trp Ile Asn Leu Gly Glu Lys Lys Ala Val Pro Ala Ala
      195                      200                      205
Asn His Ala Gly Ala Ala Ser Thr Ala Ala Ala
      210                      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 948:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 143 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 920866..921294

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 948:

```

Met Asn Gln Tyr Ala Lys Ala Ala Gly Lys Arg Thr Lys Phe Arg Lys
1      5      10      15
Gln Gln Lys Gly Gln Phe Ala Gly Leu Ser Lys Gly Ala Thr Phe Val
      20      25      30
Asp Phe Gly Glu Phe Gly Met Gln Thr Leu Glu Arg Gly Trp Ile Thr
      35      40      45
Ser Arg Gln Ile Glu Ala Cys Arg Val Ala Ile Asn Arg Tyr Leu Lys
      50      55      60
Arg Lys Gly Lys Val Trp Ile Arg Val Phe Pro Asp Lys Ser Val Thr
      65      70      75      80
Lys Lys Pro Ala Glu Thr Arg Met Gly Lys Gly Lys Gly Ala Pro Asp
      85      90      95
His Trp Val Ala Val Val Arg Pro Gly Arg Ile Leu Phe Glu Val Ala
      100      105      110
Asn Val Ser Lys Glu Asp Ala Gln Asp Ala Leu Arg Arg Ala Ala Ala
      115      120      125
Lys Leu Gly Ile Arg Thr Arg Phe Val Lys Arg Val Glu Arg Val
      130      135      140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 949:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 72 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921299..921514

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 949:

Met	Gly	Ala	Lys	Lys	Asn	Leu	Leu	Ala	Glu	Leu	Arg	Glu	Lys	Ser	Ser
1				5					10					15	
Glu	Glu	Leu	Asp	Glu	Phe	Ile	Arg	Asp	Asn	Lys	Lys	Ala	Leu	Phe	Ala
			20					25					30		
Leu	Arg	Ala	Glu	Ala	Ala	Leu	Gln	Asn	Lys	Val	Val	Lys	Thr	His	Gln
			35				40					45			
Phe	Ser	Leu	Tyr	Lys	Lys	Ser	Ile	Ala	Arg	Ala	Leu	Ile	Ile	Lys	Gln
	50					55					60				
Glu	Lys	Lys	Asp	Arg	Val	His	Gly								
65					70										

(2) INFORMATIONS POUR LA SEQ ID NO: 950:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 83 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921510..921758

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 950:

Met	Ala	Ser	Asp	Val	Arg	Gly	Arg	Arg	Lys	Thr	Lys	Ile	Gly	Val	Val
1				5					10					15	
Val	Ser	Ser	Lys	Met	Glu	Lys	Thr	Val	Val	Val	Arg	Val	Glu	Arg	Val
			20					25					30		
Tyr	Ser	His	Pro	Gln	Tyr	Ala	Lys	Val	Val	Arg	Asp	Ser	Ser	Lys	Tyr
		35					40					45			
Tyr	Ala	His	Asn	Glu	Leu	Asp	Val	Lys	Glu	Gly	Asp	Thr	Val	Arg	Ile
	50					55					60				
Gln	Glu	Thr	Arg	Pro	Leu	Ser	Lys	Thr	Lys	Arg	Trp	Arg	Val	Val	Gly
65					70					75					80
Arg	Val	Asn													

(2) INFORMATIONS POUR LA SEQ ID NO: 951:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921778..922143

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 951:

Met	Ile	Gln	Gln	Glu	Ser	Gln	Leu	Lys	Val	Ala	Asp	Asn	Thr	Gly	Ala
1				5					10					15	
Lys	Lys	Val	Lys	Cys	Phe	Lys	Val	Leu	Gly	Gly	Ser	Arg	Arg	Arg	Tyr

		20					25				30				
Ala	Thr	Val	Gly	Asp	Val	Ile	Val	Cys	Ser	Val	Arg	Asp	Ile	Glu	Pro
		35					40					45			
Asp	Ser	Ser	Val	Lys	Lys	Gly	Asp	Val	Val	Lys	Ala	Val	Ile	Val	Arg
		50				55					60				
Thr	Arg	Asn	Asp	Ile	His	Arg	Lys	Asp	Gly	Ser	Thr	Leu	Arg	Phe	Asp
65					70					75					80
Thr	Asn	Ser	Cys	Val	Ile	Ile	Asp	Asp	Lys	Gly	Asn	Pro	Lys	Gly	Thr
				85					90					95	
Arg	Ile	Phe	Gly	Pro	Val	Ala	Arg	Glu	Ile	Arg	Asp	Arg	Gly	Phe	Val
			100					105					110		
Lys	Ile	Ser	Ser	Leu	Ala	Pro	Glu	Val	Ile						
		115					120								

(2) INFORMATIONS POUR LA SEQ ID NO: 952:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 922159..922491

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 952:

Met	Lys	Arg	Arg	Ser	Val	Cys	Val	Gly	Asp	Thr	Val	Tyr	Val	Leu	Ala
1				5					10					15	
Gly	Asn	Asp	Lys	Gly	Lys	Gln	Gly	Lys	Val	Leu	Arg	Cys	Leu	Lys	Asp
			20					25					30		
Lys	Val	Val	Val	Glu	Gly	Ile	Asn	Val	Arg	Val	Lys	Asn	Ile	Lys	Arg
			35				40					45			
Ser	Gln	Glu	Asn	Pro	Lys	Gly	Lys	Arg	Ile	Asn	Ile	Glu	Ala	Pro	Leu
			50			55				60					
His	Ile	Ser	Asn	Val	Arg	Leu	Ser	Ile	Asp	Asn	Gln	Pro	Ala	Arg	Leu
65					70				75						80
Phe	Val	Lys	Val	Thr	Glu	Lys	Gly	Arg	Glu	Leu	Trp	Asn	Lys	His	Ser
				85				90						95	
Asp	Gly	Ser	Ser	Ser	Leu	Tyr	Arg	Leu	Val	Arg	Glu	Arg	Lys	Gly	
			100					105					110		

(2) INFORMATIONS POUR LA SEQ ID NO: 953:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 155 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 922571..923035

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 953:

```

Met Gln Ile Pro Val Leu Lys Lys Ile Val Ile Ser Met Gly Leu Ala
1      5      10      15
Glu Ala Ala Lys Asp Lys Asn Leu Phe Gln Ala His Leu Glu Glu Leu
20      25      30
Ala Val Ile Ser Gly Gln Lys Pro Leu Val Thr Arg Ala Lys Asn Ser
35      40      45
Ile Ala Gly Phe Lys Leu Arg Glu Gly Gln Gly Ile Gly Ala Lys Val
50      55      60
Thr Leu Arg Gly Ile Arg Met Tyr Asp Phe Met Asp Arg Phe Cys Asn
65      70      75      80
Ile Val Ser Pro Arg Ile Arg Asp Phe Arg Gly Phe Ser Cys Lys Gly
85      90      95
Asp Gly Arg Gly Cys Tyr Ser Leu Gly Leu Asp Asp Gln Gln Ile Phe
100      105      110
Pro Glu Val Asp Leu Asp Arg Val Lys Arg Ser Gln Gly Met Asn Ile
115      120      125
Thr Trp Val Thr Thr Ala Gln Thr Asp Ala Glu Cys Leu Thr Leu Leu
130      135      140
Glu Cys Met Gly Leu Arg Phe Lys Lys Ala Gln
145      150      155

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 954:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 98 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 923160..923453

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 954:

```

Ser Asn Ile Arg Ile Leu Lys Gln His Gly Phe Val Ala His Phe Leu
1      5      10      15
Val Lys Glu Glu Asn Arg Lys Arg Leu Met Arg Val Phe Leu Arg Tyr
20      25      30
Gly Glu Asp Arg Arg Pro Val Ile His Ala Leu Lys Arg Val Ser Lys
35      40      45
Pro Ser Arg Arg Val Tyr Val Ser Ala Ala Lys Ile Pro Tyr Val Phe
50      55      60
Gly Asn Met Gly Ile Ala Val Leu Ser Thr Pro Gln Gly Val Leu Glu
65      70      75      80
Gly Ser Val Ala Arg Ala Lys Asn Val Gly Gly Glu Leu Leu Cys Leu
85      90      95
Val Trp

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 955:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 923484..924032

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 955:

```

Met Ser Arg Lys Ala Arg Asp Pro Ile Val Leu Pro Gln Gly Val Glu
1      5      10      15
Val Ser Ile Gln Asn Asp Glu Ile Ser Val Lys Gly Pro Lys Gly Ser
      20      25      30
Leu Thr Gln Val Leu Ala Lys Glu Val Glu Ile Ala Val Lys Gly Asn
      35      40      45
Glu Val Phe Val Ala Pro Ala Ala His Val Val Asp Arg Pro Gly Arg
      50      55      60
Met Gln Gly Leu Tyr Trp Ala Leu Ile Ala Asn Met Val Lys Gly Val
65      70      75      80
His Thr Gly Phe Glu Lys Arg Leu Glu Met Ile Gly Val Gly Phe Arg
      85      90      95
Ala Ala Val Gln Gly Ser Leu Leu Asp Leu Ser Ile Gly Val Ser His
      100     105     110
Pro Thr Lys Met Pro Ile Pro Thr Gly Leu Glu Val Ser Val Glu Lys
      115     120     125
Asn Thr Leu Ile Ser Ile Lys Gly Ile Asn Lys Gln Leu Val Gly Glu
      130     135     140
Phe Ala Ala Cys Val Arg Ala Lys Arg Pro Pro Glu Pro Tyr Lys Gly
145      150      155      160
Lys Gly Ile Arg Tyr Glu Asn Glu Tyr Val Arg Arg Lys Ala Gly Lys
      165      170      175
Ala Ala Lys Thr Gly Lys Lys
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 956:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924057..924425

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 956:

```

Met Glu Ser Ser Leu Tyr Lys Lys Thr Ser Gly Lys Ala Arg Arg Ala
1      5      10      15
Leu Arg Val Arg Lys Ala Leu Lys Gly Cys Ser Leu Lys Pro Arg Leu
      20      25      30
Ser Val Val Lys Thr Asn Lys His Val Tyr Val Gln Leu Ile Asp Asp
      35      40      45
Val Glu Gly Lys Thr Leu Ala Phe Ile Ser Thr Leu Ala Lys Val Ala
      50      55      60
Lys Thr Ser Gly Leu Thr Arg Lys Asn Gln Asp Asn Ala Lys Ala Leu
65      70      75      80
Gly Ile Lys Ile Ala Glu Leu Gly Lys Gly Leu Gln Val Asp Arg Val
      85      90      95

```



Val Phe Asp Arg Gly Ala His Lys Tyr His Gly Val Val Ala Met Val  
                   100                  105                  110  
 Pro Asp Gly Ala Arg Glu Gly Gly Leu Gln Phe  
                   115                  120

(2) INFORMATIONS POUR LA SEQ ID NO: 957:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 165 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924443..924937

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 957:

Xaa Thr Leu Ser Arg Asn Ser His Lys Glu Asp Gln Leu Glu Glu Lys  
 1                  5                  10                  15  
 Val Leu Val Val Asn Arg Cys Cys Lys Val Val Lys Gly Gly Arg Lys  
                   20                  25                  30  
 Phe Ser Phe Ser Ala Leu Ile Leu Val Gly Asp Arg Lys Gly Arg Leu  
                   35                  40                  45  
 Gly Phe Gly Phe Ala Lys Ala Asn Glu Leu Thr Asp Ala Ile Arg Lys  
                   50                  55                  60  
 Gly Gly Asp Ala Ala Arg Lys Asn Leu Val Ser Ile Asn Ser Leu Glu  
 65                  70                  75                  80  
 Gly Gly Ser Ile Pro His Glu Val Leu Val Asn His Asp Gly Ala Glu  
                   85                  90                  95  
 Leu Leu Leu Lys Pro Ala Lys Pro Gly Thr Gly Ile Val Ala Gly Ser  
                   100                  105                  110  
 Arg Ile Arg Leu Ile Leu Glu Met Ala Gly Val Lys Asp Ile Val Ala  
                   115                  120                  125  
 Lys Ser Leu Gly Ser Asn Asn Pro Met Asn Gln Val Lys Ala Ala Phe  
                   130                  135                  140  
 Xaa Ala Leu Leu Thr Leu Ser Cys Lys Asp Asp Ile Met Lys Arg Arg  
 145                  150                  155                  160  
 Ala Val Ile Asn Asp  
                   165

(2) INFORMATIONS POUR LA SEQ ID NO: 958:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924933..925364

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 958:

Met Ile Lys Leu Glu Cys Leu Gln Asp Pro Ser Pro Arg Lys Arg Arg

1				5				10				15			
Thr	Lys	Leu	Leu	Gly	Arg	Gly	Pro	Ser	Thr	Gly	His	Gly	Lys	Thr	Ser
			20					25					30		
Gly	Arg	Gly	His	Lys	Gly	Asp	Gly	Ser	Arg	Ser	Gly	Tyr	Lys	Arg	Arg
		35					40					45			
Phe	Gly	Tyr	Glu	Gly	Gly	Gly	Val	Pro	Leu	Tyr	Arg	Arg	Val	Pro	Thr
	50					55					60				
Arg	Gly	Phe	Ser	His	Lys	Arg	Phe	Asp	Lys	Cys	Val	Glu	Glu	Ile	Thr
65					70					75					80
Thr	Gln	Arg	Leu	Asn	Glu	Ile	Phe	Asp	Asn	Gly	Ala	Glu	Val	Ser	Leu
				85					90					95	
Glu	Ala	Leu	Lys	Glu	Arg	Lys	Val	Ile	His	Arg	Glu	Thr	Ser	Arg	Val
			100					105						110	
Lys	Val	Ile	Leu	Lys	Gly	Ala	Leu	Asp	Lys	Lys	Leu	Val	Trp	Lys	Asp
		115					120					125			
Ala	Ala	Ile	Val	Leu	Ser	Glu	Gly	Val	Lys	Ser	Leu	Ile	Glu	Ala	Val
	130						135					140			

(2) INFORMATIONS POUR LA SEQ ID NO: 959:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 457 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 925390..926760

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 959:

Met	Ala	Thr	Leu	Arg	Gln	Val	Phe	Ser	Ile	Ser	Glu	Leu	Arg	Gln	Lys
1				5					10					15	
Ile	Phe	Phe	Thr	Phe	Ser	Leu	Leu	Ala	Leu	Cys	Lys	Ile	Gly	Val	Phe
			20					25					30		
Ile	Pro	Val	Pro	Gly	Ile	Asn	Gly	Asp	Arg	Ala	Val	Ala	Tyr	Phe	Asn
		35					40					45			
Gln	Leu	Leu	Gly	Ser	Ser	Gln	Asn	Leu	Phe	Gln	Leu	Ala	Asp	Ile	Phe
	50					55					60				
Ser	Gly	Gly	Ala	Phe	Ala	Gln	Met	Thr	Val	Ile	Ala	Leu	Gly	Val	Val
65					70					75					80
Pro	Tyr	Ile	Ser	Ala	Ser	Ile	Ile	Val	Gln	Leu	Leu	Val	Val	Phe	Met
				85					90					95	
Pro	Thr	Leu	Gln	Arg	Glu	Met	Arg	Glu	Ser	Pro	Asp	Gln	Gly	Lys	Arg
			100					105					110		
Lys	Leu	Gly	Arg	Met	Thr	Arg	Leu	Phe	Thr	Leu	Val	Leu	Ala	Cys	Val
		115					120					125			
Gln	Ser	Leu	Leu	Phe	Ala	Lys	Phe	Ala	Leu	Arg	Met	Asn	Leu	Val	Val
	130					135					140				
Pro	Gly	Ile	Val	Leu	Pro	Ala	Met	Leu	Ser	Leu	Lys	Leu	Phe	Gly	Val
145					150					155					160
Pro	Trp	Val	Phe	Tyr	Leu	Thr	Thr	Val	Val	Val	Met	Thr	Thr	Gly	Thr
			165						170					175	
Leu	Leu	Leu	Met	Trp	Val	Gly	Glu	Gln	Ile	Ser	Asp	Lys	Gly	Ile	Gly
		180					185						190		
Asn	Gly	Ile	Ser	Leu	Ile	Ile	Thr	Leu	Gly	Ile	Leu	Ala	Ser	Phe	Pro
	195						200					205			

```

Ser Val Leu Gly Ser Ile Phe Asn Lys Leu Asn Leu Gly Ser Gln Asp
210                215                220
Pro Ser Glu Phe Gly Ile Val Ser Leu Leu Ile Leu Cys Ala Val Phe
225                230                235                240
Val Phe Val Leu Ile Ala Thr Val Leu Ile Ile Glu Gly Val Arg Lys
                245                250                255
Ile Pro Val Gln His Ala Arg Arg Ile Ile Gly Arg Arg Glu Val Val
                260                265                270
Gly Gly Gly Ser Tyr Leu Pro Leu Lys Val Asn Tyr Ala Gly Val Ile
275                280                285
Pro Val Ile Phe Ala Ser Ser Leu Leu Met Phe Pro Ala Thr Ile Gly
290                295                300
Gln Phe Leu Ser Ser Glu Ser Ser Trp Leu Lys Arg Ile Ala Thr Met
305                310                315                320
Leu Ser Pro Gly Ser Val Ala Tyr Ser Ile Phe Tyr Val Leu Leu Ile
                325                330                335
Ile Phe Phe Thr Tyr Phe Trp Thr Ala Thr Gln Phe Arg Pro Glu Gln
340                345                350
Ile Ala Ser Glu Met Lys Lys Asn Gly Ala Phe Ile Pro Gly Ile Arg
355                360                365
Gln Gly Lys Pro Thr Gln Thr Tyr Leu Glu Tyr Thr Met Asn Arg Val
370                375                380
Thr Leu Leu Gly Ala Val Phe Leu Ala Val Val Ala Ile Leu Pro Ser
385                390                395                400
Val Leu Gly Arg Ile Leu Arg Val Asp Ala Asn Val Ser Tyr Phe Leu
                405                410                415
Gly Gly Thr Ala Met Leu Ile Val Val Gly Val Ile Leu Asp Thr Met
                420                425                430
Lys Gln Ile Asp Ala Phe Leu Leu Val Arg Arg Tyr Asp Gly Val Leu
435                440                445
Lys Lys Asp Arg Pro Lys Gly Arg Pro
450                455

```

(2) INFORMATIONS POUR LA SEQ ID NO: 960:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 122 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 926819..927184

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 960:

```

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
1          5          10          15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Leu Ser Lys Glu
20        25        30
Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu
35        40        45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln Ser Asp Tyr
50        55        60
Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65        70        75        80
Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu

```

				85					90					95					
Pro	Val	Arg	Gly	Gln	Arg	Thr	Lys	Thr	Asn	Ser	Arg	Thr	Arg	Lys	Gly				
			100					105					110						
Lys	Arg	Lys	Thr	Ile	Ala	Gly	Lys	Lys	Lys										
			115				120												

(2) INFORMATIONS POUR LA SEQ ID NO: 961:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 132 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 927209..927604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 961:

Leu	Val	Lys	Asn	Gln	Ala	Gln	Lys	Arg	Gly	Val	Lys	Arg	Lys	Gln	Val				
1			5						10				15						
Lys	Asn	Ile	Pro	Ser	Gly	Val	Val	His	Val	Lys	Ala	Thr	Phe	Asn	Asn				
			20					25					30						
Thr	Ile	Val	Thr	Ile	Thr	Asp	Pro	Ala	Gly	Asn	Val	Ile	Ser	Trp	Ala				
		35				40					45								
Ser	Ala	Gly	Lys	Val	Gly	Tyr	Ser	Gly	Ser	Arg	Lys	Ser	Ser	Ala	Phe				
	50				55					60									
Ala	Ala	Thr	Val	Ala	Ala	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Met	Ser	Ser				
65				70					75					80					
Gly	Leu	Lys	Glu	Val	Glu	Val	Gly	Leu	Lys	Gly	Thr	Gly	Ala	Gly	Arg				
			85					90					95						
Glu	Ser	Ala	Val	Arg	Ala	Leu	Ile	Ser	Ser	Gly	Leu	Ile	Val	Ser	Val				
			100					105					110						
Ile	Arg	Asp	Glu	Thr	Pro	Val	Pro	His	Asn	Gly	Cys	Arg	Pro	Arg	Lys				
		115				120						125							
Arg	Arg	Arg	Val																
			130																

(2) INFORMATIONS POUR LA SEQ ID NO: 962:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 927628..928155

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 962:

Met	Ser	Asp	Ser	Ser	His	Asn	Leu	Leu	Tyr	Asn	Lys	Phe	Glu	Leu	Pro				
1			5					10				15							
Glu	Ser	Val	Lys	Met	Ser	Pro	Val	Glu	Gly	Ala	Val	Gly	Gly	Ile	Asp				
			20					25				30							

Lys	Val	Ala	Arg	Phe	Val	Ala	Asp	Pro	Leu	Glu	Lys	Gly	Met	Gly	His
		35					40					45			
Thr	Leu	Gly	Ser	Ala	Leu	Arg	Arg	Ala	Leu	Leu	Ile	Gly	Leu	Glu	Ala
	50					55					60				
Pro	Ala	Ile	Val	Ser	Phe	Ser	Met	Thr	Gly	Val	Leu	His	Glu	Tyr	Met
65					70					75					80
Ala	Val	Glu	Gly	Ile	Ile	Glu	Asp	Val	Thr	Asn	Ile	Val	Leu	Asn	Leu
				85					90					95	
Lys	Gly	Ser	Leu	Leu	Lys	Lys	Tyr	Pro	Leu	Gln	Asp	Cys	Glu	Gly	Gly
			100					105					110		
Arg	Cys	Ser	Gln	Lys	Leu	Arg	Ala	Thr	Ile	Ser	Val	Asp	Ala	Ser	Asp
		115					120					125			
Leu	Ala	Ala	Ala	Gly	Gly	Gln	Lys	Glu	Val	Thr	Leu	Gly	Asp	Leu	Leu
	130					135					140				
Gln	Glu	Gly	Thr	Phe	Glu	Ala	Val	Asn	Pro	Glu	His	Val	Ile	Phe	Thr
145					150					155					160
Val	Thr	Arg	Pro	Met	Gln	Leu	Glu	Val	Met	Leu	Pro	Ser	Cys	Phe	Trp
				165					170					175	

(2) INFORMATIONS POUR LA SEQ ID NO: 963:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 220 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 928100..928759

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 963:

Phe	Leu	Arg	Ser	Arg	Val	Gln	Cys	Asn	Leu	Arg	Leu	Cys	Cys	Arg	Val
1				5					10					15	
Ala	Phe	Gly	Arg	Gly	Tyr	Ser	Pro	Ser	Glu	Arg	Ile	Val	Leu	Glu	Glu
		20						25					30		
Arg	Gly	Met	Asn	Glu	Ile	Val	Leu	Asp	Ala	Ala	Phe	Ser	Pro	Val	Val
	35						40					45			
Leu	Val	Asn	Tyr	Phe	Val	Glu	Asp	Thr	Arg	Val	Gly	Gln	Asp	Thr	Asp
	50					55					60				
Phe	Asp	Arg	Leu	Val	Leu	Gln	Val	Glu	Thr	Asp	Gly	Arg	Val	Ala	Pro
65					70					75					80
Lys	Glu	Ala	Val	Ala	Phe	Ala	Thr	Gln	Ile	Leu	Ser	Lys	His	Phe	Ser
				85					90					95	
Val	Phe	Glu	Lys	Met	Asp	Glu	Lys	Arg	Ile	Val	Phe	Glu	Glu	Ala	Ile
			100					105					110		
Ser	Val	Glu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	His	Lys	Leu	Val	Leu	
		115					120					125			
Gly	Ile	Asn	Glu	Ile	Glu	Leu	Ser	Val	Arg	Ser	Thr	Asn	Cys	Leu	Ser
	130					135					140				
Asn	Ala	Asn	Ile	Glu	Thr	Ile	Gly	Glu	Leu	Val	Ile	Met	Pro	Glu	Pro
145					150					155					160
Arg	Leu	Leu	Gln	Phe	Arg	Asn	Phe	Gly	Lys	Lys	Ser	Leu	Cys	Glu	Ile
				165					170					175	
Lys	Asn	Lys	Leu	Lys	Glu	Met	Lys	Leu	Glu	Leu	Gly	Met	Asp	Leu	Ser
			180					185					190		
Gln	Phe	Gly	Val	Gly	Leu	Asp	Asn	Val	Lys	Glu	Lys	Met	Lys	Trp	Tyr

	195		200		205
Ala	Glu Lys Ile Arg Ser	Ser Lys Asn Thr Lys Gly			
210		215		220	

(2) INFORMATIONS POUR LA SEQ ID NO: 964:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 341 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 929222..930244

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 964:

Leu	Thr	Thr	Trp	Asp	Leu	Ala	Met	Arg	Ile	Val	Ile	Asn	Gly	Phe	Gly
1			5						10					15	
Arg	Ile	Gly	Arg	Leu	Val	Leu	Arg	Gln	Ile	Leu	Lys	Arg	Asn	Ser	Pro
		20						25					30		
Ile	Glu	Val	Val	Ala	Ile	Asn	Asp	Leu	Val	Ala	Gly	Asp	Leu	Leu	Thr
		35					40					45			
Tyr	Leu	Phe	Lys	Tyr	Asp	Ser	Thr	His	Gly	Ser	Phe	Ala	Pro	Gln	Ala
	50					55					60				
Thr	Phe	Ser	Asp	Gly	Cys	Leu	Val	Met	Gly	Glu	Arg	Lys	Ile	Arg	Phe
65				70					75					80	
Leu	Ala	Glu	Lys	Xaa	Val	Gln	Lys	Leu	Pro	Trp	Lys	Asp	Leu	Asp	Val
			85					90					95		
Asp	Val	Val	Ile	Glu	Ser	Thr	Gly	Leu	Phe	Val	Asn	Arg	Asp	Asp	Ala
			100					105					110		
Ala	Lys	His	Leu	Asp	Ser	Gly	Ala	Lys	Arg	Val	Leu	Ile	Thr	Ala	Pro
		115				120						125			
Ala	Lys	Gly	Asp	Val	Pro	Thr	Phe	Val	Met	Gly	Val	Asn	His	Gln	Gln
	130					135				140					
Phe	Asp	Pro	Ala	Asp	Val	Ile	Ile	Ser	Asn	Ala	Ser	Cys	Thr	Thr	Asn
145				150					155					160	
Cys	Leu	Ala	Pro	Leu	Ala	Lys	Val	Leu	Leu	Asp	Asn	Phe	Gly	Ile	Glu
			165					170					175		
Glu	Gly	Leu	Met	Thr	Thr	Val	His	Ala	Ala	Thr	Ala	Thr	Gln	Ser	Val
		180					185						190		
Val	Asp	Gly	Pro	Ser	Arg	Lys	Asp	Trp	Arg	Gly	Gly	Arg	Gly	Ala	Phe
		195				200						205			
Gln	Asn	Ile	Ile	Pro	Ala	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Val	Gly	Leu
	210					215					220				
Cys	Leu	Pro	Glu	Leu	Lys	Gly	Lys	Leu	Thr	Gly	Met	Ala	Phe	Arg	Val
225				230					235					240	
Pro	Val	Ala	Asp	Val	Ser	Val	Val	Asp	Leu	Thr	Val	Lys	Leu	Ser	Ser
			245					250					255		
Ala	Thr	Thr	Tyr	Glu	Ala	Ile	Cys	Glu	Ala	Val	Lys	His	Ala	Ala	Asn
			260					265					270		
Thr	Ser	Met	Lys	Asn	Ile	Met	Tyr	Tyr	Thr	Glu	Glu	Ala	Val	Val	Ser
		275				280						285			
Ser	Asp	Phe	Ile	Gly	Cys	Glu	Tyr	Ser	Ser	Ile	Phe	Asp	Ala	Gln	Ala
	290					295					300				
Gly	Val	Ala	Leu	Asn	Asp	Arg	Phe	Phe	Lys	Leu	Val	Ala	Trp	Tyr	Asp
305				310					315					320	

Asn Glu Ile Gly Tyr Ala Thr Arg Ile Val Asp Leu Leu Glu Tyr Val  
                                   325                                  330                                  335  
 Gln Glu Asn Ser Lys  
                                   340

(2) INFORMATIONS POUR LA SEQ ID NO: 965:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 930222..930656

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 965:

Ser	Thr	Tyr	Lys	Lys	Thr	Leu	Asn	Lys	Gly	Ser	Phe	Val	Tyr	Phe	Thr
1				5					10					15	
Arg	Asp	Pro	Val	Ile	Glu	Thr	Val	Ile	Thr	Ser	Arg	Glu	Gly	Tyr	Lys
			20					25					30		
Leu	Ser	Ile	Arg	Asn	Ser	Lys	His	Leu	Ser	Gln	Asp	Pro	Phe	Val	Val
			35				40					45			
Glu	Ala	Ile	Glu	Val	Val	Arg	Leu	Gly	Gly	Thr	Ser	Phe	Phe	Arg	Asn
	50					55					60				
Cys	Asp	His	Ser	Lys	Pro	Phe	Leu	Leu	Pro	Ala	Ser	Asp	Tyr	Glu	Val
65					70				75					80	
Met	Glu	Ile	Arg	Asp	Ala	Lys	Ile	Asn	Leu	Lys	Ala	Val	Gly	Leu	Asp
				85				90					95		
Arg	Gly	Val	Lys	Ile	Val	Gly	Ser	Arg	Glu	Ala	Leu	Leu	Lys	Met	Pro
			100					105					110		
Lys	Val	Ala	Pro	Ile	Val	Ser	Val	Ser	Glu	Asp	Asn	Thr	Ile	Val	Ser
		115					120					125			
Glu	Glu	Glu	Val	Val	Ala	Asp	Ser	Thr	Val	Ala	Leu	Pro	Leu	Leu	His
	130					135					140				
Leu															
145															

(2) INFORMATIONS POUR LA SEQ ID NO: 966:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 930608..931078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 966:

Arg	Arg	Gly	Ser	Cys	Arg	Leu	Tyr	Cys	Cys	Thr	Pro	Ala	Ser	Thr	Pro
1				5					10					15	
Val	Ala	Pro	Met	Ser	Lys	Lys	Glu	Arg	Arg	Lys	Glu	Phe	Lys	Asn	Glu

(iii) HYPOTHETIQUE: oui



(viii) POSITION DANS LE GENOME: 931549..931959

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 968:

Tyr	Cys	Gly	Met	Gly	Glu	Tyr	Leu	Ser	Asp	Val	Val	Trp	Cys	Leu	Phe
1				5					10					15	
Lys	Asn	Glu	Arg	Ser	Leu	Leu	Arg	Asn	Lys	Lys	Gln	Met	Gln	Ile	Gln
			20					25					30		
Ser	Ala	Ser	Lys	Glu	Gln	Ser	Leu	Ala	Glu	Trp	Glu	Gln	Gln	Val	Cys
		35					40					45			
Glu	Leu	Lys	Ser	Gln	Leu	Ala	Ser	Gln	Glu	Asn	Ala	Asn	Gln	Gln	Glu
	50						55				60				
Ile	Ser	Lys	Leu	Gln	Ala	Glu	Asn	His	Trp	Leu	Gln	Asn	Arg	Leu	Ala
65				70					75					80	
Glu	Lys	Leu	Gln	Gln	Ala	Arg	His	Gln	Asn	Asp	Val	Ile	Asp	Glu	Leu
			85					90					95		
Lys	Arg	Asp	Leu	Val	Glu	Ser	Val	Gln	Gln	Met	Glu	Val	Ser	Glu	Gly
			100					105					110		
Arg	Arg	Leu	Cys	Tyr	Glu	His	Lys	Ile	Arg	Val	Leu	Glu	Gln	Ile	
		115					120					125			
Asp	Arg	Phe	Leu	Ala	Lys	Glu	Glu	Val							
	130					135									

(2) INFORMATIONS POUR LA SEQ ID NO: 969:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 932070..932579

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 969:

Met	Ala	Asp	Leu	Ile	Met	Gly	Ile	Asp	Pro	Gly	Thr	Leu	Val	Cys	Gly
1				5					10					15	
Tyr	Ala	Leu	Ile	Lys	Val	Glu	Asn	Arg	Tyr	His	Ile	His	Pro	His	Ser
			20					25					30		
Phe	Gly	Lys	Val	Lys	Leu	Ser	Gln	Lys	Leu	Ala	Leu	Ala	His	Arg	Tyr
		35					40					45			
Lys	Gln	Leu	Phe	Thr	Glu	Ile	Ser	Thr	Ile	Leu	Gln	Gln	Glu	Ser	Pro
	50					55					60				
Lys	Ala	Val	Val	Leu	Glu	Thr	Gln	Tyr	Val	His	Lys	Asn	Pro	Gln	Ser
65				70					75					80	
Thr	Ile	Lys	Leu	Gly	Met	Ala	Arg	Gly	Val	Leu	Leu	Leu	Ala	Ala	Ser
			85					90					95		
Leu	Gln	Asp	Val	Pro	Val	Phe	Glu	Tyr	Ala	Pro	Asn	Thr	Ala	Lys	Lys
		100					105					110			
Ala	Ala	Val	Gly	Lys	Gly	Asn	Ala	Ser	Lys	Lys	Gln	Val	Gln	Leu	Met
		115				120					125				
Val	Ser	Lys	Leu	Leu	Arg	Val	Pro	Asp	Leu	Leu	Ala	Glu	Asp	Asn	Glu
	130					135					140				
Asp	Ile	Ala	Asp	Ala	Phe	Ala	Leu	Ala	Met	Cys	His	Ala	His	Leu	Ala
145				150					155					160	
Pro	Tyr	Gln	Asp	Leu	Lys	Lys	Thr	Leu	Val						

165

170

(2) INFORMATIONS POUR LA SEQ ID NO: 970:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 200 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 932602..933201

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 970:

Met	Tyr	Glu	Tyr	Ile	Lys	Gly	Thr	Leu	Thr	His	Ile	Asp	Gly	Ser	Tyr
1				5				10					15		
Val	Val	Ile	Glu	Ser	Phe	Gly	Ile	Gly	Tyr	Ala	Ile	Met	Leu	Ser	Glu
		20						25					30		
Arg	Phe	Leu	Val	Asp	Leu	Arg	Ala	Phe	Met	His	Gln	Glu	Val	Leu	Ile
	35					40						45			
Tyr	Val	His	Ser	Val	Ile	Arg	Glu	Thr	Glu	His	Val	Leu	Tyr	Gly	Phe
	50					55					60				
Ser	Ser	Arg	Ala	Glu	Arg	Glu	Cys	Phe	Arg	Leu	Leu	Ile	Ser	Phe	Ser
65					70				75					80	
Gly	Ile	Gly	Pro	Lys	Thr	Gly	Leu	Ser	Ile	Leu	Asn	Met	Phe	Pro	Leu
				85				90						95	
Gln	Glu	Leu	Cys	Ser	Ile	Ala	Arg	Leu	Glu	Asn	Val	Lys	Ala	Ile	Ala
			100					105					110		
Ser	Val	Pro	Gly	Ile	Gly	Lys	Lys	Thr	Ala	Glu	Lys	Leu	Met	Val	Asp
		115					120					125			
Leu	Lys	Gln	Lys	Leu	Pro	Thr	Leu	Met	Pro	Leu	Tyr	Leu	Glu	Glu	Pro
	130					135					140				
Val	Val	Pro	Ser	Ser	Thr	Ala	Asn	Ser	Ser	Phe	Lys	Glu	Gly	Ile	Gly
145					150					155					160
Ala	Leu	Met	Asn	Leu	Gly	Phe	Ser	Arg	Leu	Ala	Ala	Asp	Arg	Met	Met
				165				170						175	
Thr	Glu	Ala	Val	Lys	Glu	Leu	Ser	Glu	Glu	Ala	Ser	Val	Ala	Glu	Leu
			180					185					190		
Leu	Pro	Ile	Ala	Leu	Arg	Lys	Ser								
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 971:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 86 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 933364..933621

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 971:

Met	Glu	Gln	Thr	Leu	Ser	Ile	Ile	Lys	Pro	Asp	Ser	Val	Gly	Lys	Ala
1				5				10					15		
His	Ile	Gly	Glu	Ile	Ile	Ala	Ile	Phe	Glu	Lys	Ser	Gly	Leu	Arg	Ile
		20						25					30		
Ala	Ala	Met	Lys	Met	Val	His	Leu	Ser	Val	Lys	Glu	Ala	Glu	Gly	Phe
		35					40					45			
Tyr	Val	Val	His	Lys	Glu	Arg	Pro	Phe	Phe	Gln	Glu	Leu	Val	Asp	Phe
	50					55					60				
Met	Ile	Ser	Gly	Pro	Val	Val	Val	Met	Val	Leu	Gln	Gly	Glu	Asn	Leu
65					70					75					80
Ser	Pro	Val	Thr	Glu	Ser										
				85											

(2) INFORMATIONS POUR LA SEQ ID NO: 972:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 933522..933785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 972:

Arg	Glu	Thr	Phe	Phe	Pro	Arg	Thr	Gly	Arg	Leu	Tyr	Asp	Leu	Trp	Ser
1				5				10					15		
Cys	Cys	Ser	Asn	Gly	Thr	Ala	Arg	Gly	Lys	Pro	Val	Ala	Arg	Asn	Arg
			20					25					30		
Glu	Leu	Met	Gly	Ala	Thr	Asn	Pro	Lys	Glu	Ala	Ala	Glu	Gly	Ser	Ile
		35					40					45			
Arg	Ala	Leu	Phe	Gly	Glu	Ser	Ile	Gly	Val	Asn	Ala	Val	His	Gly	Ser
	50					55					60				
Asp	Ser	Leu	Glu	Asn	Ala	Ala	Ile	Glu	Val	Ser	Tyr	Phe	Phe	Ala	Lys
65					70					75					80
Thr	Glu	Val	Val	Asn	Ser	Val	Ala								
				85											

(2) INFORMATIONS POUR LA SEQ ID NO: 973:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 233 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(933848..934546)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 973:

Met	Leu	Ile	Asn	Cys	Val	Phe	Val	His	Cys	Glu	Gly	Leu	Pro	Ile	Phe
1				5				10					15		
Lys	Gln	Leu	Gln	Leu	Glu	Glu	Ala	Leu	Leu	Arg	Thr	Ser	Ser	Gln	Asn



Leu	Leu	Asp	Asn	Gly	Glu	Lys	Val	Leu	Gly	Val	Ser	Thr	Lys	Glu	Gly
130						135					140				
Trp	Ala	Tyr	Leu	Gly	Lys	Thr	Val	Val	Leu	Ser	Ser	Gly	Thr	Phe	Met
145					150					155					160
Arg	Gly	Leu	Ile	His	Ile	Gly	Thr	Gln	Asn	Phe	Ser	Gly	Gly	Arg	Leu
				165					170					175	
Gly	Asp	Ala	Ala	Ser	Leu	Gly	Leu	Ser	Glu	Asp	Leu	Lys	Arg	Leu	Gly
			180					185					190		
Phe	Pro	Leu	Gly	Arg	Leu	Lys	Thr	Gly	Thr	Pro	Ala	Arg	Leu	Leu	Ala
		195					200					205			
Ser	Ser	Ile	Asp	Phe	Ser	Val	Met	Glu	Glu	Gln	Pro	Gly	Asp	His	Asn
	210					215					220				
Val	Cys	Phe	Val	His	Arg	Asn	Glu	Met	Phe	Val	Pro	Thr	Leu	Pro	Gln
225					230					235					240
Val	Ser	Cys	His	Ile	Thr	His	Thr	Thr	Asp	Gln	Thr	Lys	Asp	Leu	Ile
				245					250					255	
Thr	Lys	Asn	Leu	His	Arg	Ser	Ala	Leu	Tyr	Gly	Gly	Arg	Ile	Glu	Gly
			260					265					270		
Val	Gly	Pro	Arg	Tyr	Cys	Pro	Ser	Ile	Glu	Asp	Lys	Ile	Val	Lys	Phe
		275					280					285			
Ala	Asp	Lys	Asp	Arg	His	His	Ile	Phe	Ile	Glu	Pro	Glu	Gly	Leu	Asn
	290					295					300				
Thr	Gln	Glu	Val	Tyr	Val	Asn	Gly	Leu	Ser	Thr	Ser	Met	Pro	Phe	Asp
305					310					315					320
Val	Gln	Tyr	Asp	Ile	Ile	Arg	Ser	Val	Ser	Gly	Leu	Glu	Asn	Ala	Ile
				325					330					335	
Ile	Thr	Arg	Pro	Ala	Tyr	Ala	Ile	Glu	Tyr	Asp	Tyr	Val	His	Gly	Asn
			340					345					350		
Val	Ile	Phe	Pro	Ser	Leu	Glu	Ser	Lys	Leu	Ile	Glu	Gly	Leu	Phe	Leu
		355					360					365			
Cys	Gly	Gln	Ile	Asn	Gly	Thr	Thr	Gly	Tyr	Glu	Glu	Ala	Ala	Ala	Gln
	370					375					380				
Gly	Leu	Ile	Ala	Gly	Val	Asn	Ala	Val	Asn	Lys	Val	Leu	Arg	Arg	Pro
385					390					395					400
Pro	Phe	Val	Pro	Ser	Arg	Gln	Glu	Ser	Tyr	Ile	Gly	Val	Met	Leu	Asp
				405					410					415	
Asp	Leu	Thr	Thr	Gln	Val	Leu	Asp	Glu	Pro	Tyr	Arg	Met	Phe	Thr	Ser
			420					425					430		
Arg	Ala	Glu	His	Arg	Leu	Leu	Leu	Arg	Gln	Asp	Asn	Ala	Gly	Met	Arg
		435					440					445			
Leu	Ser	His	Tyr	Gly	His	Ser	Leu	Gly	Leu	Leu	Ser	Ser	Glu	Arg	Tyr
	450					455					460				
Ala	Met	Phe	Gln	Glu	Gln	Lys	Ala	Cys	Ile	Glu	Gln	Glu	Lys	Glu	Arg
465					470					475					480
Leu	Ser	Lys	Thr												

Ala His 595 600 605  
610

(2) INFORMATIONS POUR LA SEQ ID NO: 975:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 466 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(936666..938063)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 975:

Lys	Pro	Gln	Pro	Thr	Gln	Leu	Leu	Ser	Leu	Pro	Asn	Ser	Lys	Glu	Ser
1				5					10					15	
Glu	Met	Ile	Val	Leu	Gly	Cys	Met	Leu	Thr	Ser	Val	Asn	His	Leu	Asn
			20					25				30			
Leu	Ala	Ala	Asn	Leu	Leu	Gln	Glu	Asp	Asp	Phe	Tyr	Phe	Leu	Glu	His
		35					40					45			
Arg	Ile	Ile	Phe	Arg	Val	Leu	Gln	Asp	Ala	Phe	Lys	Ser	Asp	Arg	Pro
50						55					60				
Met	Asp	Pro	His	Leu	Thr	Gly	Glu	Glu	Leu	Lys	Arg	Arg	Asp	Gln	Leu
65					70					75				80	
Asn	Ile	Ile	Gly	Gly	Pro	Ser	Tyr	Leu	Ile	Thr	Leu	Ser	Glu	Phe	Ala
			85					90					95		
Gly	Thr	Ser	Ala	Tyr	Ile	Glu	Glu	Tyr	Ala	Glu	Ile	Ile	Arg	Ser	Lys
			100					105					110		
Ser	Ile	Leu	Arg	Lys	Met	Ile	Gln	Ala	Ala	Lys	Asp	Ile	Glu	Lys	Lys
		115				120						125			
Ala	Ala	Glu	Glu	Pro	Arg	Asp	Val	Thr	Thr	Ala	Leu	Asp	Asp	Ala	Gln
		130				135					140				
Asn	Leu	Leu	Phe	Arg	Ile	Ser	Gln	Thr	Thr	Asn	Leu	Ala	Pro	Tyr	Val
145					150					155					160
Leu	Val	Ala	Asp	Lys	Leu	Lys	Gly	Val	Ala	Ser	Ser	Lys	Asp	Lys	Ser
			165					170					175		
Phe	Leu	Leu	Ala	Leu	Gln	Glu	Arg	Gln	Glu	Ala	Phe	Gln	Ala	Ser	Ala
			180					185					190		
His	Asp	Ser	Ser	Ser	Pro	Met	Leu	Ser	Gly	Phe	Pro	Thr	His	Phe	Leu
		195				200						205			
Asp	Leu	Asp	Arg	Met	Ile	Ser	Gly	Phe	Ser	Pro	Ser	Asn	Leu	Ile	Ile
	210					215					220				
Leu	Ala	Ala	Arg	Pro	Ala	Met	Gly	Lys	Thr	Ala	Leu	Ala	Leu	Asn	Ile
225					230					235				240	
Val	Glu	Asn	Phe	Cys	Phe	Asp	Ser	Arg	Leu	Pro	Val	Gly	Ile	Phe	Ser
			245					250					255		
Leu	Glu	Met	Thr	Val	Asp	Gln	Leu	Ile	His	Arg	Ile	Ile	Cys	Ser	Arg
			260					265					270		
Ser	Glu	Val	Glu	Ala	Lys	Lys	Ile	Ser	Val	Gly	Asp	Ile	Ser	Gly	Arg
		275				280						285			
Asp	Phe	Gln	Arg	Val	Val	Ser	Val	Val	Arg	Glu	Met	Glu	Glu	His	Thr
	290					295					300				
Leu	Leu	Ile	Asp	Asp	Tyr	Pro	Gly	Leu	Lys	Ile	Thr	Asp	Leu	Arg	Ala
305					310					315					320

```

Arg Ala Arg Arg Met Lys Glu Ser Tyr Asp Ile Gln Phe Leu Val Ile
          325          330          335
Asp Tyr Leu Gln Leu Ile Ser Ser Ser Gly Asn Leu Arg Asn Ser Asp
          340          345          350
Ser Arg Asn Gln Glu Ile Ser Xaa Ile Ser Arg Met Leu Xaa Asn Leu
          355          360          365
Ala Arg Glu Leu Asn Ile Pro Ile Leu Cys Xaa Ser Gln Leu Ser Arg
          370          375          380
Glu Val Glu Asp Arg Ala Asn His Arg Pro Leu Met Ser Asp Leu Arg
385          390          395          400
Glu Ser Gly Ser Ile Glu Gln Asp Ala Asp Gln Ile Met Phe Leu Leu
          405          410          415
Arg Arg Glu Tyr Tyr Asp Pro Asn Asp Lys Pro Gly Thr Ala Glu Leu
          420          425          430
Ile Val Ala Lys Asn Arg His Gly Ser Ile Gly Ser Ile Gln Leu Val
          435          440          445
Phe Glu Lys Asp Phe Ala Arg Phe Arg Asn Tyr Ala Gly Cys Glu Phe
          450          455          460
Pro Gly
465

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 976:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 187 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 938538..939098

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 976:

```

Tyr Val Ser Leu Arg Trp Arg Leu Arg Ile Phe Lys Thr Ser Phe Arg
1          5          10          15
Ile Asn Val Met Arg Gln Phe Cys Asn Leu Leu Ser Leu Ser Arg Val
          20          25          30
Trp Leu Ala Leu Leu Phe Cys Gln Glu Arg Ile Ile Thr Arg Leu Leu
          35          40          45
Val Ile Phe Ala Ala Met Val Ser Asp Val Leu Asp Gly Tyr Leu Ala
50          55          60
Arg Arg Tyr Asn Ala Thr Ser Arg Leu Gly Ser Ile Leu Asp Pro Ala
65          70          75          80
Thr Asp Lys Ile Phe Phe Leu Ile Cys Val Gly Val Leu Phe Trp Glu
          85          90          95
Asn Ser Leu Gly Leu Thr His Leu Ala Leu Ile Phe Ser Arg Asp Ile
          100          105          110
Phe Leu Val Phe Phe Gly Phe Tyr Leu Ser Trp Val Arg Gly Trp Lys
          115          120          125
Gly Tyr Asp Tyr Arg Ala Leu Ser Phe Gly Lys Phe Phe Thr Val Val
130          135          140
Gln Phe Phe Ile Leu Phe Gly Val Thr Ile Gly Met Glu Ile Pro Val
145          150          155          160
Leu Trp Leu Ala Pro Leu Val Ile Leu Gly Ala Leu Tyr Phe Leu Glu
          165          170          175
Arg Val Leu Asp Tyr Arg Arg His Cys Leu Glu

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180

185

(2) INFORMATIONS POUR LA SEQ ID NO: 977:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 535 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 939329..940933

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 977:

Asn	Pro	Phe	Arg	Ser	Ser	Gly	Asp	Xaa	Phe	Phe	Pro	Ile	Tyr	Arg	Ser	1	5	10	15
Glu	Phe	Ser	Lys	Phe	Ile	Pro	Leu	Phe	Phe	Leu	Ala	Phe	Phe	Val	Gly	20	25	30	
Val	Asn	Tyr	Ala	Leu	Leu	Lys	Thr	Lys	Asp	Ser	Leu	Val	Leu	Val		35	40	45	
Gly	Ser	Arg	Ala	Gly	Ala	Glu	Val	Ile	Pro	Phe	Leu	Lys	Val	Trp	Gly	50	55	60	
Ile	Val	Pro	Gly	Ala	Val	Ile	Val	Thr	Met	Ile	Tyr	Gly	Trp	Met	Ser	65	70	75	80
Arg	Arg	Tyr	Ser	Arg	Gly	Thr	Val	Phe	Ile	Ser	Leu	Val	Gly	Gly	Phe	85	90	95	
Leu	Gly	Phe	Phe	Ala	Leu	Phe	Ala	Thr	Val	Ile	Tyr	Pro	Ile	Gly	Asp	100	105	110	
Ala	Leu	His	Leu	Asn	Lys	Leu	Ala	Lys	Leu	Gln	Ser	Ile	Leu	Pro		115	120	125	
Pro	Gly	Gly	Arg	Gly	Phe	Val	Val	Met	Val	Gln	Tyr	Trp	Ser	Tyr	Ser	130	135	140	
Leu	Tyr	Tyr	Val	Met	Ser	Glu	Leu	Trp	Ser	Ser	Val	Val	Leu	Ser	Thr	145	150	155	160
Leu	Phe	Trp	Gly	Val	Ala	Asn	His	Ile	Thr	Ser	Val	Arg	Glu	Ala	Gly	165	170	175	
Arg	Phe	Tyr	Ala	Leu	Ile	Asn	Thr	Gly	Leu	Asn	Leu	Ser	Ser	Val	Phe	180	185	190	
Ala	Gly	Glu	Val	Ser	Leu	Trp	Leu	Gly	Arg	Ser	Pro	Val	Ile	Ala	Phe	195	200	205	
Pro	Met	Ala	Val	Asp	Pro	Trp	His	Glu	Met	Leu	Leu	Asn	Ile	Thr	Leu	210	215	220	
Leu	Ile	Val	Leu	Ala	Gly	Gly	Val	Ile	Leu	Tyr	Leu	Tyr	Gln	Lys	Leu	225	230	235	240
Asp	Arg	Leu	Met	Asp	Glu	Thr	Ser	Met	Leu	Glu	Glu	Gly	Leu	Ala	Ala	245	250	255	
Glu	Met	Ser	Val	Ala	Gln	Leu	Lys	Lys	Glu	Lys	Lys	Arg	Ser	Lys	Ala	260	265	270	
Lys	Ala	Lys	Ser	Leu	Phe	Ala	Leu	Leu	Arg	Ser	Arg	Tyr	Leu	Leu		275	280	285	
Gly	Ile	Ala	Val	Val	Val	Leu	Ser	Tyr	Asn	Leu	Val	Ile	His	Leu	Phe	290	295	300	
Glu	Val	Val	Trp	Lys	Asp	Gln	Val	Cys	Arg	Ile	Tyr	Ala	Ser	Arg	Val	305	310	315	320
Glu	Phe	Asn	Ser	Tyr	Met	Ser	Arg	Ile	Thr	Thr	Leu	Thr	Gly	Ile	Val	325	330	335	



```

Ser Ala Leu Ala Gly Ile Phe Ala Ala Gly Gln Thr Ile Arg Arg Trp
      340      345      350
Gly Trp Thr Val Gly Ala Leu Val Pro Pro Leu Thr Ile Leu Ile Thr
      355      360      365
Gly Ala Leu Phe Phe Gly Ala Ile Tyr Ala Val Lys Gly Asp Ala Met
      370      375      380
Ile Phe Gly Gly Ile Leu Gly Ile Ser Pro Leu Val Leu Thr Ala Trp
385      390      395      400
Leu Gly Gly Val Gln Asn Val Phe Ser Arg Ala Ile Lys Phe Thr Tyr
      405      410      415
Phe Asp Gln Thr Lys Glu Met Ala Phe Ile Pro Leu Glu Asp Asp Glu
      420      425      430
Lys Asn Tyr Gly Lys Ala Ala Ile Asp Gly Val Ile Ser Arg Val Gly
      435      440      445
Lys Ser Gly Gly Ser Leu Val Tyr Gln Gly Leu Leu Ile Ile Phe Ser
      450      455      460
Ser Val Ala Ala Ser Leu Asn Ala Ile Thr Ile Val Leu Leu Leu Ala
465      470      475      480
Leu Gly Ser Trp Ile Phe Val Ile Ala Trp Leu Gly Arg Glu Tyr Thr
      485      490      495
Ala Lys Thr Glu Thr Leu Val Arg Val Asn Ala Ser Glu Glu Asp Val
      500      505      510
Leu Gln Glu Glu Arg Glu Ala Ser Ser Leu Val Asp Ala Glu Ser Arg
      515      520      525
Glu Glu Pro Ala Thr Thr Leu
530      535

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(2) INFORMATIONS POUR LA SEQ ID NO: 978:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 331 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 941076..942068

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 978:

```

Met Lys Asn Phe Phe Arg Phe Leu Leu Lys Gly Phe Leu Ser Ala Cys
1      5      10      15
Gly Leu Phe Leu Gly Val Ile Gly Ala Ala Gly Phe Ile Phe Val Leu
      20      25      30
Ser Ala Ser Val Leu Gly Ala Gly Asp Gly Val Leu Phe Val Asn Phe
      35      40      45
Pro Asn Ala Gln Gly Val Val Gln Glu Leu Gly Lys Thr Ala Pro Ile
      50      55      60
Ile Ala Val Ile Asp Ile Asn Asp Ala Ile Ile Ala Ser Ser Gly Ala
65      70      75      80
Ala Lys Arg Leu Gln Ser Ala Leu Gln Pro Leu Asn Glu Ala Pro Tyr
      85      90      95
Lys Gly Arg Val Lys Gly Ile Leu Val Lys Ile Asp Cys Pro Gly Gly
      100      105      110
Glu Val Phe Glu Ile Asp Arg Met Cys Ala Thr Leu Ser Phe Trp Lys
      115      120      125
Lys Gln Trp Gly Ile Pro Val His Val Phe Val Ser Gly Leu Cys Ala

```

130		135		140
Ser Gly Gly Tyr Tyr Val Ala Cys Ile Ala Asp Lys Ile Gly Thr Thr				
145		150		155
Ser Ser Ser Leu Ile Gly Ser Ile Gly Val Arg Ser Gly Pro Tyr Phe				
	165		170	
Asn Val Lys Glu Gly Leu Gln Arg His Gly Val Glu Thr Ala Ile Leu				
	180		185	
Thr Ala Gly Asp Asp Lys Ala Pro Leu Asn Pro Phe Ser Ser Trp Thr				
	195		200	
Glu Glu Glu Tyr Ala Glu Arg Gln Gly Ile Val Asp Ala Phe Tyr Glu				
	210		215	
Gln Phe Val Asp His Val Val Lys Tyr Arg Ser Lys Leu Ser Lys Glu				
225		230		235
Lys Leu Thr Lys Val Leu Gly Ala Arg Val Phe Ile Ala Lys Gln Ala				
	245		250	
Leu Glu Glu Gly Leu Val Asp Ala Ile Asn Gln Thr Gln Glu Gln Ala				
	260		265	
Leu Glu Glu Leu Ala Glu Ala Cys Gly Ile Lys Asp Asn Tyr Arg Val				
	275		280	
Ile Gly Leu Gly Ser Gly His Phe Leu Lys Arg Phe Ser Ser Tyr Leu				
	290		295	
Ser Asn Ser Pro Leu Val Thr Gly Lys Leu Gln Val Thr Ala Leu Pro				
305		310		315
Asp Gln Gln Gln Lys Ser Leu Trp Tyr Met Gly				
	325		330	

(2) INFORMATIONS POUR LA SEQ ID NO: 979:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 866 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 942088..944685

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 979:

Met Lys Lys Leu Phe Val Leu Asp Val Ser Gly Phe Val Phe Arg Ala		
1	5	10
Tyr Phe Ala Leu Pro Glu Met Arg Gly Pro Asn Gly Glu Ser Thr Gln		
	20	25
Xaa Val Phe Gly Phe Ile Arg Ser Leu Asp Lys Leu Ile Lys Asp Leu		
	35	40
Ser Pro Glu Tyr Val Val Ala Val Phe Asp Gly Pro Asn Asn Lys Gln		
	50	55
Ser Arg Gln Glu Leu Tyr Ala Asp Tyr Lys Ser Asn Arg Asp Arg Gln		
65	70	75
Leu Glu Asp Leu Pro Glu Gln Ile Arg Leu Val Lys Gln Tyr Cys Glu		
	85	90
Leu Leu Gly Ile Ser Cys Leu Glu Glu Lys Gly Val Glu Ala Asp Asp		
	100	105
Val Ile Ala Ser Ile Thr Lys Lys Ala Val Ala Asp Gly Phe Glu Val		
	115	120
Cys Ile Cys Thr Ala Asp Lys Asp Leu Leu Gln Leu Val Ser Ser Arg		
	130	135
		140

Val	Ser	Val	Phe	Asn	Pro	Trp	Lys	Glu	Gln	Glu	Ile	Gln	Tyr	Asn	Glu
145					150					155					160
Val	Leu	Leu	Gln	Phe	Gly	Val	Pro	Pro	Glu	Gln	Ile	Ala	Asp	Tyr	Leu
				165					170					175	
Ala	Leu	Val	Gly	Asp	Ser	Ser	Asp	Asn	Ile	Pro	Gly	Val	Ser	Gly	Cys
			180					185					190		
Gly	Pro	Lys	Lys	Ala	Gln	Ala	Leu	Leu	Lys	Glu	Phe	Gln	Ser	Val	Glu
		195					200					205			
Glu	Leu	Val	Ala	Asn	Thr	Glu	Arg	Leu	Ser	Gly	Lys	Thr	Lys	Gln	Met
	210					215						220			
Ile	Glu	Asp	Gln	Lys	Glu	Thr	Leu	Leu	Leu	Ser	Lys	Arg	Leu	Ala	Thr
225					230					235					240
Leu	His	Met	Asp	Leu	Ala	Phe	Pro	Leu	Thr	Thr	Glu	Glu	Phe	Ala	Phe
				245					250					255	
Ser	Pro	Gln	Ala	Ile	Asp	Ser	Ala	Gln	Leu	Asn	Thr	Phe	Tyr	Leu	Gln
			260					265					270		
His	Gly	Phe	Lys	Ala	Leu	Val	Lys	His	Ser	Glu	Thr	Ala	Thr	Ser	Ser
		275					280					285			
Ile	Ala	Val	Gln	Thr	Val	Thr	Asp	Pro	Val	Thr	Leu	Lys	Thr	Val	Leu
	290					295					300				
Glu	Gln	Leu	Lys	Gly	Gly	Glu	Val	Gly	Tyr	Cys	Ala	Ala	Tyr	Thr	Gly
305					310					315					320
Glu	His	Leu	Pro	Ser	Leu	Gln	Leu	His	Gly	Val	Ala	Leu	Ala	Gly	Ala
				325					330					335	
Asn	Gln	Val	Phe	Tyr	Ile	Glu	Val	Ser	Gly	Val	Gln	Glu	Ile	Ala	Leu
			340					345					350		
Leu	Lys	Asp	Phe	Phe	Ala	Asp	Lys	Ala	Thr	Gln	Phe	Phe	Gly	Tyr	Arg
		355					360					365			
Ser	Lys	Arg	Asp	Asn	His	Ala	Leu	Arg	Asn	Ser	Gly	Ile	Asp	Val	His
	370					375					380				
Val	Thr	Ala	Asp	Leu	Val	Leu	Ala	Glu	His	Leu	Val	Ser	Gly	Gly	Ala
385					390					395					400
Lys	Ile	Ser	Phe	Gln	Thr	Leu	Leu	Met	Glu	Ser	Gly	His	Ile	Gln	Glu
				405					410					415	
Ala	Val	Phe	Phe	Ser	Lys	Glu	Trp	Gly	Ala	Gly	Ser	Leu	Pro	Val	Gln
			420					425					430		
Ser	Leu	Pro	Arg	Asp	Pro	Ala	Gln	Tyr	Phe	Gly	Met	Phe	Ala	Ser	Lys
		435				440						445			
Leu	Leu	Ala	Ile	Lys	Asn	Tyr	Leu	Phe	Val	Lys	Leu	Glu	Glu	Lys	Gly
	450				455						460				
Leu	Lys	Asp	Ile	Phe	Glu	Thr	Val	Glu	Gln	Pro	Glu	Glu	Ala	Val	Leu
465					470					475					480
Phe	Ala	Met	Glu	Cys	Val	Gly	Met	Pro	Leu	Asp	Ser	Gln	Gly	Leu	Ala
				485					490					495	
Val	Leu	Asp	Arg	Asp	Leu	Thr	Lys	Glu	Leu	Glu	Glu	Cys	Ser	Gln	Glu
			500					505					510		
Ile	Tyr	Asp	Leu	Thr	Gly	Cys	Glu	Phe	Asn	Ile	Lys	Ser	Pro	Lys	Gln
		515					520					525			
Leu	Ser	Asp	Ile	Leu	Tyr	Gln	Arg	Leu	Gly	Ile	Glu	Pro	Val	Asp	Lys
	530					535					540				
Ala	Lys	Ser	Thr	Lys	Ala	Glu	Val	Leu	Glu	Ala	Leu	Glu	Asp	Arg	His
545					550					555					560
Glu	Ile	Ile	Pro	Lys	Ile	Leu	Met	Phe	Arg	Ala	Thr	Glu	Lys	Met	Leu
				565					570					575	
Ser	Thr	Tyr	Val	Arg	Ala	Leu	Pro	Lys	Gln	Ile	Asn	Ala	Gly	Thr	Gln
			580					585					590		
Arg	Ile	His	Pro	Thr	Phe	Asn	Gln	Val	Gly	Thr	Val	Thr	Gly	Arg	Leu
		595					600					605			
Ser	Cys	Gln	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Ser	Glu	Arg

610	615	620
Gly Arg Ser Leu Arg Glu Ala Phe Arg Val Lys Lys Asp Asn Asp Tyr		
625	630	635
Phe Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Phe Leu Ala His		
	645	650
Leu Ser Gln Asp Glu Thr Leu Lys Arg Ala Phe Asn Ser Gly Glu Asp		
	660	665
Ile His Ala Phe Thr Ala Ser Gln Val Phe Asn Val Pro Leu Glu Gln		
	675	680
Val Thr Lys Gln Glu Arg Tyr Gln Ala Lys Ala Val Asn Phe Gly Leu		
	690	695
Val Tyr Gly Gln Gln Ala Tyr Gly Leu Ser Lys Ile Leu Lys Ile Ser		
705	710	715
Val Ser Glu Ala Gln Gly Leu Met Asp Ala Tyr Phe Ala Arg Tyr Pro		
	725	730
Leu Ala Ala Glu Phe Ile Thr Gln Thr Ile Glu Gln Ala Ser Lys Asn		
	740	745
Gln Lys Val Thr Thr Met Leu Gly Arg Glu Arg Ile Leu Ser Asp Trp		
	755	760
Glu Ser Ser Pro Gly Ala Arg Ala Ala Ser Gly Arg Leu Ala Val Asn		
	770	775
Thr Arg Ile Gln Gly Ser Ala Ala Glu Leu Ile Lys Leu Ala Met Leu		
785	790	795
Asn Ile Ser Asp Glu Met Arg Ser Arg Gly Leu Lys Ser Arg Leu Leu		
	805	810
Leu Gln Ile His Asp Glu Leu Leu Phe Glu Val Pro Ala Glu Glu Leu		
	820	825
Glu Glu Met Arg Ser Leu Val Gln Glu Lys Met Glu Ser Ala Met Glu		
	835	840
Leu Ser Val Pro Leu Val Val Asn Val Leu Ile Gly Lys Asn Trp Ala		
	850	855
Glu Cys		860
865		

(2) INFORMATIONS POUR LA SEQ ID NO: 980:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 218 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 944634..945287

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 980:

Val Cys Ser Phe Ser Cys Glu Cys Leu Asn Trp Lys Lys Leu Gly Gly	
1	5 10 15
Met Leu Asp Leu Leu Lys Ile Ser Val Thr Gly Asp Pro Ser Ser Gly	
	20 25 30
Lys Thr Glu Ala Cys Gln Val Phe Glu Asp Leu Gly Ala Tyr Val Ile	
	35 40 45
Ser Ala Asp Lys Val Ser His Ser Phe Leu Val Pro Tyr Thr Ser Val	
	50 55 60
Gly Gln Arg Ile Ile Asp Leu Leu Gly Pro Glu Ile Ile Ile Glu Asn	
65	70 75 80

```

Thr Leu Ser Arg Lys Ala Ile Ala Glu Lys Val Phe Gly Asn Arg Asp
      85                      90                      95
Leu Leu Leu Ser Leu Glu Glu Ile Leu His Pro Glu Val Cys Arg Phe
      100                      105                      110
Val Glu Glu Lys Tyr Ala His Val Val Gln Glu Gln Lys Tyr Pro Leu
      115                      120                      125
Phe Ile Val Glu Phe Pro Leu Leu Tyr Glu Ile Gln Tyr Ala Asp Trp
      130                      135                      140
Phe Asp Gln Val Ile Leu Ile Ser Ala Asp Thr Gly Ile Arg Lys Glu
      145                      150                      155                      160
Arg Phe Leu Lys Lys Thr Gly Gly Ser Asp Thr Ser Phe Asp Leu Arg
      165                      170                      175
Cys Ala Arg Phe Ser Ser Leu Glu Glu Lys Ile Leu Arg Ala Asp Val
      180                      185                      190
Val Ile Glu Asn Asn Gly Thr Lys Glu Glu Phe Arg Arg Lys Val Lys
      195                      200                      205
Gln Cys Phe Lys Ala Leu Lys Gly Thr Ile
      210                      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 981:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 287 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 945434..946294

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 981:

```

Lys Ile Ala Lys Leu Gln Arg Met Gly Ile Asn Glu Leu Asn Val Leu
1      5      10      15
Ala Arg Gln Tyr Gly Val Lys Asn Val Gly Ser Leu Thr Lys Ser Gln
      20      25      30
Val Val Phe Glu Ile Val Lys Ala Lys Ser Glu Arg Pro Asp Glu Phe
      35      40      45
Leu Ile Gly Glu Gly Val Leu Glu Val Leu Pro Asp Gly Phe Gly Phe
      50      55      60
Leu Arg Ser Pro Thr Tyr Asn Tyr Leu Pro Ser Ala Glu Asp Ile Tyr
      65      70      75      80
Val Ser Pro Ala Gln Ile Arg Arg Phe Asp Leu Lys Lys Gly Asp Thr
      85      90      95
Ile Val Gly Thr Ile Arg Ser Pro Lys Glu Lys Glu Lys Tyr Phe Ala
      100     105     110
Leu Leu Lys Val Asp Lys Ile Asn Gly Ser Thr Pro Asp Lys Ala Lys
      115     120     125
Glu Arg Val Leu Phe Glu Asn Leu Thr Pro Leu His Pro Asn Glu Arg
      130     135     140
Leu Ile Met Glu Ile Gly Lys Glu Asn Leu Ala Glu Arg Val Leu Asp
      145     150     155     160
Leu Thr Ala Pro Ile Gly Lys Gly Gln Arg Gly Leu Ile Val Ala Pro
      165     170     175
Pro Arg Ser Gly Lys Thr Val Ile Leu Gln Ser Ile Ala His Ala Ile
      180     185     190
Ala Val Asn Asn Pro Asp Ala Glu Leu Ile Val Leu Leu Ile Asp Glu

```

(2) INFORMATION POUR LA SEQ ID NO: 982:

(A) LONGUEUR: 128 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 946293..946676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 982:

(2) INFORMATION POUR LA SEQ ID NO: 983:

(A) LONGUEUR: 450 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 947105..948454

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 983:

Asn	Tyr	Phe	Leu	Trp	Trp	Arg	Gly	Gln	Met	Ala	Gly	Arg	Arg	Thr	Lys
1				5					10					15	
Glu	Glu	Gln	Ile	Asn	Arg	Lys	Arg	Ser	His	Phe	Tyr	Arg	Asp	Asn	Val
			20					25					30		
Gly	Val	Ile	Val	Leu	Cys	Gly	Gly	Glu	Gly	Lys	Arg	Leu	Ser	Pro	Leu
		35				40						45			
Thr	Cys	Trp	Arg	Cys	Lys	Pro	Thr	Val	Ser	Phe	Gly	Gly	Arg	Tyr	Lys
	50					55					60				
Leu	Ile	Asp	Val	Pro	Ile	Ser	His	Ala	Phe	Ala	Ser	Glu	Phe	Ser	Lys
65					70					75					80
Ile	Phe	Val	Ile	Gly	Gln	Tyr	Leu	Thr	Tyr	Thr	Leu	Gln	Gln	His	Leu
			85						90					95	
Phe	Lys	Thr	Tyr	Phe	Tyr	His	Gly	Val	Met	Gln	Asp	Gln	Ile	His	Leu
			100					105					110		
Leu	Val	Pro	Glu	Arg	Arg	Asp	Gly	Ser	Gln	Val	Trp	Tyr	Gln	Gly	Thr
		115					120					125			
Ala	Asp	Ala	Ile	Arg	Gln	Asn	Leu	Leu	Tyr	Leu	Gln	Asp	Ser	Arg	Val
		130				135					140				
Glu	Tyr	Phe	Leu	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Asn	Met	Asp	Phe
145					150					155					160
Arg	Ser	Ile	Val	Asp	Tyr	Ala	Ile	Asp	Ala	Gln	Ala	Asp	Met	Val	Ile
				165					170					175	
Ala	Ser	Gln	Pro	Val	Ser	Asp	Lys	Asp	Val	Ser	Arg	Phe	Gly	Val	Leu
			180					185					190		
Lys	Val	Asp	Asp	Glu	Ser	Lys	Leu	Ile	Asp	Phe	Tyr	Glu	Lys	Pro	Gln
		195					200					205			
Ser	Glu	Glu	Ile	Leu	Lys	His	Phe	Arg	Leu	Ser	Asn	Thr	Ala	Met	Lys
		210				215					220				
Lys	Phe	Gly	Leu	Asp	Pro	Gln	His	Gly	Asn	Phe	Leu	Gly	Ser	Met	Gly
225					230					235					240
Ile	Tyr	Leu	Phe	Arg	Lys	Asp	Cys	Leu	Phe	Gln	Leu	Leu	Leu	Glu	Glu
			245						250					255	
Thr	Gly	Asp	Asp	Phe	Gly	Lys	Glu	Leu	Ile	His	Arg	Gln	Met	His	Arg
			260					265					270		
Gly	Lys	Thr	Val	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Thr	Asp	Ile	Gly
		275					280					285			
Thr	Ile	Glu	Ser	Tyr	Tyr	Glu	Ala	Asn	Met	Ala	Leu	Thr	Gln	Arg	Pro
		290				295					300				
Ser	His	Asn	Ile	Arg	Gly	Phe	Asn	Cys	Tyr	Asp	Asp	Gly	Gly	Ile	Ile
305					310					315					320
Tyr	Ser	Lys	Asn	Asn	His	Leu	Pro	Gly	Ala	Ile	Ile	Ser	Asp	Ser	Arg
			325						330					335	
Ile	Ser	Ser	Ser	Leu	Leu	Cys	Glu	Gly	Ala	Met	Ile	Glu	Ser	Gly	Gln
			340					345					350		
Val	Ser	Asn	Ser	Val	Val	Gly									

## (2) INFORMATIONS POUR LA SEQ ID NO: 984:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 252 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 948522..949277

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 984:

Phe	Phe	Tyr	Gln	Ala	Arg	Gly	Phe	Met	Arg	Ile	Phe	Ala	Leu	Ala	Asp	1	5	10	15
Leu	His	Leu	Ser	Leu	Gly	Val	Pro	Glu	Lys	Thr	Met	Glu	Val	Phe	Gly	20	25	30	
Glu	Pro	Trp	Val	Gly	Tyr	His	Gln	Lys	Ile	Glu	Lys	His	Trp	Arg	Asp	35	40	45	
Ile	Val	Ser	Ser	Asp	Asp	Ile	Val	Cys	Leu	Pro	Gly	Asp	Ile	Ser	Trp	50	55	60	
Ala	Met	Arg	Leu	Glu	Glu	Ala	Gln	Val	Asp	Phe	Arg	Phe	Leu	Gly	Ala	65	70	75	80
Leu	Pro	Gly	Ile	Lys	Tyr	Met	Ile	Arg	Gly	Asn	His	Asp	Tyr	Trp	Ser	85	90	95	
Ser	Ala	Ser	Ser	Ala	Lys	Leu	Ala	Asn	Val	Leu	Pro	Glu	Thr	Leu	His	100	105	110	
Tyr	Leu	Ser	Lys	Gly	Tyr	Val	Leu	Leu	Asn	Ala	His	Gln	Ala	Ile	Val	115	120	125	
Gly	Val	Arg	Leu	Trp	Asp	Ser	Ser	Asp	Ile	Cys	Leu	His	Trp	Glu	Thr	130	135	140	
Gln	His	Asp	Gly	Pro	Gln	Arg	Val	Leu	Thr	Glu	Gln	Asp	Asp	Lys	Ile	145	150	155	160
Phe	Leu	Arg	Glu	Tyr	Gly	Arg	Leu	Glu	Arg	Ala	Leu	Lys	Glu	Leu	Pro	165	170	175	
Ala	Ser	Val	Glu	Asp	Val	Leu	Val	Met	Thr	His	Tyr	Pro	Pro	Val	Ser	180	185	190	
Asn	Asp	Gly	Thr	Pro	Gly	Arg	Val	Ser	Asn	Leu	Leu	Glu	Met	Asp	Gly	195	200	205	
Arg	Val	Ser	Arg	Cys	Leu	Phe	Gly	His	Leu	His	Lys	Val	Pro	Arg	Pro	210	215	220	
Phe	Pro	Gly	Phe	Gly	Asn	Ile	Arg	Gly	Ile	Glu	Tyr	Thr	Leu	Val	Ala	225	230	235	240
Ala	Asp	Tyr	Val	Asp	Phe	Ile	Pro	Gln	Val	Val	Ser	245	250						

## (2) INFORMATIONS POUR LA SEQ ID NO: 985:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 106 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui



(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 985:

(2) INFORMATION POUR LA SEQ ID NO: 986:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 949849..950676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 986:

Ala	Lys	Arg	Asn	His	Ser	Gly	Trp	Ile	Lys	Ile	Phe	Leu	Leu	Asn	Met
1				5					10					15	
Ile	Arg	Gly	Ser	Ser	Leu	Ile	Ser	Glu	Val	Arg	Val	Lys	Phe	Lys	Tyr
			20					25					30		
Leu	Arg	Pro	Leu	Ser	Phe	Leu	Val	Leu	Val	Ile	Val	Ala	Phe	Cys	Tyr
			35				40					45			
Gly	Cys	Ser	Arg	Glu	Lys	Gln	Glu	Val	Leu	Val	Gly	Arg	Asp	Ala	Thr
			50			55					60				
Trp	Phe	Pro	Gln	Gln	Phe	Gly	Ile	Tyr	Thr	Ser	Gly	Ile	Asn	Ala	Phe
65					70					75					80
Val	Asn	Asp	Leu	Val	Ser	Glu	Ile	Asn	Tyr	Lys	Glu	Gly	Leu	Asn	Ile
				85					90					95	
Ser	Ile	Val	Asn	Gln	Asp	Trp	Val	His	Leu	Phe	Glu	Asn	Leu	Asp	Asp
			100					105					110		
Lys	Lys	Thr	Ser	Gly	Ala	Phe	Thr	Ser	Ala	Ser	Pro	Ser	Ile	Glu	Met
			115				120					125			
Leu	Ala	Arg	Tyr	Gln	Phe	Ser	Asp	Pro	Val	Leu	Leu	Thr	Gly	Pro	Val
			130			135					140				
Leu	Val	Val	Leu	Glu	Asn	Ser	Pro	Tyr	His	Ser	Leu	Gln	Asp	Leu	Glu
145					150					155					160
Gly	Lys	Leu	Ile	Gly	Val	Tyr	Lys	Phe	Asp	Ser	Ser	Val	Leu	Ile	Ala
				165					170					175	
Gln	Asn	Val	Pro	Asn	Ala	Val	Ile	Asp	Ser	Tyr	Gln	His	Ile	Pro	Val
			180					185					190		
Ala	Leu	Glu	Ala	Leu	Ser	Thr	Gln	Arg	Tyr	Asp	Ala	Leu	Leu	Val	Pro

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          195                200                205
Val Ile Glu Ala Thr Ala Leu Val Glu Thr Ala Tyr Lys Gly Arg Leu
    210                215                220
Arg Ile Ala Ser Glu Pro Leu Asn Glu Glu Gly Leu Arg Leu Val Val
    225                230                235                240
Leu Arg Gly Gly Gly Ser Asp Ser Leu Leu Glu Gly Phe Asn Ala Gly
          245                250                255
Leu Ala Lys Ile Arg Arg Ser Gly Arg Tyr Lys Ala Ile Lys Met Gln
          260                265                270
Ser Arg Leu Pro
          275

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(2) INFORMATIONS POUR LA SEQ ID NO: 987:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 217 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 950680..951330

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 987:

```

Asn Lys Glu Phe Lys Glu Thr Val Val Thr Tyr Leu Leu Ala Asn Phe
1          5          10          15
Gly Gly Pro Arg Thr Ser Gln Glu Ile Val Ser Phe Leu Gln Ala Leu
    20          25          30
Leu Thr Asp Arg Asp Val Thr Gly Met Ile Pro Ser Val Leu His
    35          40          45
Arg Pro Leu Phe Ser Tyr Ile Ala Lys Arg Arg Ala Pro His Val Ala
    50          55          60
Arg Gln Tyr Ala Tyr Leu Gly Gly Gly Ser Pro Ile Phe Gln Asp Thr
    65          70          75          80
Glu Arg Leu Ala Gln Asn Leu Ser Gln Glu Leu Gln Ala Ser Val Ile
          85          90          95
Pro Phe His Thr Tyr Leu Pro Glu Thr His Arg Glu Thr Leu Gln Ala
    100          105          110
Leu Gln Glu Ser Gln Gly Ser Ile Val Gly Ile Pro Leu Phe Pro His
    115          120          125
Tyr Thr Phe Ala Val Thr Gly Ser Ile Ile Arg Phe Phe Leu Gln His
    130          135          140
Leu Pro Glu Lys Pro Ile Ser Trp Ile Thr Gln Phe Gly Val His Pro
    145          150          155          160
Gln Phe Val Ser Cys Met Gln Gln His Ile Arg Asp Cys Leu Ala Ala
          165          170          175
Gln Xaa Ile Ala Val Glu Asp Cys Tyr Phe Leu Phe Ser Val His Gly
          180          185          190
Leu Pro Gln Arg His Ile Arg Leu Gly Asp Pro Tyr Ala Gln Gln Cys
          195          200          205
Gln Ala Ser Phe Glu Ala Leu Arg Arg
    210          215

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(2) INFORMATIONS POUR LA SEQ ID NO: 988:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 951281..951643

Glu	Ile	Leu	Met	Leu	Ser	Asn	Val	Arg	Leu	Leu	Ser	Lys	His	Tyr	Gly
1				5					10					15	
Gly	Glu	Leu	Glu	Gly	Glu	Ile	Ala	Phe	Gln	Ser	Lys	Phe	Gly	Ile	Gly
			20					25					30		
Lys	Trp	Leu	Asp	Pro	Ser	Thr	Gln	Glu	Val	Cys	Gln	Ser	Leu	Arg	Thr
		35					40					45			
Lys	Lys	Arg	Tyr	Ile	Val	Ile	Val	Pro	Phe	Gly	Phe	Val	Ser	Asp	His
	50					55					60				
Ile	Glu	Thr	Leu	Tyr	Glu	Ile	Asp	His	Leu	Tyr	Val	Pro	Ile	Leu	Leu
65					70					75					80
Gln	Lys	Glu	Tyr	Arg	Val	Val	Arg	Ile	Pro	Ala	Ile	Asn	Ala	Ser	Ser
			85						90					95	
Arg	Trp	Val	Ser	Ser	Leu	Ala	Ala	Ile	Val	Arg	Ser	Ser	Pro	Gln	Glu
			100					105					110		
Thr	Ser	Leu	Glu	Pro	Leu	Leu	Met	Pro							
		115					120								

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 951788..952798

Glu	Cys	Gly	Ile	Ser	Met	Lys	Ser	Arg	Asn	Ala	Gln	Ser	Ile	Leu	Glu
1				5					10					15	
Ser	Leu	Cys	Lys	Lys	Thr	His	Arg	Leu	Leu	Leu	Arg	Tyr	Leu	Leu	Lys
			20					25					30		
Gln	Thr	Leu	Leu	Val	Ala	Leu	Gly	Met	Thr	Leu	Met	Val	Ala	Glu	Leu
			35				40					45			
Gly	Ile	Phe	Leu	Tyr	Phe	Phe	Leu	Phe	Ser	Gly	Lys	Thr	Leu	Leu	Pro
	50					55					60				
Ala	Phe	Cys	Leu	Ala	Cys	Phe	Val	Leu	Thr	Ile	Phe	Ile	Cys	Leu	Val
65					70					75					80
Ile	Arg	Leu	Tyr	Ile	Leu	Ser	Lys	Lys	Thr	Glu	Phe	Phe	Asp	Lys	Leu
				85					90					95	
Leu	Ala	Asp	Phe	Val	His	Gln	Ala	Gln	Val	Ile	Phe	Lys	Lys	Lys	Asn
			100					105					110		
Met	Met	Glu	Glu	His	Pro	Glu	Ile	Ala	Ala	Ala	Val	Thr	Gln	Leu	Ser

1

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 953581..954264

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 990:

Arg	Thr	Val	Cys	Phe	Tyr	Arg	Val	Arg	Lys	Thr	Met	Phe	Glu	Ile	Leu
1				5					10					15	
Arg	Lys	Lys	Ile	Ser	Ser	Tyr	Ser	Val	Val	Leu	Phe	Cys	Leu	Val	Val
			20					25					30		
Leu	Ser	Ile	Phe	Leu	Ser	Gly	Lys	Ile	Val	Val	Asn	Val	Lys	Thr	Tyr
		35				40					45				
Arg	Val	Glu	Arg	Gln	Asn	Ser	Leu	Val	Leu	Leu	Ser	Arg	Ser	Val	Glu
	50					55					60				
Ala	Ala	Tyr	Ser	Arg	Gly	Ile	Phe	Pro	Pro	Glu	Thr	Ala	Met	Pro	Met
65					70					75				80	
Leu	Glu	Gln	Ala	Tyr	Arg	Arg	Gly	Gly	Lys	Glu	Ala	Val	Ser	Tyr	Ala
			85						90					95	
Gly	Phe	Leu	Ala	Ser	Cys	Phe	His	Ile	His	Asn	Asp	Pro	Leu	Arg	Gly
			100					105					110		

Ala Tyr Tyr Ser Gly Leu Ala Tyr Gln His Gly Thr His Leu Gln Leu  
 115 120 125  
 Pro Ser Pro Gln His Ile Leu Lys Glu Ile Ala Asp Ala His Ala  
 130 135 140  
 Thr Lys Gln Tyr Gln Glu Val Leu Asp Lys Ser Arg Glu Leu Leu Ser  
 145 150 155 160  
 Ser Ile Ser Ser Ser Lys Asp Phe Pro Met Leu Arg Phe Leu Thr Leu  
 165 170 175  
 Leu Arg Met Ile Glu Val Lys Glu Ser Leu Asn Gln Asp Phe Ser Leu  
 180 185 190  
 Glu Leu Thr Glu Leu Lys Ala Leu Pro Gly Phe Glu Asp Tyr Glu Gln  
 195 200 205  
 Leu Tyr Lys Asp Gly Val Trp Thr Ile Ser Lys Arg Tyr Ser Ser Leu  
 210 215 220  
 Arg Ala Leu Tyr  
 225

## (2) INFORMATIONS POUR LA SEQ ID NO: 991:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 244 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 954426..955157

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 991:

Ser Met Leu Arg Val Leu Ala Tyr Arg Gln Val Ser Phe Ser Lys Phe  
 1 5 10 15  
 Pro His Leu Phe Lys Ser Phe Val Ser Leu Leu Ser Ser Leu Lys Gln  
 20 25 30  
 His Tyr Ser Phe Met Leu Pro Gly Asp Pro Leu Pro Lys Lys Lys Ala  
 35 40 45  
 Leu Met Leu Thr Phe Asp His Ala Ser Val Asp Phe Tyr Thr His Val  
 50 55 60  
 Phe Pro Leu Leu Gln Asn Leu Gln Ile Pro Ala Val Ile Gly Val Ala  
 65 70 75 80  
 Trp Arg Tyr Val Ala Asp Leu Glu Gly Glu Asp Leu Pro Ile Asp Val  
 85 90 95  
 Arg Ile Ala Pro Ser Asp Phe Leu Ala Phe Gln Asp Glu Ile Phe Ser  
 100 105 110  
 Tyr His Gln Pro Phe Cys Ser Val Arg Glu Leu Cys His Met Ala Ala  
 115 120 125  
 Ser Pro Leu Val Arg Phe Ala Ser Ser Gly Phe Ala Ile Arg Asn Leu  
 130 135 140  
 Lys Tyr Ala Pro Pro Tyr Leu Asp Thr Glu Ile Leu Leu Ser Lys Ile  
 145 150 155 160  
 Leu Leu Glu Asn Ala Ile Gln Ser Pro Val Glu Ser Phe Phe Phe Pro  
 165 170 175  
 Leu Gly Lys Ser Asp Val Val Ser Gln His Phe Val Gln Glu Thr Tyr  
 180 185 190  
 Arg Tyr Ser Phe Val Leu Gly Asn Thr Ala Ser Phe Ser Tyr Pro Thr  
 195 200 205  
 Gln Ser Leu His Gly Ile Pro Arg Ile Asp Met Pro Leu Asp Ser Gln

	210		215		220	
Arg	Val	Pro	Ser	Leu	Tyr	Gln
225				230		235
Leu	Val	Leu	Arg			

(2) INFORMATIONS POUR LA SEQ ID NO: 992:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 729 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 955754..957940

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 992:

Arg	Arg	Gln	Arg	Met	Ile	Asp	Lys	Ile	Ile	Arg	Thr	Val	Leu	Val	Leu
1				5					10					15	
Ser	Leu	Phe	Leu	Leu	Tyr	Trp	Ser	Ser	Asp	Leu	Leu	Glu	Lys	Asp	Val
			20					25					30		
Lys	Ser	Ile	Lys	Arg	Glu	Leu	Lys	Ala	Leu	His	Glu	Asp	Val	Leu	Glu
		35					40					45			
Leu	Val	Arg	Ile	Ser	His	Gln	Gln	Lys	Asn	Trp	Val	Gln	Ser	Ile	Asp
	50					55					60				
Phe	Ser	Val	Ser	Pro	Glu	Ile	Ser	Val	Leu	Lys	Asp	Cys	Gly	Asp	Pro
65				70						75					80
Ala	Phe	Pro	Asn	Leu	Cys	Glu	Asp	Pro	Tyr	Val	Glu	Lys	Val	Val	
			85					90					95		
Pro	Ser	Leu	Leu	Lys	Glu	Gly	Phe	Val	Pro	Lys	Gly	Ile	Leu	Arg	Thr
			100					105					110		
Ala	Gln	Val	Gly	Arg	Pro	Asp	Asn	Leu	Ser	Pro	Phe	Asn	Gly	Phe	Val
		115					120					125			
Asn	Ile	Val	Arg	Phe	Tyr	Glu	Leu	Cys	Val	Pro	Asn	Leu	Ala	Val	Glu
	130					135					140				
His	Val	Gly	Lys	Tyr	Glu	Glu	Phe	Ala	Pro	Ser	Leu	Ala	Leu	Lys	Ile
145				150						155					160
Glu	Glu	His	Tyr	Val	Glu	Asp	Gly	Ser	Gly	Asp	Lys	Glu	Phe	His	Ile
			165					170						175	
Tyr	Leu	Arg	Pro	Asn	Met	Phe	Trp	Glu	Pro	Ile	Asp	Pro	Thr	Leu	Phe
		180						185					190		
Pro	Lys	Asn	Ile	Thr	Leu	Ala	Asp	Thr	Phe	Leu	Arg	Pro	His	Pro	Val
		195					200					205			
Thr	Ala	His	Asp	Val	Lys	Phe	Tyr	Tyr	Asp	Val	Val	Met	Asn	Pro	Tyr
	210					215					220				
Val	Ala	Glu	Met	Arg	Ala	Val	Ala	Met	Arg	Ser	Tyr	Phe	Glu	Asp	Met
225				230						235					240
Val	Ser	Val	Arg	Val	Glu	Asn	Asp	Leu	Lys	Leu	Ile	Val	Arg	Trp	Arg
			245					250						255	
Ala	His	Thr	Val	Arg	Asn	Glu	Gln	Gly	Glu	Glu	Glu	Lys	Lys	Val	Leu
		260						265					270		
Tyr	Ser	Ala	Phe	Ala	Asn	Thr	Leu	Ala	Leu	Gln	Pro	Leu	Pro	Cys	Phe
		275					280					285			
Val	Tyr	Gln	Tyr	Phe	Ala	Asn	Gly	Glu	Lys	Ile	Val	Pro	Glu	Asp	Ser
	290					295					300				

Asp	Pro	Asp	Thr	Tyr	Arg	Lys	Asp	Ser	Val	Trp	Ala	Gln	Asn	Phe	Ser	305	310	315	320
Ser	His	Trp	Ala	Tyr	Asn	Tyr	Ile	Val	Ser	Cys	Gly	Ala	Phe	Arg	Phe	325	330	335	335
Ala	Gly	Met	Asp	Asp	Glu	Lys	Ile	Thr	Leu	Val	Arg	Asn	Pro	Asn	Tyr	340	345	350	350
His	Asn	Pro	Phe	Ala	Ala	Leu	Val	Glu	Lys	Arg	Tyr	Ile	Tyr	Met	Lys	355	360	365	365
Asp	Ser	Thr	Asp	Ser	Leu	Phe	Gln	Asp	Phe	Lys	Ala	Gly	Lys	Val	Asp	370	375	380	380
Ile	Ala	Tyr	Phe	Pro	Pro	Asn	His	Val	Asp	Asn	Leu	Ala	Ser	Phe	Met	385	390	395	400
Gln	Thr	Ser	Ala	Tyr	Lys	Glu	Gln	Ala	Ala	Arg	Gly	Glu	Ala	Ile	Leu	405	410	415	415
Glu	Lys	Asn	Ser	Ser	Asp	Arg	Ser	Tyr	Ser	Tyr	Ile	Gly	Trp	Asn	Cys	420	425	430	430
Leu	Ser	Leu	Phe	Phe	Asn	Asn	Arg	Ser	Val	Arg	Gln	Ala	Met	Asn	Met	435	440	445	445
Leu	Ile	Asp	Arg	Asp	Arg	Ile	Ile	Glu	Gln	Cys	Leu	Asp	Gly	Arg	Gly	450	455	460	460
Val	Ser	Val	Ser	Gly	Pro	Phe	Ser	Leu	Cys	Ser	Pro	Ser	Tyr	Asn	Arg	465	470	475	480
Asp	Val	Glu	Gly	Trp	Gln	Tyr	Ser	Pro	Glu	Glu	Ala	Ala	Arg	Lys	Leu	485	490	495	495
Glu	Glu	Glu	Gly	Trp	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Ile	Arg	Glu	Lys	500	505	510	510
Val	Ile	Asp	Gly	Val	Val	Val	Pro	Phe	Arg	Phe	Arg	Leu	Cys	Tyr	Tyr	515	520	525	525
Val	Lys	Ser	Val	Thr	Ala	Arg	Thr	Ile	Ala	Glu	Tyr	Val	Ala	Thr	Val	530	535	540	540
Cys	Lys	Glu	Val	Gly	Ile	Glu	Cys	Cys	Leu	Leu	Gly	Leu	Asp	Met	Ala	545	550	555	560
Asp	Tyr	Ser	Gln	Ala	Leu	Glu	Glu	Lys	Asn	Phe	Asp	Ala	Ile	Leu	Ser	565	570	575	575
Gly	Trp	Cys	Leu	Gly	Thr	Pro	Pro	Glu	Asp	Pro	Arg	Ala	Leu	Trp	His	580	585	590	590
Ser	Glu	Gly	Ala	Leu	Glu	Lys	Gly	Ser	Ala	Asn	Ala	Val	Gly	Phe	Cys	595	600	605	605
Asn	Glu	Glu	Ala	Asp	Arg	Ile	Ile	Glu	Gln	Leu	Ser	Tyr	Glu	Tyr	Asp	610	615	620	620
Ser	Asn	Lys	Arg	Gln	Ala	Leu	Tyr	His	Arg	Phe	His	Glu	Val	Ile	His	625	630	635	640
Glu	Glu	Ser	Pro	Tyr	Ala	Phe	Leu	Tyr	Ser	Arg	Gln	Tyr	Ser	Leu	Val	645	650	655	655
Tyr	Lys	Glu	Phe	Val	Lys	Asn	Ile	Phe	Val	Pro	Thr	Glu	His	Gln	Asp	660	665	670	670
Leu	Ile	Pro	Gly	Ala	Gln	Asp	Glu	Thr	Val	Asn	Leu	Ser	Met	Leu	Trp	675	680	685	685
Val	Asp	Lys	Glu	Glu	Gly	Arg	Ser	Pro	Leu	Tyr	Leu	Lys	Thr	Ser	Ala	690	695	700	700
Phe	Asp	Ser	Leu	Asn	Ala	Leu	Cys	Tyr	His	Leu	Cys	Glu	Phe	Cys	Asp	705	710	715	720
Ser	Gln	Cys	Cys	Ser	Arg	Arg	Pro	Ala								725			

(2) INFORMATIONS POUR LA SEQ ID NO: 993:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 957837..959312

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 993:

Asp 1	Leu	Arg	Tyr	Ile 5	Leu	Lys	Arg	Leu 10	Leu	Ile	Pro	Leu 15	Thr	Leu
Phe	Ala	Ile	Ile 20	Ser	Val	Asn	Phe 25	Val	Ile	Leu	Asn 30	Ala	Ala	Pro Gly
Asp	Leu	Leu	Glu 35	Glu	His	Ser 40	Val 45	Asp	Ala	Gln	Gly 50	Glu	Ala	Gly Arg
Ser	Asp	Lys	Ile 50	Arg	Thr	Tyr 55	Lys 60	Gly	Pro	Asp	Arg 65	Tyr	Leu	Gln Phe
Arg 65	Glu	His	Tyr 70	Gly	Leu	Thr 75	Leu	Pro	Ile	Phe 80	Asn	Thr	Arg	Pro 85
Gln	Ile	Ser	Arg 85	Ser	Glu	Leu 90	Arg	Ala	Gly 95	Ile	Gln	Glu	Ile	Ile Asp
Gly	Thr	Ile	His 100	Lys	Lys	Ser 105	Lys	Thr	Gly 110	Ser	Ile	Thr	Asn	Ile Lys
Val	Tyr	Trp	Gly 115	Asp	Cys	Ala 120	Lys	Phe	Ile	Met 125	Pro	Ala	Leu	Leu Ala
Glu	Ala	Glu	Asp 130	Ser	Ser	Lys 135	Glu	Asp	Ile	Tyr 140	Arg	His	Val	Ala Ala
Asp 145	Leu	Phe	Ile 150	Arg	Gly	Gly 155	Ile	Arg	Gln	Gly 160	Ile	Val	Glu	Pro Arg
Leu	Leu	Glu	Glu 165	Gln	Arg	Glu 170	Tyr	Asn	Gln	Lys 175	Val	Ser	Lys	Ser Asn
Ala	Glu	Leu	Val 180	Arg	Leu	Leu 185	Asn	Glu	Asp	Asn 190	Ile	Glu	Val	Lys Val
Ala	Ala	Leu	Gln 195	Glu	Trp	Val 200	Glu	Gln	Glu	Gly 205	Gly	Arg	Gly	Gln Leu
Met	Arg	Arg	Asp 210	Leu	Trp	Arg 215	Ile	Phe	Phe	Leu 220	Glu	Thr	Arg	Phe Ala
Lys 225	Tyr	Leu	Ser 230	Arg	Ile	Val 235	Arg	Leu	Asp	Phe 240	Gly	Thr	Leu	Arg Asn
Asp	Cys	His	Lys 245	Thr	Val	Val 250	Ser	Glu	Val	Ile 255	Lys	Arg	Leu	Gly Ser
Ser	Leu	Ile	Leu 260	Ser	Leu	Leu 265	Pro	Met	Ile	Val 270	Val	Phe	Ile	Leu Cys
Gln	Val	Phe	Gly 275	Met	Ile	Met 280	Ala	Val	Asn	Lys 285	Asn	His	Trp	Ile Asp
His	Leu	Leu	Asn 290	Phe	Leu	Phe 295	Leu	Ile	Leu	Phe 300	Ser	Ile	Pro	Val Phe
Val 305	Ala	Val	Pro 310	Trp	Ile	Ile 315	Asp	Asn	Phe	Val 320	Leu	Asn	Lys	Thr Val
Pro	Phe	Thr	Ser 325	Ile	Ser	Met 330	Pro	Tyr	Ser	Gly 335	Leu	Cys	Ser	Ser Pro
Glu	Ile	Phe	Lys 340	Glu	Met	Thr 345	Ser	Phe	Glu	Lys 350	Leu	Thr	Asp	Ile Val
Leu	His	Ser	Phe 355	Leu	Pro	Phe 360	Cys	Ala	Val	Ser 365	Tyr	Gly	Ala	Phe Ala
Ala	Gln	Ser	Arg 370	Leu	Ser	Arg 375	Ala	Val	Phe	Leu 380	Glu	Val	Leu	Gly Glu



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Asp His Ile Ser Ala Leu Arg Ala Arg Gly Ile Ser Gln Tyr Asp Ile
385                      390                      395                      400
Leu Val Arg His Val Gly Lys Asn Ser Ala Ala Thr Leu Ile Thr Ser
                      405                      410                      415
Leu Ala Ser Ser Leu Ser Ala Leu Leu Gly Gly Ala Leu Val Val Glu
                      420                      425                      430
Thr Leu Phe Asp Ile Asp Gly Phe Gly Lys Phe Phe Tyr Gln Ala Ile
                      435                      440                      445
Leu Asn Arg Asp His Asn Val Val Met Phe Ser Val Ile Met Gly Ser
                      450                      455                      460
Val Ile Ser Leu Ile Gly Tyr Leu Ile Gly Asp Ile Cys Tyr Val Leu
465                      470                      475                      480
Leu Asp Pro Arg Val Gln Leu Glu Glu Arg Lys Val
                      485                      490

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 994:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 584 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 959299..961050

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 994:

```

Lys Lys Gly Arg Cys Glu Met Lys Glu Pro Gln Thr Ser Tyr Gln Arg
1                      5                      10                      15
Phe Phe Arg Ala Tyr Asn Arg Arg Ala Leu Pro Ser Ile Ala Leu Lys
                      20                      25                      30
Phe Phe Ile Gly Leu Met Leu Ile Gly Ile Tyr Ala Pro Leu Phe Ala
                      35                      40                      45
Ser Ser Lys Pro Ile Leu Val Arg Trp His Gly Glu Trp Tyr Ser Pro
50                      55                      60
Leu Phe Arg Tyr Leu Leu Phe Pro Gly Phe Tyr Thr Lys Ser Ile Asp
65                      70                      75                      80
Leu Phe Phe Asn Val Leu Met Leu Thr Leu Pro Phe Phe Ile Leu Gly
                      85                      90                      95
Phe Arg Tyr Leu Ser Gly Val Trp Lys Lys Leu Phe Leu Gly Val Val
                      100                      105                      110
Thr Gly Ile His Ile Ala Val Phe Ser Phe Ala Leu Ser Gly Arg Val
                      115                      120                      125
Gln Asp Pro Cys Arg Asp Glu Leu Leu Lys Gln Lys Arg Ala Lys His
130                      135                      140
Leu Gln Gln Glu Leu Lys Thr Thr Pro Lys Thr Glu Phe Leu Pro Thr
145                      150                      155                      160
Ile Ala Lys Arg Thr Arg Thr Trp Glu Ser Glu Arg Ala Tyr Met Ser
                      165                      170                      175
Lys Tyr Glu Gln Leu Gly Met Leu Val Lys Ala Lys Tyr Arg Lys Met
180                      185                      190
Gln His Asp His Leu Glu Lys Gln Arg Glu Ala Tyr Glu Leu Cys Lys
195                      200                      205
Gln Ser Pro Met Pro Thr Leu Arg Phe Leu Glu Met Lys Asn Glu Thr
210                      215                      220
Ala Ser Leu Arg Phe Phe Lys Asn Lys Ile Asn Lys Leu Lys Ala Ser

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225					230					235					240
Tyr	Pro	Glu	Gly	Phe	Glu	Gly	Trp	Gly	Thr	Leu	Leu	Glu	Asp	Tyr	Arg
				245					250					255	
Pro	Tyr	Leu	Met	Ala	Arg	Ala	Arg	Ser	Glu	His	Ala	Leu	Asn	Met	Ala
			260					265					270		
Ile	Tyr	Glu	Gln	His	Pro	Gln	Glu	Glu	Leu	Arg	Ala	Ala	Phe	Glu	Ala
		275					280					285			
Leu	Glu	Glu	Lys	Glu	Ala	Pro	Phe	Arg	Glu	Gln	Leu	Ala	Phe	Val	Arg
	290					295					300				
Ser	Leu	Leu	Glu	Glu	Arg	Glu	Ala	Leu	Asn	Asn	Ser	Ile	Thr	Phe	Ile
305					310					315					320
Met	Asp	Lys	Arg	Asn	Trp	Ile	Glu	Thr	Glu	Ser	Glu	Gln	Val	Gln	Met
				325					330					335	
Val	Leu	Asn	Pro	Leu	Leu	Ser	Ser	Phe	His	Trp	Glu	Asp	Asp	Ala	Gly
			340					345					350		
Gly	Ser	Arg	Glu	Met	Asn	Lys	Tyr	Val	His	Trp	Trp	Gln	Leu	Thr	Arg
		355					360					365			
Ile	Asn	Arg	Lys	Asp	Leu	Leu	Ala	Ser	Leu	Ile	Phe	Gly	Ile	Arg	Ile
	370					375					380				
Ala	Ile	Val	Val	Gly	Gly	Leu	Gly	Val	Ser	Ile	Ala	Leu	Phe	Ile	Gly
385					390					395					400
Ile	Ile	Val	Gly	Leu	Leu	Ser	Gly	Tyr	Phe	Gly	Gly	Lys	Val	Asp	Met
			405						410					415	
Leu	Leu	Ser	Arg	Val	Thr	Glu	Ile	Trp	Glu	Thr	Met	Pro	Met	Leu	Phe
			420					425					430		
Ile	Leu	Met	Leu	Val	Val	Ala	Ile	Thr	Gln	Lys	Lys	Ser	Leu	Ile	Leu
	435						440					445			
Asp	Ser	Val	Leu	Leu	Gly	Cys	Phe	Gly	Trp	Val	Ser	Ile	Ser	Arg	Tyr
	450					455					460				
Val	Arg	Ile	Glu	Thr	Leu	Lys	Gln	Arg	Asn	Leu	Gly	Tyr	Val	Leu	Ala
465					470					475					480
Ala	Thr	Asn	Leu	Cys	Tyr	Ser	His	Tyr	His	Ile	Met	Val	His	Gln	Ile
				485					490					495	
Leu	Pro	Asn	Val	Ile	Val	Pro	Val	Ile	Ser	Leu	Leu	Pro	Phe	Ser	Met
		500						505					510		
Met	Ala	Met	Ile	Ser	Cys	Glu	Ala	Gly	Leu	Thr	Phe	Leu	Gly	Leu	Gly
		515					520					525			
Glu	Glu	Ser	Ser	Ala	Ser	Trp	Gly	Asn	Leu	Leu	Arg	Glu	Gly	Val	Thr
	530					535					540				
Ala	Phe	Pro	Ser	Glu	Ser	Ala	Ile	Leu	Trp	Pro	Pro	Ala	Ile	Met	Leu
545					550				555						560
Thr	Leu	Leu	Leu	Met	Ala	Ile	Ala	Val	Ile	Gly	Asp	Gly	Ile	Arg	Asp
				565				570						575	
Ala	Leu	Asp	Pro	Lys	Met	Gln	Asp								
			580												

(2) INFORMATIONS POUR LA SEQ ID NO: 995:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(961053..961514)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 995:

Ala	Gln	Ala	Cys	Ser	Gln	Gly	Leu	Pro	Ile	Asn	Arg	Thr	Pro	Pro	Ile
1				5					10					15	
Gln	Ile	Ile	Val	His	Phe	Arg	Gly	Asp	Ser	Ile	Phe	His	Ser	Arg	Leu
			20					25					30		
Ser	Pro	Ala	Pro	Val	Phe	Thr	Cys	Leu	Phe	Leu	Gly	Pro	Gly	Ala	His
		35					40					45			
Lys	Ala	Met	Glu	Gly	Leu	Val	Arg	Trp	Cys	Glu	Ala	Tyr	Ala	Asn	Lys
	50					55				60					
Met	Pro	Pro	Lys	Leu	Ser	Phe	Leu	Asp	Leu	Ser	Phe	Lys	Glu	Lys	
65					70					75				80	
Arg	Leu	Ala	Ile	Leu	Gln	Glu	Ile	Arg	Gln	Ile	Pro	Phe	Gly	Thr	Arg
				85					90					95	
His	Thr	Cys	Glu	Glu	Ile	Ala	Glu	Arg	Thr	Lys	Thr	His	Thr	Glu	Glu
			100					105					110		
Val	Leu	Ile	Ala	Cys	Gln	Glu	Asn	Pro	Leu	Pro	Leu	Leu	Ile	Pro	Cys
		115					120						125		
His	Arg	Val	Leu	Ser	Ile	His	Asp	Tyr	Pro	Gly	Gly	Glu	Lys	Leu	Tyr
	130					135					140				
Lys	Ala	Leu	Thr	Glu	Phe	Glu	Glu	Leu	Ser						
145					150										

## (2) INFORMATIONS POUR LA SEQ ID NO: 996:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 363 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(961487..962575)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 996:

Glu	Ile	Ser	Gln	His	Arg	Thr	Arg	Gln	Leu	Met	Lys	Arg	Leu	Phe	Phe
1				5					10					15	
Ile	Cys	Ala	Leu	Ala	Leu	Ser	Pro	Leu	Ala	Tyr	Gly	Ala	Val	Gln	Lys
			20					25					30		
Asp	Pro	Met	Leu	Met	Lys	Glu	Thr	Phe	Arg	Asn	Asn	Tyr	Gly	Ile	Ile
		35					40					45			
Val	Phe	Lys	Gln	Glu	Trp	Asn	Lys	Arg	Gly	Cys	Asp	Gly	Ser	Ile	Thr
	50					55					60				
Arg	Val	Phe	Lys	Asp	Gly	Thr	Thr	Thr	Leu	Glu	Val	Tyr	Ala	Gln	Gly
65					70					75				80	
Ala	Leu	His	Gly	Glu	Val	Thr	Arg	Thr	Phe	Pro	His	Ser	Thr	Thr	Leu
			85						90					95	
Ala	Val	Ile	Glu	Thr	Tyr	Asp	Gln	Gly	Arg	Leu	Leu	Ser	Lys	Lys	Thr
			100					105					110		
Phe	Phe	Pro	Asn	Ala	Leu	Pro	Ala	Lys	Glu	Ala	Val	Tyr	His	Glu	Asp
		115					120					125			
Gly	Ser	Phe	Ser	Leu	Thr	Arg	Trp	Pro	Asp	Asn	Asn	Asn	Ser	Asp	Thr
	130					135					140				
Ile	Thr	Asp	Pro	Cys	Phe	Val	Glu	Lys	Thr	Tyr	Gly	Gly	Arg	Val	Leu
145					150					155				160	
Glu	Gly	His	Tyr	Thr	Ser	Phe	Asn	Gly	Lys	Tyr	Ser	Ser	Lys	Ile	Leu



(2) INFORMATIONS POUR LA SEQ ID NO: 998:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 790 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(962545..964914)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 998:

Met	Leu	Val	Pro	Leu	Ser	Leu	Leu	Gln	Lys	Phe	Phe	Ser	Ser	Pro	Leu	1	5	10	15
Ser	Ile	Glu	Glu	Ile	Leu	Gln	Ala	Cys	Asp	Arg	Ile	Gly	Ile	Glu	Ala	20	25	30	
Glu	Cys	Ser	Asn	Val	Phe	Pro	Asp	Ser	Leu	Asn	Thr	Val	Val	Thr	Gly	35	40	45	
Lys	Ile	Leu	Ser	Ala	Ser	Pro	His	Pro	Asp	Ala	Glu	Arg	Leu	Thr	Val	50	55	60	
Ala	Ile	Val	Phe	Asp	Gly	Lys	Gly	Lys	Arg	Gln	Ile	Ile	Cys	Gly	Ala	65	70	75	80
Pro	Asn	Cys	Arg	Ala	Gly	Ile	Ile	Val	Pro	Ile	Ala	Leu	Pro	Gly	Ala	85	90	95	
Lys	Leu	Arg	Asn	Ala	Ser	Gly	Glu	Ile	Thr	Thr	Ile	Lys	Lys	Ala	Lys	100	105	110	
Ile	Arg	Gly	Leu	Glu	Ser	Gln	Gly	Met	Cys	Cys	Gly	Ala	Asp	Glu	Leu	115	120	125	
Gly	Phe	Pro	His	Leu	Gln	Lys	Ala	Gln	Arg	Gly	Ile	Phe	Glu	Phe	Pro	130	135	140	
Ala	Asp	Thr	Pro	Leu	Gly	Glu	Ser	Ala	Cys	Met	Leu	Leu	Ala	Gly	Ala	145	150	155	160
Ser	Leu	Glu	Cys	Ser	Leu	Thr	Pro	Asn	Leu	Gly	His	Cys	Ala	Ser	Leu	165	170	175	
Leu	Gly	Leu	Ala	Arg	Glu	Ile	Ser	Phe	Leu	Ser	Pro	Val	Ser	Leu	Asn	180	185	190	
Ile	Pro	Glu	Phe	Ser	Phe	Ala	Ser	Leu	Pro	Gln	Glu	Thr	Ser	Ile		195	200	205	
Cys	Asp	Met	His	Asp	Ala	Gly	Ala	Cys	Pro	Val	Phe	Tyr	Ser	Val	Lys	210	215	220	
Ile	Ser	Gly	Leu	Ser	Cys	Arg	Arg	Ser	Pro	Glu	Tyr	Leu	Gln	Ala	Ala	225	230	235	240
Leu	Thr	Ala	Leu	Gly	Gln	Lys	Pro	Leu	Asn	Ala	Ile	Val	Asp	Ile	Thr	245	250	255	
Asn	Tyr	Val	Met	Leu	Ser	Leu	Gly	Gln	Pro	Leu	His	Ala	Tyr	Asp	Ser	260	265	270	
Gln	Ala	Val	Glu	Gln	Lys	Ser	Leu	His	Ala	Ala	Thr	Leu	Gln	Ser	Ala	275	280	285	
Gln	Pro	Leu	Thr	Leu	Leu	Asn	Gln	Glu	Thr	Tyr	Thr	Leu	Pro	Ala	Gly	290	295	300	
Ser	Leu	Val	Val	Ala	Asp	Gln	His	Asn	Ile	Leu	Gly	Leu	Ala	Gly	Val	305	310	315	320
Met	Gly	Ser	Ala	Ala	Ser	Ser	Cys	Ser	Glu	Asn	Thr	Thr	Glu	Ile	Ile	325	330	335	
Leu	Glu	Ala	Ala	Tyr	Phe	Gln	Pro	Gln	Ala	Val	Arg	Lys	Tyr	Gln	Arg				

340										345					350					
Thr	Ile	Gln	Leu	His	Thr	Glu	Ala	Ala	Tyr	Arg	Phe	Thr	Arg	Gly	Val					
355										360					365					
Asp	Pro	Gln	Gly	Val	Leu	Pro	Ala	Leu	His	Ala	Ala	Ile	His	Met	Ile					
370										375					380					
Gln	Ser	Leu	Phe	Pro	Asp	Ala	Gln	Ile	Ser	Pro	Ile	Gln	Lys	Ile	Gly					
385	390										395					400				
Asp	Asp	Ser	Phe	Phe	Pro	Leu	Ser	Leu	Ser	Val	Arg	Pro	Lys	Thr	Ile					
405										410					415					
Lys	Arg	Leu	Leu	Asp	Ile	Glu	Leu	Ser	Thr	Ala	Glu	Ile	Val	Ala	Lys					
420										425					430					
Leu	Phe	Ser	Leu	Gly	Phe	Gln	Thr	Ala	Val	Glu	Glu	Gln	Ala	Val	Arg					
435										440					445					
Val	Glu	Val	Pro	Ser	Tyr	Arg	His	Asp	Ile	Gln	Glu	Glu	Thr	Asp	Leu					
450										455					460					
Val	Glu	Glu	Ile	Cys	Arg	Thr	Thr	Pro	Phe	Val	Gln	Lys	Thr	Gln	Lys					
465	470										475					480				
Ile	Leu	Pro	Thr	Tyr	Thr	Pro	Ile	Tyr	Ser	Leu	Lys	Arg	Glu	Leu	Thr					
485										490					495					
Ala	Phe	Leu	Ala	Asn	Gly	Gly	Leu	Gln	Gln	Phe	Phe	Thr	Cys	Ser	Leu					
500										505					510					
Leu	Asp	Thr	Glu	Val	Ser	Ser	Leu	Ser	Leu	Gln	Glu	Ser	Ser	Leu	Ile					
515										520					525					
Pro	Val	Gln	Asn	Ser	Ser	Trp	Lys	Leu	Arg	Asp	Ser	Leu	Leu	Pro	Gly					
530										535					540					
Met	Leu	Lys	Ser	Ala	Ala	Thr	Asn	Leu	His	Arg	Gln	Ala	Pro	Tyr	Val					
545	550										555					560				
Tyr	Ala	Phe	Glu	Ile	Gly	Asn	Val	Tyr	Ser	Lys	Glu	Gln	Asn	Arg	Tyr					
565										570					575					
Gln	Glu	Glu	Glu	Arg	Val	Ala	Ile	Leu	Leu	Ser	Arg	Gln	Val	Met	Asp					
580										585					590					
Asp	Ser	Trp	Gln	Gly	Lys	Thr	Pro	Leu	Ser	Phe	Tyr	Thr	Ile	Lys	Gly					
595										600					605					
Trp	Val	Glu	Lys	Leu	Leu	Cys	Gln	Ser	Gly	Ala	Ser	Ile	Glu	Asp	Phe					
610										615					620					
Ser	Leu	Gln	Pro	Ser	Gln	His	Pro	Asn	Phe	His	Pro	Tyr	Gln	Gln	Ala					
625	630										635					640				
Ala	Leu	Tyr	Gln	Lys	Lys	His	Leu	Leu	Gly	Ile	Phe	Gly	Thr	Leu	His					
645										650					655					
Pro	Gln	Leu	Cys	Arg	Lys	Ala	Gln	Ile	Lys	His	Asp	Val	Val	Phe	Ala					
660										665					670					
Glu	Leu	Ser	Leu	Asn	Val	Leu	Leu	Ser	Leu	Lys	Lys	Lys	Ser	Gly	Pro					
675										680					685					
His	Tyr	Val	Pro	Tyr	Pro	Ile	Tyr	Pro	Ala	Ser	Ser	Arg	Asp	Ile	Thr					
690										695					700					
Ile	Thr	Ile	Asp	Arg	Asp	Leu	Pro	Ala	Asp	Leu	Val	Arg	Arg	Glu	Leu					
705	710										715					720				
Leu	Ser	Phe	Glu	Ser	Lys	Trp	Leu	Glu	Ser	Val	His	Ile	Val	Ser	Val					
725										730					735					
Tyr	Gln	Gly	Arg	Asp	Ser	Ala	Ser	Gln	Ser	Lys	Asn	Val	Ser	Leu	Arg					
740										745					750					
Met	Val	Phe	Arg	Asp	His	Glu	Arg	Thr	Leu	Ser	Gly	Gln	Glu	Ile	Glu					
755										760					765					
Glu	Glu	Tyr	Glu	Arg	Leu	Thr	Ala													

## (2) INFORMATIONS POUR LA SEQ ID NO: 999:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 256 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 964941..965708

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 999:

Ile	Leu	Arg	Ser	Gly	Val	Tyr	Ser	Ser	Lys	Tyr	Phe	Glu	Gly	Glu	Gly	1	5	10	15
Cys	Arg	Ser	Phe	Met	Gly	Ile	Glu	Gly	Arg	Gly	Ser	Gly	Ala	Met	Gln	20	25	30	
Ser	Lys	Lys	Thr	Ile	Lys	Trp	Leu	Lys	Gln	Ala	Leu	Val	Leu	Ser	Ser	35	40	45	
Ile	Val	Asn	Ile	Leu	Leu	Leu	Leu	Ile	Tyr	Ser	Thr	Val	Phe	Arg	50	55	60		
Lys	Asp	Ile	Tyr	Lys	Leu	Arg	Val	Phe	Pro	Gly	Asn	Leu	Ile	Ala	Lys	65	70	75	80
Ser	Ser	Arg	Ile	Gly	Lys	Ile	Pro	Glu	Asp	Ile	Leu	Glu	Arg	Leu	Glu	85	90	95	
Asn	Ala	Ser	Phe	Ala	Asp	Leu	Leu	Ala	Leu	Leu	Xaa	Glu	Glu	Arg	Met	100	105	110	
Val	Phe	Gly	His	Pro	Leu	Lys	Ser	Trp	Ala	Gln	Gly	Val	Ser	Ile	Gln	115	120	125	
Lys	Tyr	Phe	Val	Asp	Ile	Ala	Pro	Met	Leu	Xaa	His	Xaa	Leu	Thr	Phe	130	135	140	
Ile	Lys	Leu	Lys	Ser	Pro	Glu	Arg	Thr	Trp	Leu	Leu	Pro	Asp	Ile	Asn	145	150	155	160
Asp	Gln	Glu	Phe	Thr	Arg	Ile	Cys	Gln	Tyr	Leu	Leu	Thr	Xaa	Arg	Phe	165	170	175	
Pro	Phe	Ser	Ser	Arg	Gly	Phe	Phe	Arg	Ile	Met	Val	Arg	Asp	Cys	Glu	180	185	190	
Ala	Gly	Val	Val	Asp	Glu	Asp	Val	Leu	Tyr	Arg	Phe	Cys	His	Leu	Pro	195	200	205	
Glu	Phe	Leu	Tyr	Val	Arg	Ser	Leu	Leu	Phe	Gly	Ala	Glu	Ile	Glu	Ala	210	215	220	
Ala	Ser	Val	Ala	Ser	Leu	Ala	Arg	Met	Ile	Ile	Gln	Gly	Gly	Glu	Asp	225	230	235	240
Leu	Phe	Phe	Ser	Leu	Cys	Cys	Leu	Glu	Asn	Arg	Gln	Thr	Ala	Asp	Phe	245	250	255	

## (2) INFORMATIONS POUR LA SEQ ID NO: 1000:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 277 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(966193..967023)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1000:

```

Asp Thr Leu Pro Phe Asn Asp Ile Asp Val Ile Ser Thr Met Arg Cys
1          5          10          15
Ser Ala Tyr Cys Thr Ala Ser Ser Tyr His Leu His Val Leu Phe His
20          25          30
Leu Leu Lys Val Asn Tyr Pro Ser Val Leu Ser Arg Glu Tyr Val Leu
35          40          45
Ile Ser Ser Glu Glu Leu Asp Glu Ser Asp Lys Ala Ala Val Phe Phe
50          55          60
Pro Phe Gly Val Cys Val Phe Trp Gly Trp Glu Thr Glu Glu Leu
65          70          75          80
Gln Val Ile Arg Ala Ile Thr Pro Ser Ala Val Asn Pro Leu Pro Asn
85          90          95
Pro Glu Ile Asp Ser Tyr Asp Phe His Tyr Gly Glu Lys Leu Gln Ile
100         105         110
Arg Arg Asp Arg Leu Val Leu Thr Asn Ser Asn Leu Asn Thr Lys Leu
115         120         125
Ala Ile Ser Phe Gly Leu Ala Gln Ser Ile Lys Leu Thr Val Phe Glu
130         135         140
Glu Thr Ile Tyr Lys Thr Val Glu Asn Ser Lys Ser Leu Pro Gln Glu
145         150         155         160
Leu Ala Ser Lys Gly Lys Ile Ser Leu Ser Arg Lys Thr Ile Ala Lys
165         170         175
Lys Ile Gly Glu Leu Phe Leu Asp Lys Ala Ser Val Asn Leu His Ser
180         185         190
Asp Ile Leu Asp Glu Pro Asp Phe Phe Trp Glu His Pro Glu Thr Gln
195         200         205
Pro Phe Tyr Ile Asn Val Leu Thr Cys Leu Asp Val Asn Ala Arg Val
210         215         220
Asn Val Leu Asn His Arg Leu Ala Ile Leu Gly Asp Val Leu Glu Ile
225         230         235         240
Leu Asn Asp Gln Leu Asn His Gln His Ser Ser Ala Leu Glu Trp Thr
245         250         255
Val Ile Trp Leu Ile Ala Leu Glu Val Leu Val Thr Leu Leu Lys Asp
260         265         270
Val Phe Asn Ile Ile
275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1001:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 967444..968061

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1001:

```

Ser Phe Val Ser Phe Val Met Glu Lys Arg Gly Val Ile Val His Ile
1          5          10          15
Leu Val Cys Leu Leu Thr Ile Phe Gly Thr Leu Ser Leu Pro Ala Phe
20          25          30

```



(2) INFORMATION POUR LA SEQ ID NO: 1002:

(A) LONGUEUR: 280 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(968064..968903)

Arg 1	Lys	Leu	Ser	Ala 5	His	Arg	Phe	Phe	Ile 10	Pro	Lys	Asp	Lys	Asn 15	Ile
Arg	Phe	Leu	Pro 20	Arg	Asp	Ser	Phe	Ile 25	Phe	Ser	Thr	Asp	Glu 30	Leu	Leu
Tyr	Pro	Tyr 35	Ile	Phe	Met	Gln	Ile 40	Thr	Leu	Pro	Gly	Val 45	Val	Leu	Thr
Asn	Ser 50	Pro	Ala	Glu	Lys	Gln 55	His	Val	Ile	Val	Lys 60	Ile	Phe	Ser	Pro
Ala 65	Gly	Leu	Leu	Ser 70	Ala	Phe	Ala	Lys	Asn 75	Gly	Ala	Ser	Leu	Ser	Cys 80
Asp	Phe	Arg	Glu 85	Ser	Leu	Phe	Pro	Ile	Ser 90	Phe	Ser	Leu	Phe	Thr 95	Ile
Gln	Gln	Ser 100	Pro	Pro	Lys	Met	Arg	Lys 105	Val	Ile	Gln	Gly 110	Glu 115	Leu	Gln
Asn	Pro 115	Phe	Thr	Thr	Ile	Lys	Ser 120	Ser	Tyr	Pro	Leu	Leu 125	Gln	Ser	Ala
Gly	Lys 130	Met	Ile	Gln	Ala	Ile 135	Leu	Lys	Thr	Gln	Trp 140	His	Glu	Lys	Pro
Ser 145	Pro	His	Leu	Phe 150	Ser	Leu	Phe	Phe	Asn 155	Phe	Leu	Gln	Arg	Ile	Pro 160
Glu	Thr	Gln	Tyr	Pro	Asn	Phe	Phe	Ser	Ser	Met	Phe	Leu	Leu	Lys	Leu



Lys Lys Val Gly Arg Phe Glu Leu Ala His Gln Gly Thr Leu Leu Leu  
 225 230 235 240  
 Asp Glu Ile Thr Glu Ile Pro Ile His Leu Gln Ala Lys Leu Leu Arg  
 245 250 255  
 Ala Ile Gln Glu Gln Glu Phe Xaa His Ile Gly Gly Ile Lys Thr Leu  
 260 265 270  
 Pro Val Asn Ile Arg Phe Leu Ala Thr Ser Asn Arg Asp Leu Glu Glu  
 275 280 285  
 Ala Ile Glu Thr Lys Val Leu Arg Gln Asp Leu Tyr Tyr Arg Leu Ser  
 290 295 300  
 Val Ile Ser Leu His Ile Pro Pro Leu Arg Asp Arg Lys Glu Asp Ile  
 305 310 315 320  
 Leu Pro Leu Ala His Tyr Tyr Leu Glu Lys Phe Cys Lys Met Asn Asn  
 325 330 335  
 Lys Pro Pro Lys Thr Leu Ser Leu Glu Ala Gln Arg Asn Leu Leu Asp  
 340 345 350  
 Tyr Ser Trp Pro Gly Asn Val Arg Glu Leu Ser Asn Val Leu Glu Arg  
 355 360 365  
 Thr Val Ile Leu Glu Asn Asp Pro Ala Ile Thr Pro Ser Met Leu Ala  
 370 375 380  
 Leu Leu  
 385

(2) INFORMATIONS POUR LA SEQ ID NO: 1004:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(971024..971806)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1004:

Glu Lys Glu Asn Trp Glu Leu Met Pro Lys Ile Asp Thr Cys Asp Ser  
 1 5 10 15  
 Cys Val Ser Asn Thr Glu Leu Leu Ala Ile Arg Thr Arg Val Thr Gln  
 20 25 30  
 Ser Tyr Asn Glu Ala Gln Thr Ile Leu Ser Ser Ile Pro Asp Gly Ile  
 35 40 45  
 Phe Leu Leu Ser Glu Ser Gly Glu Ile Leu Ile Cys Asn Pro Gln Ala  
 50 55 60  
 Arg Ala Ile Leu Gly Ile Pro Lys Asp Ile Gln Leu Val Thr Arg Arg  
 65 70 75 80  
 Phe His Asp Phe Phe Pro Asp Thr Phe Phe Gly Phe Ser Val Gln Glu  
 85 90 95  
 Ala Leu Glu Lys Glu Val Pro Pro Lys Thr Ile Arg Leu Thr Leu Ser  
 100 105 110  
 Gln Glu Leu Ser Gln Lys Glu Val Glu Val Phe Val Arg Lys Asn Ile  
 115 120 125  
 Ser His Gly Phe Leu Phe Leu Leu Ile Arg Asp Arg Ser Asp Tyr Arg  
 130 135 140  
 Gln Leu Glu Gln Ala Ile Glu Lys Tyr Arg Ser Ile Ser Glu Leu Gly  
 145 150 155 160  
 Lys Ile Ala Ala Thr Leu Ala His Glu Ile Arg Asn Pro Leu Thr Ser

				165				170					175				
Ile	Ser	Gly	Phe	Ala	Thr	Leu	Leu	Lys	Glu	Glu	Leu	Ser	Ser	Glu	Arg		
			180					185					190				
His	Gln	Arg	Met	Leu	Asn	Val	Ile	Ile	Glu	Gly	Thr	Arg	Ser	Leu	Asn		
		195					200					205					
Ser	Leu	Val	Ser	Ser	Met	Leu	Glu	Tyr	Thr	Lys	Ile	Gln	Pro	Leu	Asn		
	210					215					220						
Leu	Arg	Ser	Ile	Asp	Leu	Gln	Asp	Phe	Phe	Ser	Ser	Leu	Ile	Pro	Glu		
225					230					235					240		
Leu	Ser	Leu	Thr	Phe	Leu	Leu	Val	His	Leu	Glu	Glu	Pro	Ser	Tyr	Leu		
				245					250					255			
Leu	Tyr	Ser	Ala	Leu													
				260													

(2) INFORMATIONS POUR LA SEQ ID NO: 1005:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(972388..973053)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1005:

Ala	Phe	Phe	His	Ser	Ala	Gly	Asn	Phe	Met	Asn	Leu	Ile	Leu	Leu	Leu		
1			5						10				15				
Thr	Leu	Cys	Leu	Ser	Ser	Leu	Leu	Ser	Gly	Cys	Ser	Thr	Asp	Asn	Arg		
		20						25				30					
Gln	Thr	Ser	Tyr	Ile	Glu	Ala	Ala	Arg	Ile	Thr	Thr	Gln	Ser	Ser	Gly		
		35				40						45					
Ser	Leu	Ile	Leu	Tyr	Pro	Val	Ile	Glu	Pro	Arg	Ser	Ala	Pro	Thr	Tyr		
	50					55				60							
His	Trp	Pro	Thr	Pro	Lys	Ser	Pro	Val	Ile	Thr	Asn	Tyr	Ser	Phe	His		
65					70					75				80			
Cys	His	Gly	Thr	Ser	Gly	Ser	Leu	Ser	Thr	Glu	Glu	Thr	Leu	Val	Phe		
				85					90				95				
Asp	Cys	Asn	Gly	Ile	Lys	His	Leu	Ala	Lys	Pro	Phe	Ser	Ile	His	Pro		
		100						105					110				
Leu	Leu	Val	Thr	Ile	Ala	Gln	Tyr	Ile	His	His	His	Phe	Pro	Ile	Thr		
		115				120						125					
Ile	Glu	Glu	Gly	Tyr	Cys	Cys	Pro	Met	His	Tyr	Lys	Phe	Leu	Leu	Thr		
	130					135					140						
Ser	Asp	Thr	Ser	Ile	Ser	Glu	Gln	His	Cys	Lys	Gly	Leu	Ala	Ala	Ile		
145					150					155					160		
Val	Ser	Thr	Gln	Gln	Pro	Val	Ser	Pro	Gln	Met	Leu	Ala	Pro	Ile	Leu		
				165					170					175			
Ser	Lys	Leu	Tyr	Arg	Gly	Leu	Pro	Leu	Pro	Ser	Lys	Thr	Phe	Thr	Leu		
		180						185					190				
Ser	His	Asn	Thr	Ile	Gln	Asn	Glu	Asp	Phe	Ile	Ile	Thr	Ser	Thr	Phe		
		195				200						205					
Lys	Lys	Gly	Lys	Pro	Val	Leu	Val	Ile	Glu	Val	His	His	Glu				
	210					215					220						

## (2) INFORMATIONS POUR LA SEQ ID NO: 1006:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(973746..974546)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1006:

```

Met Thr Lys Lys Ile Val Leu Gln Ile Ala Tyr Gln Gly Thr Ser Tyr
1      5      10      15
Ser Gly Trp Gln Tyr Gln Pro Asn Ala Leu Ser Ile Gln Glu Val Leu
20      25      30
Lys Thr Ile Leu Lys Lys Ile Ala Gly Phe Arg Ile Ser Val Ile Ser
35      40      45
Ser Gly Arg Thr Asp Ala Gly Val His Ala Gln Gly Gln Ile Ala His
50      55      60
Phe His Cys Pro Asp His Pro His Phe Thr Asp Pro Arg Gln Ile Gln
65      70      75      80
Lys Met Leu Asn Ala Leu Leu Pro His Asp Ile Val Ile Arg Asp Ala
85      90      95
Val Met Thr Asp Gly Asp Phe His Ser Arg Phe Ser Ala Ile Ala Lys
100     105     110
Glu Tyr Arg Tyr Thr Leu Ser Leu Leu Pro Lys Pro Leu Pro His His
115     120     125
Arg Leu Phe Cys Phe Ser Pro Arg Tyr Lys Leu Asn Ile Ala Arg Met
130     135     140
Gln Glu Ala Ala Gln Tyr Leu Val Gly Thr His Asp Phe Ala Ser Phe
145     150     155     160
Ala Asn Leu Gly Arg Glu Tyr Ser Ser Thr Ile Arg Thr Leu Tyr Thr
165     170     175
Leu Asp Leu Ser Glu Gln Glu His Leu Val Thr Val Ile Cys Arg Gly
180     185     190
Asn Gly Phe Leu Tyr Lys Met Val Arg Asn Ile Val Gly Ala Leu Leu
195     200     205
Asp Ile Gly Lys Gly Lys Tyr Pro Pro Glu His Leu Leu Asp Met Leu
210     215     220
Ala Thr Lys Asp Arg Arg Lys Gly Pro Pro Ser Ala Pro Pro Tyr Gly
225     230     235     240
Leu Ser Leu His His Val Cys Tyr Pro Pro Pro Tyr Gln Trp Phe Cys
245     250     255
Lys His Glu His Asn Asn Ser Ser Glu Gly Lys
260     265

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1007:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(974558..975223)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1007:

Gly	Ala	Ser	Met	Asn	Leu	Ser	Cys	Ser	Leu	Val	Leu	Leu	Gly	Gly	Gly
1				5					10				15		
Lys	Gly	Glu	Arg	Phe	Asn	Ser	Leu	Gln	Pro	Lys	Gln	Tyr	Thr	His	Leu
			20					25				30			
Cys	Gly	Glu	Pro	Leu	Ile	Leu	His	Ala	Leu	His	Ala	Tyr	Gln	Arg	Leu
		35					40					45			
Pro	Phe	Val	Gln	Glu	Val	Val	Val	Cys	Glu	Glu	Gln	Tyr	Arg	Glu	
	50					55				60					
Leu	Phe	Leu	Pro	Tyr	Ser	Val	Lys	Phe	Ala	Ser	Pro	Gly	Thr	Leu	Arg
65				70						75				80	
Gln	Asp	Ser	Val	Phe	Ser	Gly	Leu	Gln	Gln	Val	Phe	Thr	Pro	Trp	Val
			85					90					95		
Cys	Ile	His	Asp	Gly	Val	Arg	Pro	Phe	Val	Tyr	Ala	Asp	Glu	Val	Ile
			100					105				110			
Glu	Val	Cys	Ser	Ala	Ala	Arg	Lys	Thr	Gly	Ala	Ala	Ala	Leu	Ala	Ser
		115					120					125			
Pro	Ala	Thr	Tyr	Thr	Ile	Lys	Ser	Cys	Ala	Pro	Val	Arg	Thr	Leu	Asp
	130					135					140				
Arg	Asp	Ala	Leu	Ala	Val	Ile	His	Thr	Pro	Gln	Cys	Leu	Asp	Thr	Glu
145					150					155					160
Val	Leu	Arg	Glu	Gly	Leu	Leu	Leu	Ala	Arg	Ala	Met	Asp	Phe	Ser	Leu
			165					170					175		
Ser	Asp	Asp	Thr	Glu	Ala	Ala	Glu	Leu	Leu	Gly	Ile	Glu	Pro	Thr	Leu
			180				185					190			
Val	Phe	Ser	Asn	Arg	Val	Gln	Ile	Lys	Val	Thr	Tyr	Pro	Glu	Asp	Leu
		195				200						205			
Leu	Phe	Ala	Glu	Thr	Leu	Leu	Ser	Lys	Ser	Ser	Thr	Tyr	Lys		
	210					215					220				

(2) INFORMATIONS POUR LA SEQ ID NO: 1008:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(975207..975989)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1008:

Ala	Phe	Leu	Lys	Lys	Val	Ser	Arg	Lys	Ile	Ser	Ser	Leu	Ser	Pro	Asp
1				5					10					15	
Ile	Leu	Val	Phe	Thr	Gly	Asp	Phe	Val	Cys	Arg	Ala	Lys	Val	Glu	Thr
			20					25					30		
Pro	Glu	Arg	Leu	Lys	His	Phe	Leu	Cys	Ser	Leu	His	Ala	Pro	Leu	Gly
		35					40					45			
Cys	Phe	Ala	Cys	Leu	Gly	Asn	His	Asp	Tyr	Ala	Thr	Tyr	Val	Ser	Arg
	50					55					60				
Asp	Ile	His	Gly	Lys	Ile	Asn	Thr	Ile	Ser	Ala	Met	Asn	Ser	Arg	Pro
65					70					75					80

```

Leu Lys Arg Ala Phe Thr Ser Val Tyr Gln Ser Leu Phe Ala Ser Ser
      85                      90                      95
Arg Asn Glu Phe Ala Asp Thr Leu Asn Pro Gln Ile Pro Asn Pro His
      100                    105                    110
Leu Val Ser Ile Leu Arg Asn Thr Pro Phe Gln Leu Leu His Asn Gln
      115                    120                    125
Ser Ala Thr Leu Ser Asp Thr Ile Asn Ile Val Gly Leu Gly Asp Phe
      130                    135                    140
Phe Ala Lys Gln Phe Asp Pro Lys Lys Ala Phe Thr Asn Tyr Asn Pro
      145                    150                    155                    160
Thr Leu Pro Gly Ile Ile Leu Ser His Asn Pro Asp Thr Ile His His
      165                    170                    175
Leu Gln Asp Tyr Pro Gly Asp Val Val Phe Ser Gly His Ser His Gly
      180                    185                    190
Pro Gln Ile Ser Leu Pro Trp Pro Lys Phe Ala Asn Thr Ile Thr Asn
      195                    200                    205
Lys Leu Ser Gly Leu Glu Asn Pro Glu Leu Ala Arg Gly Leu Phe Ser
      210                    215                    220
Phe Pro Glu Glu Ser Arg Leu Leu Tyr Val Asn Arg Gly Leu Gly Gly
      225                    230                    235                    240
Trp Lys Arg Ile Arg Phe Cys Ser Pro Pro Glu Ile Cys Leu Met Arg
      245                    250                    255
Cys Leu Tyr Glu Pro
      260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1009:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 89 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(976254..976520).

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1009:

```

Glu Ser Ser Met Ser Gln Asn Lys Asn Ser Ala Phe Met Gln Pro Val
1      5      10      15
Asn Val Ser Ala Asp Leu Ala Ala Ile Val Gly Ala Gly Pro Met Pro
      20      25      30
Arg Thr Glu Ile Ile Lys Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser
      35      40      45
Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu
      50      55      60
Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr
      65      70      75      80
Lys Met Val Ser Gln His Ile Ile Lys
      85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1010:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 104 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 976588..976899

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1010:

Val	Tyr	Arg	Gln	Asn	Lys	Lys	His	Ser	Gln	Val	Phe	Ser	Lys	Lys	Arg
1				5					10					15	
Gly	Lys	Ser	Glu	Leu	Glu	Asn	Asp	Leu	Phe	Leu	Gly	Leu	Leu	Arg	Lys
			20					25					30		
Lys	Leu	Ile	Pro	Lys	Arg	Arg	Ser	Cys	Tyr	His	Glu	Arg	Val	Leu	Ala
		35					40					45			
Val	Thr	Ala	Thr	Val	Ile	Val	Glu	Ile	Thr	Gly	Lys	Glu	Asn	Ser	Ser
	50					55				60					
Leu	Lys	Lys	Lys	Ser	Leu	Lys	Leu	Asp	Ile	Leu	Arg	Lys	Val	Ser	Lys
65					70					75					80
Ile	Met	His	Glu	Asn	Phe	Asp	Lys	Arg	Leu	Glu	Val	Leu	Leu	Glu	Gly
				85					90					95	
Leu	Ala	Leu	Thr	Arg	Arg	Ser	Leu								
															100

(2) INFORMATIONS POUR LA SEQ ID NO: 1011:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 976886..977635

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1011:

Leu	Gly	Gly	Leu	Phe	Asp	Pro	Glu	Gly	Lys	Glu	Asn	Glu	Leu	Lys	Glu
1				5					10					15	
Leu	Glu	Gln	Gln	Ala	Val	Gln	Asp	Gly	Phe	Trp	Asp	Asp	Val	Ala	Arg
			20					25					30		
Ala	Gly	Lys	Ile	Ser	Glu	Arg	Ile	Ala	Arg	Leu	Lys	Gln	Gln	Leu	Ser
		35					40					45			
Glu	Phe	Asn	Glu	Leu	Lys	Asn	Lys	Val	Ser	Thr	Ile	Gln	Phe	Phe	Leu
	50					55				60					
Glu	Asp	Glu	Glu	Ser	Ser	Lys	Asp	Leu	Glu	Met	Gln	Lys	Glu	Leu	Glu
65					70					75					80
Lys	Glu	Phe	Val	Phe	Cys	Glu	Lys	Lys	Ile	Thr	Glu	Trp	Glu	Thr	Leu
			85					90						95	
Arg	Leu	Leu	Ser	Gly	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Phe	Leu	Ser	Ile
			100					105					110		
Asn	Ala	Gly	Ala	Gly	Gly	Thr	Glu	Ser	Cys	Asp	Trp	Val	Glu	Met	Cys
		115					120					125			
Cys	Ala	Cys	Ile	Cys	Asp	Gly	Leu	Val	Val	Ile	Ser	Trp	Arg	Val	Glu
	130					135				140					
Val	Ile	Asp	Arg	Leu	Asp	Gly	Glu	Val	Ala	Gly	Ile	Lys	His	Ile	Thr
145					150					155					160



```

Leu Lys Leu Val Gly Glu Tyr Ala Tyr Gly Tyr Ala Lys Ala Glu Ser
      165      170      175
Gly Val His Arg Leu Val Arg Ile Ser Pro Phe Asp Ser Asn Ala Lys
      180      185      190
Arg His Thr Ser Phe Ala Ser Val Glu Val Phe Pro Glu Ile Asp Asp
      195      200      205
Lys Ile Glu Val Glu Ile His Pro Gly Asp Ile Arg Ile Asp Thr Tyr
      210      215      220
Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn Val Thr Asp Ser Ala
225      230      235      240
Val Arg Ile Thr Gln Xaa Leu Arg Glu Leu
      245      250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1012:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 91 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 977661..977933

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1012:

```

Ser Asn Ser Lys Pro Arg Ser Leu Tyr Glu Tyr Leu Arg Ala Arg Ile
1      5      10      15
Tyr Gln Lys Leu Gln Glu Arg Leu Glu Lys Gln Asn Ile Asp Arg
      20      25      30
Lys Asn Lys Lys Glu Ile Ser Trp Gly Ser Gln Ile Arg Asn Tyr Val
      35      40      45
Phe Gln Pro Tyr Thr Leu Val Lys Asp Val Arg Thr Gly Tyr Glu Val
      50      55      60
Gly Asn Ile Gln Ala Met Met Asp Gly Glu Leu Leu Asp Ala Phe Ile
65      70      75      80
Lys Ala Tyr Leu Val Asp Tyr Gly Glu Ile Thr
      85      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1013:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 172 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 977918..978433

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1013:

```

Leu Trp Arg Asn Tyr Met Thr Thr Met Arg Asp Pro Leu Leu Glu Ile
1      5      10      15
Arg Tyr Thr Val Pro Glu Asp Ala His Tyr Met Arg Leu Trp Leu Asn

```

			20					25				30							
Asp	Pro	Lys	Ile	Leu	Arg	Gly	Phe	Pro	Leu	Lys	Thr	Glu	Ala	Glu	Ile				
		35					40					45							
Arg	Asp	Ser	Val	Asn	Phe	Trp	Val	Ser	Phe	Tyr	Arg	Cys	Arg	Ser	Ser				
	50					55					60								
Leu	Thr	Ala	Val	Tyr	Asn	Gly	Glu	Val	Ala	Gly	Val	Ala	Thr	Leu	Ile				
65					70					75					80				
Leu	Asn	Pro	Tyr	Val	Lys	Val	Ala	His	His	Ser	Leu	Leu	Ser	Ile	Ile				
				85					90					95					
Val	Gly	Glu	Lys	Phe	Arg	Asn	Lys	Gly	Val	Gly	Thr	Ala	Leu	Leu	Asn				
			100				105						110						
Asn	Leu	Leu	His	Leu	Gly	Lys	Thr	Gln	Leu	Lys	Leu	Glu	Leu	Val	Tyr				
		115					120					125							
Leu	Glu	Val	Tyr	Glu	Gly	Asn	Pro	Ala	Ile	His	Leu	Tyr	Glu	Arg	Phe				
	130					135					140								
Gly	Phe	Val	Glu	Val	Gly	Arg	Gln	Lys	Thr	Phe	Tyr	Lys	Asp	Glu	Leu				
145					150					155					160				
Gly	Tyr	Leu	Ala	Lys	Ile	Thr	Met	Glu	Arg	Val	Leu								
				165						170									

(2) INFORMATIONS POUR LA SEQ ID NO: 1014:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 978619..978984

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1014:

Met	Ala	Gly	His	Ser	Lys	Trp	Ala	Asn	Thr	Lys	His	Arg	Lys	Glu	Arg				
1				5					10					15					
Ala	Asp	His	Lys	Lys	Gly	Lys	Ile	Phe	Ser	Arg	Thr	Ile	Lys	Glu	Leu				
		20					25					30							
Ile	Ser	Ala	Val	Lys	Met	Gly	Gly	Pro	Asp	Pro	Lys	Ser	Asn	Ala	Arg				
	35					40					45								
Leu	Arg	Met	Ile	Ile	Gln	Lys	Ala	Lys	Asp	Gln	Asn	Ile	Pro	Asn	Glu				
	50				55					60									
Asn	Ile	Glu	Arg	Asn	Leu	Lys	Lys	Ala	Ser	Ser	Ala	Asp	Gln	Lys	Asn				
65				70					75					80					
Tyr	Glu	Glu	Val	Thr	Tyr	Glu	Leu	Tyr	Gly	Phe	Gly	Gly	Val	Gly	Ile				
			85					90					95						
Ile	Val	Glu	Ala	Met	Thr	Asp	Asn	Lys	Asn	Arg	Thr	Ala	Ser	Asp	Met				
		100					105					110							
Arg	Val	Pro	Leu	Thr	Asn	Glu	Val	Gly	Leu										
		115					120												

(2) INFORMATIONS POUR LA SEQ ID NO: 1015:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 978933..979331

[illegible]

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(979389..981197)

Val	Thr	Gln	Lys	Ile	Arg	Val	Val	Val	Gln	Gln	Gln	His	Ser	Ile	Leu
1				5		-			10					15	
Tyr	Arg	Gly	Ser	Ser	Tyr	Thr	Thr	Gly	Pro	Arg	Asn	Glu	Gly	Val	Phe
			20					25					30		
Gly	Pro	Gly	Pro	Glu	Gly	Leu	Pro	Asp	Met	Ser	Leu	Pro	Ser	Tyr	Asp
			35				40					45			
Pro	Thr	Asn	Lys	Thr	Ser	Leu	Leu	Thr	Phe	Leu	Ser	Asn	Pro	His	Val
	50					55					60				
Lys	Xaa	Lys	Met	Leu	Glu	Asn	Ser	Gly	His	Phe	Val	Phe	Ile	Asp	Thr
65				70					75					80	
Asp	Arg	Ser	Ser	Phe	Ile	Leu	Val	Pro	Asn	Gly	Asn	Trp	Asp	Gln	Val
				85				90						95	
Cys	Ser	Ile	Lys	Val	Gln	Asn	Gly	Lys	Thr	Lys	Glu	Asp	Leu	Asp	Ile
			100					105					110		
Lys	Asp	Leu	Glu	Asn	Met	Cys	Ala	Lys	Phe	Cys	Thr	Gly	Phe	Asn	Lys
		115					120					125			
Phe	Ser	Gly	Asp	Trp	Asp	Ser	Arg	Val	Glu	Pro	Met	Met	Ser	Ala	Lys

130						135					140				
Ala	Gly	Val	Ala	Ser	Gly	Gly	Asn	Leu	Pro	Asn	Thr	Val	Ile	Ile	Asn
145					150					155					160
Asn	Lys	Phe	Lys	Thr	Cys	Val	Ala	Tyr	Gly	Pro	Trp	Asn	Ser	Arg	Glu
				165					170					175	
Ala	Ser	Ser	Gly	Tyr	Thr	Pro	Ser	Ala	Trp	Arg	Arg	Gly	His	Gln	Val
			180					185				190			
Asn	Phe	Gly	Glu	Ile	Phe	Glu	Lys	Ala	Asn	Asp	Phe	Asn	Lys	Ile	Asn
		195				200				205					
Trp	Gly	Thr	Gln	Ala	Gly	Pro	Ser	Ser	Glu	Asp	Asp	Gly	Ile	Ser	Phe
210					215					220					
Ser	Asn	Glu	Thr	Pro	Gly	Ala	Gly	Pro	Ala	Ala	Ala	Pro	Ser	Pro	Thr
225				230					235						240
Pro	Ser	Ser	Ile	Pro	Val	Ile	Asn	Val	Asn	Val	Asn	Val	Gly	Gly	Thr
			245					250						255	
Asn	Val	Asn	Ile	Arg	Asp	Thr	Asn	Val	Asn	Thr	Thr	Asn	Thr	Thr	Pro
			260					265				270			
Thr	Thr	Gln	Ser	Thr	Asp	Ala	Ser	Thr	Asp	Thr	Ser	Asp	Ile	Asp	Asn
		275				280				285					
Ile	Asn	Thr	Asn	Asn	Gln	Thr	Asp	Asp	Ile	Asn	Thr	Thr	Asp	Lys	Asp
290					295				300						
Ser	Asp	Gly	Ala	Gly	Gly	Val	Asn	Gly	Asp	Ile	Ser	Glu	Thr	Glu	Ser
305				310					315						320
Ser	Ser	Gly	Asp	Asp	Ser	Gly	Ser	Val	Ser	Ser	Ser	Glu	Ser	Asp	Lys
			325					330						335	
Asn	Ala	Ser	Val	Gly	Asn	Asp	Gly	Pro	Ala	Met	Lys	Asp	Ile	Leu	Ser
			340				345					350			
Ala	Val	Arg	Lys	His	Leu	Asp	Val	Val	Tyr	Pro	Gly	Asp	Asn	Gly	Gly
		355				360					365				
Ser	Thr	Glu	Gly	Pro	Leu	Gln	Ala	Asn	Gln	Thr	Leu	Gly	Asp	Ile	Val
370					375					380					
Gln	Asp	Met	Glu	Thr	Thr	Gly	Thr	Ser	Gln	Glu	Thr	Val	Val	Ser	Pro
385				390					395						400
Trp	Lys	Gly	Ser	Thr	Ser	Ser	Thr	Gly	Ser	Ala	Gly	Gly	Ser	Gly	Ser
			405					410						415	
Val	Gln	Thr	Leu	Leu	Pro	Ser	Pro	Pro	Pro	Thr	Pro	Ser	Thr	Thr	Thr
			420				425						430		
Leu	Arg	Thr	Gly	Thr	Gly	Ala	Thr	Thr	Thr	Ser	Leu	Met	Met	Gly	Gly
		435				440					445				
Pro	Ile	Lys	Ala	Asp	Ile	Ile	Thr	Thr	Gly	Gly	Gly	Gly	Arg	Ile	Pro
450					455				460						
Gly	Gly	Gly	Thr	Leu	Glu	Lys	Leu	Leu	Pro	Arg	Ile	Arg	Ala	His	Leu
465				470					475						480
Asp	Ile	Ser	Phe	Asp	Gly	Gln	Gly	Asp	Leu	Val	Ser	Thr	Glu	Glu	Pro
			485					490						495	
Gln	Leu	Gly	Ser	Ile	Val	Asn	Lys	Phe	Arg	Lys	Glu	Thr	Gly	Ser	Gly
			500				505					510			
Gly	Ile	Val	Ala	Ser	Val	Glu	Ser	Ala	Pro	Gly	Lys	Pro	Gly	Ser	Ala
		515				520						525			
Gln	Val	Leu	Thr	Gly	Thr	Gly	Gly	Asp	Lys	Gly	Asn	Leu	Phe	Gln	Ala
530					535						540				
Ala	Ala	Ala	Val	Thr	Gln	Ala	Leu	Gly	Asn	Val	Ala	Gly	Lys	Val	Asn
545				550					555						560
Leu	Ala	Ile	Gln	Gly	Gln	Lys	Leu	Ser	Ser	Leu	Val	Asn	Asp	Asp	Gly
			565					570						575	
Lys	Gly	Ser	Val	Gly	Arg	Asp	Leu	Phe	Gln	Ala	Ala	Thr	Gln	Thr	Thr
			580				585						590		
Gln	Ala	Leu	Ser	Ser	Leu	Ile	Asp	Thr	Val	Gly					
		595					600								

## (2) INFORMATIONS POUR LA SEQ ID NO: 1017:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 979711..980112

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1017:

Gly	Ser	Ser	Val	Leu	Thr	Arg	Ser	Pro	Cys	Pro	Ser	Lys	Asp	Met	Ser
1				5					10					15	
Lys	Cys	Ala	Arg	Ile	Arg	Gly	Ser	Ser	Phe	Ser	Asn	Val	Pro	Pro	Pro
			20					25					30		
Gly	Ile	Arg	Pro	Pro	Pro	Pro	Val	Val	Ile	Met	Ser	Ala	Leu	Ile	Gly
		35					40					45			
Pro	Pro	Ile	Ile	Lys	Asp	Val	Val	Val	Ala	Pro	Val	Pro	Val	Leu	Asn
	50					55					60				
Val	Val	Val	Asp	Gly	Val	Gly	Gly	Gly	Glu	Gly	Ser	Ser	Val	Cys	Thr
65					70				75					80	
Leu	Pro	Leu	Pro	Pro	Ala	Asp	Pro	Val	Glu	Glu	Val	Leu	Pro	Phe	His
				85					90					95	
Gly	Asp	Thr	Thr	Val	Ser	Trp	Asp	Val	Pro	Val	Val	Ser	Ile	Ser	Trp
			100					105					110		
Thr	Ile	Ser	Pro	Arg	Val	Trp	Leu	Ala	Trp	Arg	Gly	Pro	Ser	Val	Glu
		115					120						125		
Pro	Pro	Leu	Ser	Pro	Gly										
															130

## (2) INFORMATIONS POUR LA SEQ ID NO: 1018:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 323 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(981148..982116)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1018:

Phe	Val	Val	Met	Thr	Asn	Ser	Ile	Ser	Gly	Asp	Gln	Pro	Thr	Val	Thr
1				5					10					15	
Thr	Phe	Thr	Ser	Ser	Thr	Thr	Ser	Ala	Ser	Gly	Ala	Ser	Gly	Ser	Leu
			20					25					30		
Gly	Ala	Ser	Ser	Val	Ser	Thr	Thr	Ala	Asn	Ala	Thr	Val	Thr	Gln	Thr
		35					40					45			
Ala	Asn	Ala	Thr	Asn	Ser	Ala	Ala	Thr	Ser	Ser	Ile	Gln	Thr	Thr	Gly
	50				55					60					
Glu	Thr	Val	Val	Asn	Tyr	Thr	Asn	Ser	Ala	Ser	Ala	Pro	Thr	Val	Thr

65					70					75				80
Val	Ser	Thr	Ser	Ser	Ser	Ser	Thr	Gln	Ala	Thr	Ala	Thr	Ser	Asn
				85					90					95
Thr	Ser	Gln	Ala	Val	Ala	Gly	Lys	Ile	Thr	Ser	Pro	Asp	Thr	Ser
			100					105					110	
Ser	Ser	Glu	Thr	Ser	Ser	Thr	Ser	Ser	Ser	Asp	His	Ile	Pro	Ser
		115				120						125		
Tyr	Glu	Pro	Ile	Ser	Thr	Thr	Glu	Asn	Ile	Tyr	Glu	Asn	Ile	Tyr
	130					135					140			
Ser	Ile	Asp	Asp	Ser	Ser	Thr	Ser	Gly	Pro	Glu	Asn	Thr	Ser	Gly
145					150					155				160
Ala	Ala	Ala	Leu	Asn	Ser	Leu	Arg	Gly	Ser	Ser	Tyr	Ser	Asn	Tyr
			165					170						175
Asp	Ala	Ala	Ala	Asp	Tyr	Glu	Pro	Ile	Ser	Thr	Thr	Glu	Asn	Ile
			180					185					190	
Glu	Ser	Ile	Asp	Asp	Ser	Ser	Thr	Ser	Asp	Pro	Glu	Asn	Thr	Ser
	195					200						205		
Gly	Ala	Ala	Ala	Leu	Asn	Ser	Leu	Arg	Gly	Ser	Ser	Tyr	Ser	Asn
210						215					220			
Asp	Asp	Ala	Ala	Ala	Asp	Tyr	Glu	Pro	Ile	Ser	Thr	Thr	Glu	Asn
225					230					235				240
Tyr	Glu	Asn	Ile	Tyr	Glu	Ser	Ile	Asp	Asp	Ser	Ser	Thr	Ser	Gly
			245					250						255
Glu	Asn	Thr	Ser	Gly	Gly	Ala	Ala	Ala	Leu	Asn	Ser	Leu	Arg	Gly
		260					265						270	
Ser	Tyr	Ser	Asn	Tyr	Asp	Asp	Ala	Ala	Ala	Asp	Tyr	Glu	Pro	Ile
	275					280						285		
Thr	Thr	Glu	Ser	Ile	Tyr	Glu	Asn	Ile	Tyr	Glu	Ser	Ile	Asp	Gly
	290					295					300			
Ser	Ile	Ser	Asp	Pro	Glu	Asn	Thr	Ser	Gly	Gly	Ala	Ala	Ala	Ala
305					310				315					320
Asn	Ser	Leu												

(2) INFORMATIONS POUR LA SEQ ID NO: 1019:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 426 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 982321..983598

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1019:

Met	Pro	Gly	Ile	Lys	Val	Phe	Gly	Glu	Thr	Val	Leu	Arg	Gly	Ser	Val
1				5				10						15	
Arg	Val	Ser	Gly	Ala	Lys	Asn	Ala	Thr	Lys	Leu	Leu	Val	Ala	Ser	
		20						25					30		
Leu	Leu	Ser	Asp	Gln	Arg	Thr	Ile	Leu	Lys	Asn	Val	Pro	Asn	Ile	Glu
		35				40						45			
Asp	Val	Arg	Gln	Thr	Val	Asp	Leu	Cys	Arg	Val	Leu	Gly	Ala	Ile	Val
	50					55				60					
Glu	Trp	Asp	Gln	Gln	Ala	Gln	Val	Ile	Glu	Ile	His	Thr	Pro	Arg	Ile
65					70				75						80

```

Leu Leu Ser Lys Val Pro Pro Gln Phe Ser Cys Val Asn Arg Ile Pro
      85                      90                      95
Ile Leu Leu Leu Gly Ala Leu Leu Arg Arg Cys Pro Tyr Gly Ile Phe
      100                    105                    110
Val Pro Ile Leu Gly Gly Asp Ala Ile Gly Pro Arg Thr Leu His Phe
      115                    120                    125
His Leu Glu Gly Leu Lys Lys Leu Gly Ala Glu Ile Val Ile Ser Asp
      130                    135                    140
Glu Gly Tyr Trp Ala Ser Ala Pro Asn Gly Leu Val Gly Ala His Ile
      145                    150                    155                    160
Thr Leu Pro Tyr Pro Ser Val Gly Ala Thr Glu Asn Leu Ile Leu Ala
      165                    170                    175
Ser Val Gly Ala Gln Gly Arg Thr Ile Ile Lys Asn Ala Ala Leu Glu
      180                    185                    190
Val Glu Ile Ile Asp Leu Ile Val Phe Leu Gln Lys Ala Gly Val Glu
      195                    200                    205
Ile Thr Thr Asp Asn Asp Lys Thr Ile Glu Ile Phe Gly Cys Gln Asp
      210                    215                    220
Phe Tyr Ser Val Glu His Phe Ile Ile Pro Asp Lys Ile Glu Ala Ala
      225                    230                    235                    240
Ser Phe Gly Met Ala Ala Val Val Ser Gln Gly Arg Ile Phe Val Glu
      245                    250                    255
Gln Ala Arg His Glu His Met Ile Pro Phe Leu Lys Val Leu Arg Ser
      260                    265                    270
Ile Gly Gly Gly Phe Ser Val His Glu Asn Gly Ile Glu Phe Phe Tyr
      275                    280                    285
Asp Lys Pro Leu Lys Gly Gly Val Leu Leu Glu Thr Asp Val His Pro
      290                    295                    300
Gly Phe Ile Thr Asp Trp Gln Gln Pro Phe Ala Val Leu Leu Ser Gln
      305                    310                    315                    320
Ser Glu Gly Cys Ser Val Ile His Glu Thr Val His Glu Asn Arg Leu
      325                    330                    335
Gly Tyr Leu Lys Gly Leu Val Lys Met Gly Ala His Cys Asp Leu Phe
      340                    345                    350
His Glu Cys Leu Ser Ala Lys Ser Cys Arg Tyr Ser Thr Gly Asn His
      355                    360                    365
Pro His Ser Ala Val Ile His Gly Pro Thr Pro Leu Gln Ala Thr Asp
      370                    375                    380
Leu Val Ile Pro Asp Leu Arg Ala Gly Phe Ala Tyr Val Met Ala Ala
      385                    390                    395                    400
Leu Ile Ala Glu Ala Glu Pro His Gly Leu Arg Ile Pro Arg Cys Trp
      405                    410                    415
Ile Glu Gly Thr Leu Ile Gly Glu Gly Asn
      420                    425

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1020:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 209 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(983862..984488)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1020:

Trp	Arg	Ile	Gln	Leu	Arg	Asn	Asn	Arg	Cys	Arg	Ser	Tyr	Ala	Tyr	Arg
1				5					10					15	
Ile	Gln	Gln	Asp	Gln	Ala	Asp	Arg	Ile	Leu	Ile	Val	Thr	Asp	Ser	Gly
			20					25					30		
Gln	Ser	Leu	His	Phe	Gln	Leu	Leu	Glu	Ala	Thr	Cys	Leu	Ala	Ala	Gly
		35					40					45			
Tyr	Leu	Pro	Ser	Lys	Gly	Ile	Phe	Ser	His	Val	Gly	Phe	Gly	Leu	Val
	50					55					60				
Leu	Asp	Thr	Gln	Gly	Arg	Lys	Phe	Lys	Thr	Arg	Ser	Gly	Glu	Asn	Ile
65					70					75				80	
Lys	Leu	Arg	Glu	Leu	Leu	Asp	Thr	Ala	Val	Glu	Lys	Ala	Lys	Glu	Ser
				85					90					95	
Leu	Lys	Ala	His	Arg	Pro	Asp	Ile	Ser	Glu	Glu	Glu	Leu	Ala	Tyr	Gln
			100					105					110		
Gly	Pro	Ile	Leu	Gly	Ile	Asn	Ala	Ile	Lys	Tyr	Ala	Asp	Leu	Ser	Ser
		115					120					125			
His	Arg	Ile	Asn	Asp	Tyr	Val	Phe	Ser	Phe	Glu	Lys	Met	Leu	Arg	Phe
	130					135					140				
Glu	Gly	Asn	Thr	Ala	Met	Ser	Leu	Leu	Tyr	Ala	Tyr	Val	Arg	Ile	Gln
145					150					155				160	
Gly	Ile	Lys	Arg	Arg	Met	Gly	Leu	Glu	Ser	Leu	Pro	Gln	Glu	Gly	Pro
				165					170					175	
Leu	Ala	Ile	His	Glu	Pro	Ala	Glu	Glu	Ala	Leu	Xaa	Leu	Leu	Phe	Tyr
			180					185					190		
Val	Ser	Leu	Lys	Phe	Trp	Thr	Ser	Pro	Ser	Glu	Asn	Ser	Val	Leu	Xaa
		195					200					205			
Ser															

## (2) INFORMATIONS POUR LA SEQ ID NO: 1021:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(984371..985381)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1021:

Met	Thr	Thr	Leu	Leu	Ser	Phe	Leu	Thr	Ser	Leu	Cys	Ser	Ala	Ala	Ile
1				5					10					15	
His	Gln	Ala	Phe	Pro	Glu	Leu	Glu	Glu	Leu	Thr	Leu	Asp	Ile	Thr	Pro
			20					25					30		
Ser	Thr	Lys	Glu	His	Phe	Gly	His	Tyr	Gln	Cys	Asn	Asp	Ala	Met	Lys
		35					40					45			
Leu	Ala	Arg	Val	Leu	Arg	Lys	Ser	Pro	Arg	Ala	Ile	Ala	Glu	Ser	Ile
	50					55					60				
Val	Ala	His	Ile	Pro	Pro	Ala	Pro	Phe	Ser	Ser	Ile	Glu	Ile	Ala	Gly
65					70					75				80	
Ala	Gly	Phe	Ile	Asn	Phe	Thr	Phe	Ser	Lys	Glu	Phe	Leu	Ala	Ser	Gln
				85					90					95	
Leu	Gln	Thr	Phe	Ser	Lys	Glu	Leu	Ala	Asn	Gly	Phe	Arg	Ala	Ala	Ser
			100					105					110		



```

Pro Gln Lys Val Ile Ile Asp Phe Ser Ser Pro Asn Ile Ala Lys Asp
      115                      120                      125
Met His Val Gly His Leu Arg Ser Thr Ile Ile Gly Asp Cys Leu Ala
      130                      135                      140
Arg Cys Phe Ser Phe Val Gly His Asp Val Leu Arg Leu Asn His Ile
      145                      150                      155                      160
Gly Asp Trp Gly Thr Ala Phe Gly Met Leu Ile Thr Tyr Leu Gln Glu
      165                      170                      175
Thr Ser Gln Glu Ala Ile His Gln Leu Glu Asp Leu Thr Ala Leu Tyr
      180                      185                      190
Lys Lys Ala His Ala Arg Phe Ala Glu Asp Ser Glu Phe Lys Lys Arg
      195                      200                      205
Ser Gln His Asn Val Val Ala Leu Gln Ser Gly Asp Ala Gln Ala Leu
      210                      215                      220
Ala Leu Trp Ile Gln Ile Cys Ser Val Ser Glu Lys Ser Phe Gln Thr
      225                      230                      235                      240
Ile Tyr Ser Ile Leu Asp Val Glu Leu His Thr Arg Gly Glu Ser Phe
      245                      250                      255
Tyr Asn Pro Phe Leu Ala Glu Val Val Ala Asp Leu Glu Ser Lys Asn
      260                      265                      270
Leu Val Thr Leu Ser Asp Gly Ala Lys Cys Val Phe His Glu Ala Phe
      275                      280                      285
Ser Ile Pro Leu Met Ile Gln Lys Ser Asp Gly Gly Tyr Asn Tyr Ala
      290                      295                      300
Thr Thr Asp Val Ala Ala Met Pro Ile Ala Ser Asn Lys Ile Arg Pro
      305                      310                      315                      320
Ile Glu Phe Leu Ser Leu Gln Thr Gln Asp Asn Pro Tyr Thr Ser Ser
      325                      330                      335
Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1022:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 235 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(985399..986103)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1022:

```

Phe Asp Asn Lys Pro Asn Ser Gly Glu Asn Pro Thr Phe Asp Thr Leu
1      5      10
Pro Phe Asn Met Ile Phe Thr Ile Ala Lys Ser Leu Val Arg Leu Leu
      20      25      30
Phe Pro Leu Phe Tyr Arg Arg Lys Ile Leu Arg Ser Lys Ala Ser Ala
      35      40      45
Thr Val Lys Gly Ala Ala Ile Ile Ala Ala Asn His Val Ser Phe Leu
      50      55      60
Asp Pro Ile Ile Ile Pro Leu Ala Phe Pro Gly Lys Leu Tyr Gln Leu
      65      70      75      80
Ala Lys Ser Gly Leu Phe Ser Asn Ser Phe Thr Asn Arg Leu Phe Arg
      85      90      95
Glu Leu Gly Cys Tyr Pro Ile Ser Arg Asn Ala Gly Asn Ala Ala Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1023:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(986046..986693)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1023:

Met	Ile	Ile	Thr	Ile	Asp	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Ser	Thr	Leu
1				5					10					15	
Ala	Lys	Ala	Leu	Ala	Gln	Thr	Leu	Gln	Phe	Leu	Tyr	Cys	Asn	Thr	Gly
			20					25					30		
Ala	Met	Tyr	Arg	Thr	Leu	Ala	Tyr	Ala	Arg	Leu	Gln	Pro	Asp	Trp	Gln
		35					40					45			
Glu	Val	Pro	Leu	Glu	Asp	Phe	Leu	Ala	Ser	Pro	Pro	Phe	Ser	Phe	Ser
	50					55					60				
Phe	Ser	Lys	Asp	Ser	Pro	Leu	Gln	Ala	Phe	Tyr	Gly	Asp	Arg	Leu	Leu
65					70					75					80
Thr	Ser	Glu	Leu	Ser	Ser	Gln	Glu	Val	Ala	Asn	Phe	Ala	Ser	Leu	Phe
				85					90					95	
Ser	Lys	Glu	Pro	Leu	Val	Arg	Ala	Tyr	Met	Gln	Thr	Leu	Gln	Lys	Gln
			100					105					110		
Tyr	Ala	Thr	Val	Gly	Asn	Cys	Val	Phe	Glu	Gly	Arg	Asp	Met	Gly	Ser
		115					120					125			
Lys	Val	Phe	Pro	His	Ala	Glu	Val	Lys	Ile	Phe	Leu	Thr	Ala	Lys	Pro
	130					135					140				
Glu	Ile	Arg	Ala	Glu	Arg	Arg	Leu	Lys	Asp	Leu	Pro	Gln	Gly	Ser	Leu
145					150					155					160
Pro	Lys	Glu	Ala	Leu	Met	Ala	Glu	Leu	Ile	Ala	Arg	Asp	Gln	Ala	Asp
				165					170					175	
Gln	Gln	Arg	Glu	Cys	Asp	Pro	Leu	Val	Ile	Pro	Gln	Asp	Ala	Ile	Val
			180					185					190		
Ile	Asp	Ser	Ser	Asp	Leu	Thr	Ile	Ser	Gln	Ile	Leu	Glu	Lys	Ile	Leu
		195					200					205			

Met	Ile	Ile	Thr	Ile	Asp	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Ser	Thr	Leu
1				5					10					15	
Ala	Lys	Ala	Leu	Ala	Gln	Thr	Leu	Gln	Phe	Leu	Tyr	Cys	Asn	Thr	Gly
		20						25					30		
Ala	Met	Tyr	Arg	Thr	Leu	Ala	Tyr	Ala	Arg	Leu	Gln	Pro	Asp	Trp	Gln
		35					40					45			
Glu	Val	Pro	Leu	Glu	Asp	Phe	Leu	Ala	Ser	Pro	Pro	Phe	Ser	Phe	Ser
	50					55					60				
Phe	Ser	Lys	Asp	Ser	Pro	Leu	Gln	Ala	Phe	Tyr	Gly	Asp	Arg	Leu	Leu
65					70					75					80
Thr	Ser	Glu	Leu	Ser	Ser	Gln	Glu	Val	Ala	Asn	Phe	Ala	Ser	Leu	Phe
				85					90					95	
Ser	Lys	Glu	Pro	Leu	Val	Arg	Ala	Tyr	Met	Gln	Thr	Leu	Gln	Lys	Gln
			100					105					110		
Tyr	Ala	Thr	Val	Gly	Asn	Cys	Val	Phe	Glu	Gly	Arg	Asp	Met	Gly	Ser
		115					120					125			
Lys	Val	Phe	Pro	His	Ala	Glu	Val	Lys	Ile	Phe	Leu	Thr	Ala	Lys	Pro
	130					135					140				
Glu	Ile	Arg	Ala	Glu	Arg	Arg	Leu	Lys	Asp	Leu	Pro	Gln	Gly	Ser	Leu
145					150					155					160
Pro	Lys	Glu	Ala	Leu	Met	Ala	Glu	Leu	Ile	Ala	Arg	Asp	Gln	Ala	Asp
				165					170					175	
Gln	Gln	Arg	Glu	Cys	Asp	Pro	Leu	Val	Ile	Pro	Gln	Asp	Ala	Ile	Val
			180					185					190		
Ile	Asp	Ser	Ser	Asp	Leu	Thr	Ile	Ser	Gln	Ile	Leu	Glu	Lys	Ile	Leu
	195						200					205			

(2) INFORMATION POUR LA SEQ ID NO: 1024:

(A) LONGUEUR: 305 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(986693..987607)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1024:

[illegible]

## (2) INFORMATIONS POUR LA SEQ ID NO: 1025:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 168 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(987616..988119)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1025:

Ile	Glu	Ile	Gly	Ser	Arg	Arg	Ile	Ile	Phe	Phe	Ile	Gln	Leu	Ala	Val	1	5	10	15
Ala	Gln	Xaa	Leu	Ser	Phe	Leu	His	Asp	Arg	Glu	Ile	Arg	Leu	Arg	Cys	20	25	30	
Ile	Gly	Asp	Leu	Ser	Lys	Leu	Pro	Gln	Glu	Leu	Gln	Asn	Asn	Ile	Glu	35	40	45	
Gln	Ala	Ser	Ser	Ala	Thr	Ala	His	Tyr	Ser	Arg	Met	Glu	Leu	Ile	Phe	50	55	60	
Ala	Ile	Asn	Tyr	Gly	Ser	Lys	Asp	Glu	Leu	Val	Arg	Ala	Phe	Lys	Glu	65	70	75	80
Leu	His	Gln	Asp	Leu	Ala	Ser	Lys	Lys	Ile	Ser	Val	Asn	Asp	Ile	Ser	85	90	95	
Glu	Glu	Leu	Ile	Ser	Ser	Tyr	Leu	Asp	Thr	Ser	Gly	Leu	Pro	Asp	Pro	100	105	110	
Asp	Leu	Leu	Ile	Arg	Thr	Gly	Gly	Glu	Met	Arg	Val	Ser	Asn	Phe	Leu	115	120	125	
Leu	Trp	Gln	Ile	Ala	Tyr	Thr	Glu	Leu	Tyr	Val	Thr	Asp	Val	Leu	Trp	130	135	140	
Pro	Asp	Phe	Thr	Ala	Asn	Asp	Leu	Leu	Glu	Ala	Ile	Lys	Thr	Tyr	Gln	145	150	155	160
Gln	Arg	Ser	Arg	Arg	Gly	Gly	Lys									165			

## (2) INFORMATIONS POUR LA SEQ ID NO: 1026:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 106 acides aminés  
 (B) TYPE: acide aminé -  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(987936..988253)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1026:

Thr	Ile	Leu	Ser	Glu	Thr	Cys	Tyr	Ile	Trp	Pro	Pro	Ser	Gly	Ala	Asp	1	5	10	15
Ser	Ile	Pro	Gln	Ile	Val	Asp	Thr	Ala	Leu	His	Leu	Gly	Val	Glu	Ala	20	25	30	
Leu	Thr	Leu	Phe	Ala	Phe	Ser	Thr	Glu	Asn	Phe	Ser	Arg	Ser	Lys	Ser	35	40	45	

Glu Val Ala Glu Leu Phe Ser Leu Phe Asn Ser Gln Leu Arg Arg Xaa  
 50 55 60  
 Ser Leu Ser Tyr Met Ile Gly Arg Ser Asp Tyr Gly Val Leu Ala Thr  
 65 70 75 80  
 Tyr Arg Asn Phe Leu Lys Asn Tyr Lys Thr Thr Leu Ser Lys Pro Pro  
 85 90 95  
 Pro Arg Gln Leu Ile Thr Pro Ala Trp Ser  
 100 105

(2) INFORMATIONS POUR LA SEQ ID NO: 1027:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 988831..989163

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1027:

Asp Met Lys Leu Pro Glu Val Ser Phe Ser Leu Pro Thr Ala Val Trp  
 1 5 10 15  
 Ala Ser Ser Thr Lys Arg Leu Ser Gln Glu Lys Glu Phe Ser Ser Leu  
 20 25 30  
 Asp Arg Val Gln Ser Met Asn Trp Val Gln Arg Ile Val Pro Ser Leu  
 35 40 45  
 Ile Val Leu Leu Gly Ile Ser Val Leu Gly Cys Ser Val Leu Ala Phe  
 50 55 60  
 Cys Thr Cys Leu Thr Val Leu Pro Gly Leu Gly Leu Val Ile Leu Gly  
 65 70 75 80  
 Ser Leu Leu Leu Tyr Trp Ala Tyr His Gln Ile Ala Asn Met Arg Val  
 85 90 95  
 Arg Met Ala Leu Ser Phe Glu Ala Ser Ser Glu Ala Pro Ile Gln  
 100 105 110

(2) INFORMATIONS POUR LA SEQ ID NO: 1028:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 989693..993442

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1028:

Xaa Xaa Xaa Trp Thr Arg Gly Ser Gln Asp Tyr Arg Xaa Phe Thr Arg  
 1 5 10 15  
 Gln Val Ser Asp Ala Arg Asn Asp Leu Thr Leu Arg Val Ala Lys Ile  
 20 25 30  
 Leu Ser Thr Leu Lys Leu Arg Gly Asp Ile Lys Xaa His Pro Ser Ile

[illegible]

Ala	Ala	Ile	Pro	His	Lys	Asn	Val	Phe	Phe	Glu	Asn	Leu	Lys	Leu	Asn
		515					520					525			
Ile	Arg	Lys	Tyr	Ser	Arg	Gly	Glu	His	Val	Leu	Arg	Phe	Gly	Thr	Asp
	530					535					540				
Phe	Val	Gly	Gly	Lys	Gln	Ile	Arg	Ile	Ala	Phe	Arg	Asp	His	Gln	Gly
545					550					555					560
Asn	Leu	Leu	Thr	Asp	Lys	Ala	Gly	Ile	Asp	Lys	Val	Ser	Asp	Glu	Leu
				565					570					575	
Tyr	Ala	Arg	Leu	Asn	Lys	Leu	Gly	Val	Ser	Glu	Val	Gly	Met	Gln	Arg
			580					585					590		
Glu	Gly	Asp	His	Ile	Gln	Val	Ser	Val	Pro	Gly	Ala	Ala	Gly	Ile	Ser
		595						600				605			
Ser	Ala	Asp	Ile	Leu	Gly	Thr	Ser	Lys	Met	Ser	Phe	His	Val	Val	Asn
	610					615					620				
Glu	Gln	Phe	Ser	Ser	Arg	Ser	Pro	Leu	Arg	Tyr	Glu	Val	Gln	Thr	Phe
625					630					635					640
Leu	Asp	Tyr	Leu	Trp	Phe	Thr	Ala	Arg	Ser	Leu	Asp	Glu	Cys	Ser	Pro
				645					650					655	
Gln	Ala	Ile	Asn	Arg	Leu	Ala	Gly	Ala	Leu	Phe	His	Gly	Asp	Asn	Gly
			660					665					670		
Ser	Ala	Pro	Ala	Asn	Val	Arg	Val	Ala	Val	Glu	Lys	Leu	Arg	Glu	Ala
		675					680					685			
Gly	Leu	Ser	Phe	Ser	Lys	Glu	Leu	Glu	Gly	Gly	Ser	Ala	Ser	Leu	Asp
	690					695					700				
Thr	Gln	Tyr	Ser	Met	Ile	Ala	Ile	Glu	Lys	Glu	Ser	Arg	Glu	Gln	Val
705					710					715					720
Asn	Pro	Leu	Met	Ile	Val	Phe	Arg	Asn	His	Ala	Leu	Glu	Gly	Ala	Ser
				725					730					735	
Leu	Lys	Asn	Ile	Arg	Pro	Glu	Phe	Ala	Val	Gly	Glu	Gly	Tyr	Val	Leu
			740					745					750		
Asn	Phe	Gly	Val	Lys	Asp	Lys	Ala	Thr	Phe	Ser	Asp	Gly	Arg	Glu	Thr
		755					760					765			
Pro	Val	Gln	Gln	Phe	His	Ala	Trp	Thr	Ser	Lys	Phe	Cys	Gln	Glu	Gly
		770				775					780				
Val	Ser	Gly	Thr	Lys	Asn	Gly	Leu	Phe	Ser	Gly	Gly	Arg	Gly	Trp	Arg
785					790					795					800
Met	Ala	Val	Val	Leu	Asp	Gly	Tyr	Val	Ile	Ser	Asp	Pro	Val	Leu	Asn
				805					810					815	
Val	Pro	Leu	Lys	Asp	His	Ala	Ser	Val	Ser	Gly	Xaa	Phe	Ser	Tyr	Arg
			820					825					830		
Glu	Val	His	Arg	Leu	Ala	Thr	Asp	Leu	Lys	Ser	Gly	Ala	Met	Ser	Phe
		835					840					845			
Ile	Pro	Glu	Ile	Leu	Ser	Glu	Glu	Val	Val	Ser	Pro	Glu	Leu	Gly	Ser
		850				855					860				
Ser	Gln	Arg	Val	Gln	Gly	Ile	Leu	Ser	Val	Val	Leu	Gly	Leu	Val	Val
865					870					875					880
Leu	Ile	Val	Leu	Met	Ser	Val	Tyr	Tyr	Arg	Phe	Gly	Gly	Val	Ile	Ala
				885					890					895	
Ser	Ile	Ala	Val	Leu	Leu	Asn	Leu	Leu	Ile	Trp	Ala	Ser	Met	Gln	
			900					905					910		
Tyr	Leu	Asp	Ala	Pro	Leu	Thr	Leu	Ser	Gly	Leu	Ala	Gly	Ile	Ile	Leu
		915					920					925			
Ala	Met	Gly	Met	Ala	Val	Asp	Ala	Asn	Val	Leu	Val	Phe	Glu	Arg	Ile
		930				935					940				
Arg	Glu	Glu	Tyr	Leu	Leu	Thr	Arg	Ser	Leu	Ser	Glu	Ser	Val	Glu	Ala
945					950					955					960
Gly	Tyr	Lys	Lys	Ala	Phe	Ser	Ala	Ile	Phe	Asp	Ser	Asn	Leu	Thr	Thr
				965					970					975	
Ile	Leu	Ala	Ser	Ala	Leu	Leu	Leu	Met	Leu	Asp	Thr	Gly	Pro	Ile	Lys

		980					985				990				
Gly	Phe	Ala	Leu	Thr	Leu	Ile	Ile	Gly	Ile	Phe	Ser	Ser	Met	Phe	Thr
		995					1000					1005			
Ala	Leu	Phe	Met	Thr	Lys	Phe	Phe	Phe	Val	Ile	Trp	Val	Gln	Lys	Thr
	1010					1015					1020				
Arg	Glu	Thr	Gln	Leu	His	Met	Met	Asn	Lys	Phe	Ile	Gly	Ile	Lys	His
1025					1030					1035				1040	
Asn	Phe	Leu	Lys	Glu	Cys	Lys	Arg	Leu	Trp	Val	Val	Ser	Gly	Val	Val
				1045					1050					1055	
Leu	Val	Leu	Gly	Cys	Val	Gly	Leu	Gly	Phe	Gly	Ala	Trp	Asp	Ser	Val
		1060						1065				1070			
Phe	Gly	Met	Asp	Phe	Lys	Gly	Gly	Tyr	Ala	Leu	Thr	Leu	Asp	Ser	Asp
	1075						1080					1085			
Val	Cys	Glu	Tyr	Asn	Pro	Glu	Gln	Met	Cys	Ser	Val	Leu	Arg	Lys	Arg
	1090					1095					1100				
Phe	Gln	Gln	Ile	Gly	Leu	Ser	Ser	Arg	Asp	Tyr	Arg	Val	Arg	Arg	Ala
1105					1110					1115				1120	
Asp	Ser	Ser	Gly	Lys	Val	Lys	Ile	Tyr	Leu	Ser	Gln	Asn	Ala	Leu	Asp
				1125					1130					1135	
Arg	Val	Glu	Gln	Ile	Glu	Gly	Ala	Gly	Ser	Glu	Gln	Lys	Gly	Ser	Asp
		1140					1145					1150			
Tyr	His	Leu	Ala	Arg	Val	Leu	Gln	Val	Leu	Ser	Asp	Ser	Gly	Ser	Ser
	1155						1160					1165			
Thr	Thr	Ser	Met	Val	Phe	Asp	Ala	Ser	Arg	Gly	Ser	Trp	Phe	Lys	Val
	1170					1175					1180				
Ser	Gly	Gln	Leu	Ser	Asn	Lys	Met	Arg	Thr	Gln	Ala	Val	Ile	Ala	Leu
1185					1190					1195				1200	
Phe	Gly	Ala	Leu	Gly	Ile	Ile	Leu	Leu	Tyr	Val	Ser	Leu	Arg	Phe	Glu
				1205					1210					1215	
Trp	Arg	Tyr	Ala	Phe	Ser	Ala	Ile	Cys	Ala	Leu	Met	His	Asp	Leu	Leu
		1220					1225					1230			
Ala	Thr	Cys	Ala	Val	Leu	Val	Ala	Leu	His	Phe	Phe	Leu	Gln	Arg	Ile
		1235					1240					1245			
Thr	Asp														
	1250														

(2) INFORMATIONS POUR LA SEQ ID NO: 1029:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 126 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 993408..993785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1029:

Leu	Pro	Tyr	Ile	Ser	Phe	Cys	Arg	Glu	Leu	Gln	Ile	Asp	Leu	Gln	Ala
1				5				10						15	
Ile	Gly	Ala	Leu	Met	Thr	Val	Leu	Gly	Tyr	Ser	Leu	Asn	Asn	Thr	Leu
			20					25					30		
Ile	Ile	Phe	Asp	Arg	Ile	Arg	Glu	Asp	Arg	Arg	Glu	Lys	Leu	Phe	Thr
		35					40				45				
Pro	Met	Pro	Ile	Leu	Ile	Asn	Asp	Ala	Leu	Gln	Lys	Thr	Leu	Gly	Arg
	50					55						60			



```

Thr Val Met Thr Thr Ala Thr Thr Leu Ser Val Leu Val Ile Leu Leu
65                      70                      75                      80
Phe Val Gly Gly Gly Ser Ile Phe Asn Phe Ala Phe Ile Met Thr Val
                        85                      90                      95
Gly Ile Leu Leu Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu
                        100                    105                    110
Leu Leu Phe Met Val Arg Lys Glu Glu Gln Asn Ser Leu Arg
                        115                    120                    125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1030:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(993416..993835)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1030:

```

Ser Ser His Asn Phe Arg Ile Thr Tyr Ala Gln Ala Tyr Phe Ile Ile
1                      5                      10                      15
Tyr Arg Arg Glu Phe Cys Ser Ser Leu Arg Thr Met Asn Lys Arg Ser
                20                      25                      30
Gly Gly Ala Met Tyr Asn Glu Asp Ser Val Pro Asn Lys Ile Pro Thr
                35                      40                      45
Val Ile Met Asn Ala Lys Leu Lys Ile Glu Pro Pro Pro Thr Asn Asn
                50                      55                      60
Lys Met Thr Ser Thr Asp Arg Val Val Ala Val Val Ile Thr Val Arg
65                      70                      75                      80
Pro Asn Val Phe Cys Asn Ala Ser Leu Ile Lys Ile Gly Ile Gly Val
                85                      90                      95
Asn Ser Phe Ser Arg Arg Ser Ser Arg Ile Arg Ser Lys Ile Ile Asn
                100                    105                    110
Val Leu Phe Lys Glu Tyr Pro Ser Thr Val Ile Asn Aia Pro Ile Ala
                115                    120                    125
Cys Lys Ser Ile Cys Asn Ser Leu Gln Lys Glu Met
                130                    135                    140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1031:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 993882..994262

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1031:

```

Gln Glu Phe Ser Ser Gly Arg Tyr Met Glu Lys Gly Ser Leu Ser Ser

```

1		5		10		15									
Leu	Gly	Gln	Lys	Trp	Asp	Tyr	Pro	Lys	His	Asn	Glu	Val	Phe	Leu	Lys
		20					25						30		
Lys	Ile	Leu	Lys	Glu	Phe	His	Leu	His	Pro	Ala	Ile	Ala	Gln	Val	Leu
	35						40					45			
Ile	Ser	Arg	Gly	Phe	Gln	Ser	Ile	Gln	Glu	Ile	Arg	Asp	Phe	Leu	Tyr
	50					55					60				
Pro	Gln	Leu	Ser	Ser	Leu	His	Ser	Thr	Ser	Leu	Phe	Leu	Asp	Met	Glu
65					70					75					80
Lys	Ala	Val	Ala	Arg	Leu	Leu	Gln	Ala	Lys	Ala	Asn	Asn	Glu	His	Val
				85					90					95	
Met	Ile	Tyr	Gly	Asp	Gly	Asp	Val	Asp	Gly	Ile	Thr	Gly	Val	Thr	Leu
		100						105					110		
Ile	Val	Glu	Phe	Leu	Gln	Ile	Leu	Gly	Val	Lys	Thr	Ser	Tyr	Cys	
		115					120					125			

(2) INFORMATIONS POUR LA SEQ ID NO: 1032:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 477 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 994226..995656

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1032:

Ile	Ser	Thr	Asn	Thr	Trp	Ser	Glu	Asn	Lys	Leu	Leu	Leu	Thr	Gly	Thr
1			5					10						15	
Leu	Phe	Lys	Gln	His	Gly	Glu	Thr	Ala	Ser	Leu	Ile	Ser	Gln	Met	Leu
		20						25					30		
Gln	Asp	Gly	Ile	Ser	Leu	Leu	Ile	Thr	Val	Asp	Cys	Gly	Ile	Thr	Ala
	35						40					45			
Gly	Lys	Glu	Val	Gln	Ala	Ile	Asn	Lys	Gln	Gly	Ile	Asp	Val	Ile	Val
	50					55					60				
Thr	Asp	His	His	Met	Pro	Thr	Gly	Lys	Leu	Pro	His	Cys	Ile	Ala	Met
65				70					75						80
Leu	Asn	Pro	Lys	Leu	Asp	Lys	Asn	Pro	Tyr	Pro	Asn	Lys	Glu	Leu	Thr
			85					90					95		
Gly	Val	Gly	Val	Ala	Phe	Lys	Leu	Val	Cys	Ala	Thr	Tyr	Glu	Glu	Leu
		100						105					110		
Ile	Gln	Gln	Asp	Ala	Ser	Trp	Lys	Asp	Lys	Ile	Asp	Leu	Leu	Arg	Phe
	115						120					125			
Leu	Asp	Leu	Val	Ser	Leu	Gly	Thr	Ile	Ala	Asp	Val	Gly	Arg	Leu	Ser
	130					135					140				
Gly	Glu	Asn	Arg	Ile	Leu	Val	Ser	Tyr	Gly	Ile	Lys	Glu	Ile	Ala	Lys
145				150						155					160
Gly	Lys	Arg	Leu	Gly	Leu	Lys	Lys	Leu	Cys	Ser	Leu	Ser	Gly	Val	Asp
			165					170					175		
Lys	Ser	Glu	Val	Ser	Ser	Thr	Asn	Leu	Gly	Ile	Arg	Ile	Thr	Pro	Lys
		180						185					190		
Leu	Asn	Ser	Leu	Gly	Arg	Leu	Ala	Asp	Ser	Ser	Gln	Gly	Val	Lys	Leu
	195						200					205			
Leu	Leu	Ser	Gln	Asp	Pro	Lys	Asn	Ile	Gly	Thr	Ile	Val	Ser	Glu	Leu
	210						215					220			

Ser Ala Val Asn Gln Glu Arg Gln Arg Ile Glu Ala Glu Val Leu Arg  
 225 230 235 240  
 Asp Val Glu Arg Ile Leu Ala Ala Asn Pro Lys Leu Thr Ala Gln Ser  
 245 250 255  
 Ala Ile Val Leu Ala Ser Pro Asn Trp His Ser Arg Val Ile Pro Ile  
 260 265 270  
 Ile Ser Ala Arg Leu Ala Arg Thr Tyr Asn Lys Pro Val Ala Ile Ile  
 275 280 285  
 Ala Leu Gln Asp Gly Ile Gly Lys Gly Ser Leu Arg Thr Ile Gly Ser  
 290 295 300  
 Phe Pro Leu Leu Gly Val Leu Arg Lys Cys Glu Ser Phe Phe Leu Ser  
 305 310 315 320  
 Tyr Gly Gly His Asp Phe Ala Ala Gly Leu Met Ile Lys Glu Asp Gln  
 325 330 335  
 Val Glu Gly Phe Arg Lys Lys Phe Ile His Leu Val Ser Ser Ser Leu  
 340 345 350  
 Arg Lys Asp Asp Ala Met Arg Thr Leu Ser Leu Asp Val Gly Met Asp  
 355 360 365  
 Phe Ser Arg Ile Asn Arg Asp Leu Ile Ala Ser Met Glu Leu Leu Glu  
 370 375 380  
 Pro Phe Gly Lys Gly Asn Val Ser Pro Val Phe Tyr Thr Lys Ala Ile  
 385 390 395 400  
 Gln Val Arg Tyr Pro Lys Leu Leu Ala Gly Asn His Val Lys Leu Tyr  
 405 410 415  
 Leu Asn Ser Gly Glu Arg Asn Leu Glu Gly Thr Ala Phe Gly Gln Gly  
 420 425 430  
 Asp Lys Ile Ser Leu Leu Lys Ala Asn Trp Asn Ile Pro Leu Asp Ile  
 435 440 445  
 Ala Tyr Thr Leu Arg Ile Met Arg Arg Ser Ala Arg Gly Ala Ile Arg  
 450 455 460  
 Leu Leu Ile Gln Asp Phe Arg Ile Gln Ile Pro Arg Leu  
 465 470 475

(2) INFORMATIONS POUR LA SEQ ID NO: 1033:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 996063..996611

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1033:

Met Glu Cys Leu Gln Gln Asp Thr Gly Val Glu Ala Glu Gln Val Gln  
 1 5 10 15  
 Val Gln Gln Gln Glu Glu Asn Ala Val Pro Val Thr Ser Gln Arg Val  
 20 25 30  
 Ser Ile Thr Gln Ala Ala Lys Leu His Asn Val Thr Arg Gln Ala Ile  
 35 40 45  
 Tyr Val Ala Ile Lys Gln Lys Lys Leu Lys Ala Ser Lys Thr Thr Arg  
 50 55 60  
 Trp Glu Ile Asp Leu Gln Asp Leu Glu Asp Tyr Arg Arg Asn Arg Tyr  
 65 70 75 80  
 Ser Arg Ala Lys Ser Thr Tyr Gln Gly Glu Leu Leu Phe Asp Asn Glu

				85					90					95					
Lys	Gly	Phe	Tyr	Ser	Val	Gly	Gln	Val	Ala	Ser	Met	Leu	Asp	Val	Pro				
			100					105					110						
Glu	Gln	Lys	Ile	Tyr	Tyr	Ala	Thr	Arg	Ile	Gly	Ala	Met	Lys	Gly	Glu				
		115					120					125							
Arg	Arg	Gly	Ser	Ala	Trp	Val	Ile	His	Val	Ser	Glu	Val	Asp	Arg	Tyr				
		130				135					140								
Arg	Asn	Asp	Tyr	Leu	Lys	Lys	Glu	Ala	Glu	Arg	Lys	Gly	Lys	Ser	Leu				
145					150					155					160				
Ala	Ala	Met	Arg	Glu	Gly	Phe	Glu	Ala	Leu	Gly	Ala	Asp	Leu	Leu	Ala				
				165					170				175						
Asp	Ala	Glu	Asn	Phe	Ile	Ser													
				180															

(2) INFORMATIONS POUR LA SEQ ID NO: 1034:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 461 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 996885..998267

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1034:

Met	Thr	Val	Gln	Asn	Val	Arg	Val	Arg	Val	Ala	Pro	Ser	Pro	Thr	Gly				
1				5					10					15					
Asp	Pro	His	Val	Gly	Thr	Ala	Tyr	Met	Ala	Gln	Phe	Asn	Glu	Val	Phe				
			20					25					30						
Ala	Arg	Lys	Tyr	Asn	Gly	Gln	Met	Ile	Leu	Arg	Ile	Glu	Asp	Thr	Asp				
		35					40					45							
Gln	Thr	Arg	Ser	Arg	Asp	Asp	Tyr	Glu	Ala	Asn	Ile	Phe	Leu	Ala	Leu				
	50				55					60									
Lys	Trp	Cys	Gly	Ile	Arg	Trp	Asp	Glu	Gly	Pro	Asp	Val	Gly	Gly	Ala				
65					70				75						80				
Tyr	Gly	Pro	Tyr	Arg	Gln	Ser	Glu	Arg	Thr	Glu	Ile	Tyr	Lys	Lys	Tyr				
				85					90					95					
Ala	Glu	Ile	Leu	Leu	Gln	Thr	Asp	Cys	Ala	Tyr	Lys	Cys	Phe	Ala	Thr				
			100					105					110						
Pro	Gln	Glu	Leu	Gln	Glu	Met	Arg	Ala	Val	Ala	Ser	Thr	Leu	Gly	Tyr				
		115					120						125						
Arg	Gly	Gly	Tyr	Asp	Arg	Arg	Tyr	Arg	Tyr	Leu	Ser	Pro	Glu	Glu	Val				
	130					135						140							
Arg	Gln	Arg	Glu	Glu	Gln	Gly	Gln	Pro	Tyr	Thr	Ile	Arg	Leu	Lys	Val				
145					150					155					160				
Pro	Leu	Thr	Gly	Glu	Ser	Val	Phe	Glu	Asp	Gln	Cys	Lys	Gly	Arg	Val				
				165					170					175					
Val	Phe	Pro	Trp	Ala	Asp	Val	Asp	Asp	Gln	Val	Leu	Val	Lys	Ser	Asp				
			180					185					190						
Gly	Phe	Pro	Thr	Tyr	His	Phe	Ala	Asn	Val	Val	Asp	Asp	His	Leu	Met				
		195					200					205							
Gly	Ile	Thr	His	Val	Leu	Arg	Gly	Glu	Glu	Trp	Leu	Ser	Ser	Thr	Pro				
	210					215					220								
Lys	His	Leu	Leu	Leu	Tyr	Lys	Ala	Phe	Gly	Trp	Glu	Pro	Pro	Gln	Phe				
225					230					235					240				

Phe	His	Met	Pro	Leu	Leu	Leu	Asn	Pro	Asp	Gly	Ser	Lys	Leu	Ser	Lys
				245					250					255	
Arg	Lys	Asn	Pro	Thr	Ser	Ile	Phe	Tyr	Tyr	Arg	Asp	Ala	Gly	Tyr	Lys
			260					265					270		
Lys	Glu	Ala	Phe	Met	Asn	Phe	Leu	Thr	Leu	Met	Gly	Tyr	Ser	Met	Glu
		275					280					285			
Gly	Asp	Glu	Glu	Ile	Tyr	Ser	Met	Gln	Arg	Leu	Ile	Glu	Ala	Phe	Asp
	290					295					300				
Pro	Lys	Arg	Ile	Gly	Arg	Ser	Gly	Ala	Val	Phe	Asp	Ile	Arg	Lys	Leu
305					310					315					320
Asp	Trp	Met	Asn	Lys	His	Tyr	Leu	Asn	His	Glu	Gly	Ser	Pro	Glu	Ser
			325						330					335	
Leu	Leu	Gln	Glu	Leu	Lys	Gly	Trp	Leu	Trp	Asn	Asp	Glu	Phe	Leu	Leu
			340					345					350		
Lys	Ile	Leu	Pro	Leu	Cys	Gln	Ser	Arg	Ile	Thr	Thr	Leu	Ala	Asp	Phe
		355					360					365			
Val	Gly	Leu	Thr	Ser	Phe	Phe	Phe	Thr	Ala	Ile	Pro	Gln	Tyr	Ser	Lys
	370					375					380				
Glu	Glu	Leu	Leu	Pro	Ser	Ser	Leu	Lys	Gln	Glu	Gln	Ala	Ala	Val	Met
385				390						395					400
Leu	Tyr	Ser	Leu	Val	Lys	Tyr	Leu	Glu	Lys	Lys	Asp	Leu	Trp	Glu	Lys
			405					410					415		
Asp	Phe	Phe	Tyr	Gln	Gly	Ser	Lys	Trp	Leu	Ala	Glu	Ala	Phe	Gln	Val
			420					425					430		
His	His	Lys	Lys	Ala	Val	Ile	Leu	Cys	Tyr	Met	Trp	Leu	Leu	Leu	Val
		435					440					445			
Gln	Asn	Arg	Asp	Phe	Leu	Phe	Leu	Ile	Arg	Trp	Asn	Tyr			
	450					455					460				

(2) INFORMATIONS POUR LA SEQ ID NO: 1035:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 998962..999225

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1035:

Met	Lys	Lys	Thr	Ala	Leu	Leu	Ala	Ala	Leu	Cys	Ser	Val	Val	Ser	Leu
1				5					10					15	
Ser	Ser	Cys	Cys	Arg	Ile	Val	Asp	Cys	Cys	Phe	Glu	Asp	Pro	Cys	Ala
			20					25					30		
Pro	Ile	Gln	Cys	Ser	Pro	Cys	Glu	Ser	Lys	Lys	Lys	Asp	Val	Asp	Gly
		35					40					45			
Gly	Cys	Asn	Ser	Cys	Asn	Gly	Tyr	Val	Pro	Ala	Cys	Lys	Pro	Cys	Gly
	50					55					60				
Gly	Asp	Thr	His	Gln	Asp	Ala	Glu	His	Gly	Pro	Gln	Ala	Arg	Glu	Ile
65				70					75					80	
Pro	Val	Asp	Gly	Lys	Cys	Arg	Gln								
				85											

(2) INFORMATIONS POUR LA SEQ ID NO: 1036:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 547 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 999393..1001033

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1036:

Met	Asn	Lys	Leu	Ile	Arg	Arg	Ala	Val	Thr	Ile	Phe	Ala	Val	Thr	Ser	1	5	10	15
Val	Ala	Ser	Leu	Phe	Ala	Ser	Gly	Val	Leu	Glu	Thr	Ser	Met	Ala	Glu	20	25	30	
Phe	Ile	Ser	Thr	Asn	Val	Ile	Ser	Leu	Ala	Asp	Thr	Lys	Ala	Lys	Asp	35	40	45	
Asn	Thr	Ser	His	Lys	Ser	Lys	Lys	Ala	Arg	Lys	Asn	His	Ser	Lys	Glu	50	55	60	
Thr	Pro	Val	Asn	Arg	Lys	Lys	Val	Ala	Pro	Val	His	Glu	Ser	Lys	Ala	65	70	75	80
Thr	Gly	Pro	Lys	Gln	Asp	Ser	Cys	Phe	Gly	Arg	Met	Tyr	Thr	Val	Lys	85	90	95	
Val	Asn	Asp	Asp	Arg	Asn	Val	Glu	Ile	Thr	Gln	Ala	Val	Pro	Lys	Tyr	100	105	110	
Ala	Thr	Val	Gly	Ser	Pro	Tyr	Pro	Val	Glu	Ile	Thr	Ala	Thr	Gly	Lys	115	120	125	
Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln	Gln	Leu	Pro	Cys	Glu	Ala	130	135	140	
Glu	Phe	Val	Arg	Ser	Asp	Pro	Ala	Thr	Thr	Pro	Thr	Ala	Asp	Gly	Lys	145	150	155	160
Leu	Val	Trp	Lys	Ile	Asp	Arg	Leu	Gly	Gln	Gly	Glu	Lys	Ser	Lys	Ile	165	170	175	
Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	Cys	Cys	Phe	Thr	Ala	Ala	180	185	190	
Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg	Ser	Val	Thr	Lys	Cys	Gly	Gln	195	200	205	
Pro	Ala	Ile	Cys	Val	Lys	Gln	Glu	Gly	Pro	Glu	Asn	Ala	Cys	Leu	Arg	210	215	220	
Cys	Pro	Val	Val	Tyr	Lys	Ile	Asn	Val	Val	Asn	Gln	Gly	Thr	Ala	Thr	225	230	235	240
Ala	Arg	Asn	Val	Val	Val	Glu	Asn	Pro	Val	Pro	Asp	Ser	Tyr	Ala	His	245	250	255	
Ser	Ser	Gly	Gln	Arg	Val	Leu	Thr	Phe	Thr	Leu	Gly	Asp	Met	Gln	Pro	260	265	270	
Gly	Glu	His	Arg	Thr	Ile	Thr	Val	Glu	Phe	Cys	Pro	Leu	Lys	Arg	Gly	275	280	285	
Arg	Ala	Thr	Asn	Ile	Ala	Met	Val	Ser	Tyr	Cys	Gly	Gly	His	Lys	Asn	290	295	300	
Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn	Glu	Pro	Cys	Val	Gln	Val	Ser	305	310	315	320
Ile	Ala	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys	Lys	Pro	Val	Glu	Tyr	Val	325	330	335	
Ile	Ser	Val	Ser	Asn	Pro	Gly	Asp	Leu	Val	Leu	Arg	Asp	Val	Val	Val	340	345	350	
Lys	Asp	Thr	Leu	Ser	Pro	Gly	Val	Thr	Val	Leu	Glu	Ala	Ala	Gly	Ala	355	360	365	

Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu Asn Pro  
 370 375 380  
 Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr Pro Gly  
 385 390 395 400  
 Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys Gly Thr  
 405 410 415  
 Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val Ala Ala  
 420 425 430  
 Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val Gly Glu  
 435 440 445  
 Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp  
 450 455 460  
 Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln Pro Val  
 465 470 475 480  
 Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr Val Val  
 485 490 495  
 Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu Phe Ser  
 500 505 510  
 Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu Ala Ile  
 515 520 525  
 Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu Asn Thr  
 530 535 540  
 His Ile Tyr  
 545

(2) INFORMATIONS POUR LA SEQ ID NO: 1037:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1001214..1001516

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1037:

Met Ser Thr Val Pro Val Val Gln Gly Ala Gly Ser Ser Asn Ser Ala  
 1 5 10 15  
 Gln Asp Ile Ser Thr Ser Ser Ala Pro Leu Thr Leu Lys Gly Arg Ile  
 20 25 30  
 Ser Asn Leu Leu Ser Ser Thr Ala Phe Lys Val Gly Leu Val Val Ile  
 35 40 45  
 Gly Leu Leu Leu Val Met Ala Thr Ile Phe Leu Val Ser Ala Ser Phe  
 50 55 60  
 Val Cys Lys Ser His Leu Ser Ser Tyr Ser Cys Tyr Cys Gly Met Arg  
 65 70 75 80  
 Glu Tyr Leu Arg Arg Asn Phe Ile His Gly Arg Ile Leu Phe Ser Gly  
 85 90 95  
 Glu Met Glu Leu Met  
 100

(2) INFORMATIONS POUR LA SEQ ID NO: 1038:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 91 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1001392..1001664

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1038:

Phe	Arg	Pro	Ala	Ser	Phe	Val	Asn	Pro	Ile	Tyr	Leu	Ala	Ile	Pro	Ala
1				5					10					15	
Ile	Val	Gly	Cys	Val	Asn	Ile	Cys	Val	Gly	Ile	Leu	Ser	Met	Glu	Gly
		20						25					30		
Tyr	Cys	Ser	Pro	Glu	Arg	Trp	Ser	Leu	Cys	Lys	Lys	Ile	Leu	Lys	Ala
		35					40					45			
Ser	Glu	Asp	Ile	Ile	Asp	Asp	Gly	Gln	Ile	Asn	Asn	Ser	Asn	Lys	Val
	50					55					60				
Phe	Thr	Asp	Glu	Arg	Leu	Asn	Ala	Ile	Asp	Gly	Val	Val	Val	Ser	Leu
65					70					75					80
Ser	Arg	Arg	Asn	Ser	Leu	Val	Asp	Gln	Thr	Gln					
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 1039:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 625 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1001823..1003697)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1039:

Leu	Leu	Val	Leu	Thr	Leu	Phe	Pro	Gln	Leu	Ala	Phe	Ser	Ala	Glu	Pro
1				5					10					15	
Leu	Arg	Arg	Gln	Asp	Val	Arg	Lys	Thr	Val	Asp	Lys	Leu	Val	Glu	His
		20						25					30		
His	Ile	Asp	Thr	Gln	Gln	Ile	Ser	Pro	Tyr	Ile	Leu	Ser	Arg	Ser	Leu
		35					40					45			
Glu	Asp	Tyr	Val	Arg	Ser	Phe	Asp	Ser	His	Lys	Ala	Tyr	Leu	Thr	Gln
	50					55					60				
Asp	Glu	Val	Phe	Ser	His	Ala	Phe	Ser	Glu	Glu	Ala	Thr	His	Pro	Leu
65					70					75					80
Phe	Lys	Gln	Tyr	Gln	Glu	Asp	Asn	Phe	Ser	Ser	Phe	Lys	Glu	Leu	Asp
				85				90					95		
Thr	Cys	Ile	Gln	Gln	Ser	Ile	Ser	Arg	Ala	Arg	Glu	Trp	Arg	Ser	Ser
			100					105					110		
Trp	Leu	Thr	Asp	Ser	Ile	Arg	Val	Ile	Gln	Asp	Ala	Met	Ser	His	Thr
		115					120					125			
Ile	Glu	Lys	Lys	Pro	Ser	Ala	Trp	Ala	Ser	Ser	Ile	Glu	Glu	Val	Lys
	130					135					140				
Gln	Arg	Gln	Tyr	Asp	Leu	Leu	Ser	Tyr	Ala	Ser	Ile	Tyr	Leu	Glu	
145					150				155					160	



Asp	Ala	Ala	Lys	Asn	Arg	Tyr	Gln	Gly	Lys	Glu	His	Gly	Leu	Val	Lys	165	170	175
Leu	Cys	Ile	Arg	Gln	Ile	Glu	Asn	His	Glu	Asn	Pro	Tyr	Ile	Gly	Ile	180	185	190
Asn	Asp	His	Gly	Tyr	Arg	Met	Ser	Pro	Glu	Glu	Glu	Ala	Asn	Ser	Phe	195	200	205
His	Val	Arg	Ile	Ile	Lys	Ser	Ile	Ala	His	Ser	Leu	Asp	Ala	His	Thr	210	215	220
Ala	Tyr	Phe	Ser	Gln	Glu	Glu	Ala	Leu	Ser	Met	Arg	Ala	Gln	Leu	Glu	225	230	235
Lys	Gly	Met	Cys	Gly	Ile	Gly	Val	Val	Leu	Lys	Glu	Asp	Ile	Asp	Gly	245	250	255
Val	Val	Val	Lys	Glu	Val	Leu	Ala	Gly	Gly	Pro	Ala	Asp	Lys	Thr	Gly	260	265	270
Ser	Leu	Arg	Val	Gly	Asp	Ile	Ile	Tyr	Arg	Val	Asn	Gly	Lys	Asn	Ile	275	280	285
Glu	Asn	Thr	Pro	Phe	Pro	Gly	Val	Leu	Asp	Ser	Leu	Arg	Gly	Ser	Pro	290	295	300
Gly	Ser	Ser	Val	Thr	Leu	Asp	Ile	His	Arg	Gln	Asn	Asn	Asp	His	Val	305	310	315
Ile	Gln	Leu	Arg	Arg	Glu	Lys	Ile	Leu	Leu	Asp	Ser	Arg	Arg	Val	Asp	325	330	335
Val	Ser	Tyr	Glu	Pro	Tyr	Gly	Asn	Gly	Ile	Ile	Gly	Lys	Ile	Thr	Leu	340	345	350
His	Ser	Phe	Tyr	Glu	Gly	Glu	Asn	Gln	Val	Ser	Ser	Glu	Gln	Asp	Leu	355	360	365
Arg	Lys	Ala	Ile	Arg	Glu	Leu	Gln	Glu	Lys	Asn	Leu	Leu	Gly	Leu	Val	370	375	380
Leu	Asp	Ile	Arg	Glu	Asn	Thr	Gly	Gly	Phe	Leu	Ser	Gln	Ala	Ile	Lys	385	390	395
Val	Ser	Gly	Leu	Phe	Leu	Thr	Asn	Gly	Val	Val	Val	Val	Ser	Arg	Tyr	405	410	415
Ala	Asp	Gly	Ser	Val	Lys	Arg	Tyr	Arg	Thr	Ile	Ser	Pro	Gln	Lys	Phe	420	425	430
Tyr	Asp	Gly	Pro	Leu	Ala	Val	Leu	Val	Ser	Lys	Ser	Ser	Ala	Ser	Ala	435	440	445
Ala	Glu	Ile	Val	Ala	Gln	Thr	Leu	Gln	Asp	Tyr	Gly	Val	Ala	Leu	Ile	450	455	460
Val	Gly	Asp	Gln	Gln	Thr	Tyr	Gly	Lys	Gly	Thr	Ile	Gln	His	Gln	Thr	465	470	475
Ile	Thr	Gly	Ser	Asn	Ser	Gln	Glu	Asp	Phe	Phe	Lys	Val	Thr	Val	Gly	485	490	495
Arg	Tyr	Tyr	Ser	Pro	Ser	Gly	Lys	Ser	Thr	Gln	Leu	Glu	Gly	Val	Lys	500	505	510
Ser	Asp	Ile	Val	Ile	Pro	Ser	Arg	Tyr	Ala	Glu	Asp	Lys	Leu	Gly	Glu	515	520	525
Arg	Phe	Leu	Glu	Tyr	Ala	Leu	Pro	Ala	Asp	Gln	Tyr	Asp	Asn	Val	Ile	530	535	540
Asn	Asp	Asn	Leu	Gly	Asp	Leu	Asp	Ile	Asn	Ile	Arg	Pro	Trp	Phe	Gln	545	550	555
Lys	Tyr	Tyr	Ser	Pro	His	Leu	Gln	Lys	Pro	Glu	Leu	Val	Trp	Arg	Glu	565	570	575
Met	Leu	Pro	Gln	Leu	Ala	His	Asn	Ser	Gln	Glu	Arg	Leu	Glu	Lys	Asn	580	585	590
Lys	Asn	Phe	Glu	Ile	Phe	Val	Gln	His	Leu	Lys	Lys	Thr	Asn	Lys	Gln	595	600	605
Asp	Arg	Ser	Phe	Gly	Ser	Asn	Asp	Leu	Gln	Met	Glu	Glu	Cys	Glu	His	610	615	620
Arg																		

625

(2) INFORMATIONS POUR LA SEQ ID NO: 1040:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1004477..1004845

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1040:

```

Met Pro Thr Ile Asn Gln Leu Ile Arg Lys Lys Arg Gln Ser Gly Ala
1           5           10           15
Thr Arg Lys Lys Ser Pro Ala Leu Gln Lys Ser Pro Gln Lys Arg Gly
          20           25           30
Val Cys Leu Gln Val Lys Thr Lys Thr Pro Lys Lys Pro Asn Ser Ala
          35           40           45
Leu Arg Lys Val Ala Trp Val Arg Leu Ser Asn Gly Gln Glu Val Ile
          50           55           60
Ala Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Ile Val
65           70           75           80
Leu Val Gln Gly Gly Arg Xaa Lys Asp Leu Pro Gly Val Arg Tyr His
          85           90           95
Ile Val Arg Gly Ala Leu Xaa Cys Ala Ala Val Lys Asn Arg Lys Gln
          100          105          110
Ser Arg Ser Arg Tyr Gly Ala Lys Arg Pro Lys
          115          120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1041:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 131 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1004990..1005382

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1041:

```

Leu Leu His Gly Lys Lys Ser Ile Ala Arg Lys Ile Val Tyr Gly Ala
1           5           10           15
Leu Glu Arg Phe Ala Lys Arg Leu Gly Leu Glu Asn Pro Leu Glu Gly
          20           25           30
Phe Glu Glu Ala Leu Glu Asn Ala Lys Pro Ile Leu Glu Val Arg Ser
          35           40           45
Arg Arg Val Gly Gly Ala Thr Tyr Gln Val Pro Val Glu Val Ala Pro
          50           55           60
Asp Arg Arg Ser Cys Leu Ala Met Gln Trp Ile Ile Lys His Ala Arg
65           70           75           80

```

Ser	Lys	Pro	Gly	Lys	Cys	Met	Glu	Val	Gly	Leu	Ala	Asn	Glu	Leu	Ile
				85					90					95	
Asp	Cys	Phe	Asn	Lys	Gln	Gly	Ala	Thr	Ile	Lys	Lys	Arg	Glu	Asp	Thr
			100					105					110		
His	Arg	Met	Ala	Glu	Ala	Asn	Lys	Ala	Phe	Ala	His	Tyr	Lys	Trp	Xaa
		115					120					125			
Xaa	Asn	Val													
		130													

## (2) INFORMATIONS POUR LA SEQ ID NO: 1042:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 694 acides aminés  
 (B) TYPE: acide aminé  
 (D) CONFIGURATION: linéaire

## (iii) HYPOTHETIQUE: oui

## (viii) POSITION DANS LE GENOME: 1005415..1007496

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1042:

Met	Ser	Asp	Gln	Glu	Phe	Gly	Leu	Asp	Ala	Ile	Arg	Asn	Ile	Gly	Ile
1				5					10					15	
Met	Ala	His	Ile	Asp	Ala	Gly	Lys	Thr	Thr	Thr	Thr	Glu	Arg	Ile	Leu
			20					25					30		
Phe	Tyr	Ala	Gly	Arg	Thr	His	Lys	Ile	Gly	Glu	Val	His	Glu	Gly	Gly
		35					40					45			
Ala	Thr	Met	Asp	Trp	Met	Glu	Gln	Glu	Gln	Glu	Arg	Gly	Ile	Thr	Ile
	50					55					60				
Thr	Ser	Ala	Ala	Thr	Thr	Val	Phe	Trp	Leu	Gly	Ala	Lys	Ile	Asn	Ile
65				70						75				80	
Ile	Asp	Thr	Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Glu	Arg	Ser
			85					90					95		
Leu	Arg	Val	Leu	Asp	Gly	Ala	Val	Ala	Val	Phe	Asp	Ala	Val	Ser	Gly
			100					105					110		
Val	Glu	Pro	Gln	Ser	Glu	Thr	Val	Trp	Arg	Gln	Ala	Asn	Lys	Tyr	Gly
		115					120					125			
Val	Pro	Arg	Ile	Ala	Phe	Val	Asn	Lys	Met	Asp	Arg	Met	Gly	Ala	Asn
	130					135					140				
Tyr	Xaa	Gly	Ala	Val	Glu	Ser	Met	Arg	Glu	Lys	Leu	Gly	Ala	Asn	Ala
145				150	-				155					160	
Xaa	Pro	Val	His	Cys	Pro	Ile	Gly	Ser	Glu	Ser	Gln	Phe	Val	Gly	Met
			165					170					175		
Val	Asp	Leu	Ile	Ser	Gln	Lys	Ala	Leu	Tyr	Phe	Leu	Glu	Glu	Thr	Leu
		180					185					190			
Gly	Ala	Lys	Trp	Glu	Glu	Arg	Lys	Ile	Pro	Glu	Asp	Leu	Gln	Glu	Gln
		195					200					205			
Cys	Ala	Thr	Leu	Arg	Met	Gln	Leu	Leu	Glu	Glu	Leu	Ala	Thr	Val	Asp
	210					215					220				
Glu	Ser	Asn	Glu	Ala	Phe	Met	Glu	Lys	Val	Leu	Glu	Asn	Pro	Asp	Ser
225				230					235					240	
Ile	Thr	Glu	Glu	Glu	Ile	His	Thr	Val	Met	Arg	Lys	Gly	Val	Ile	Glu
			245					250					255		
Gly	Lys	Ile	Asn	Pro	Val	Leu	Cys	Gly	Ser	Ala	Phe	Lys	Asn	Lys	Gly
		260					265					270			
Val	Gln	Gln	Leu	Leu	Asp	Val	Ile	Val	Lys	Trp	Leu	Pro	Ser	Pro	Leu

275	280	285
Asp Arg Gly Asn Val Arg Gly Ile Asn Leu Lys Thr Gly Glu Glu Val		
290	295	300
Ser Leu Lys Pro Ser Lys Asp Gly Pro Leu Ala Ala Leu Ala Phe Lys		
305	310	315
Ile Met Thr Asp Pro Tyr Val Gly Arg Ile Thr Phe Ile Arg Ile Tyr		
	325	330
Ser Gly Thr Leu Lys Lys Gly Ser Ala Ile Leu Asn Ser Thr Lys Asp		
	340	345
Lys Lys Glu Arg Ile Ser Arg Leu Leu Glu Met His Ala Asn Glu Arg		
	355	360
Thr Asp Arg Asp Glu Phe Thr Val Gly Asp Ile Gly Ala Cys Val Gly		
	370	375
Leu Lys Phe Ser Val Thr Gly Asp Thr Leu Cys Asp Glu Asn Gln Glu		
385	390	395
Ile Val Leu Glu Arg Ile Glu Ala Pro Glu Pro Val Ile Asp Met Ala		
	405	410
Ile Glu Pro Lys Ser Lys Gly Asp Arg Glu Lys Leu Ala Gln Ala Leu		
	420	425
Ser Ala Leu Ser Glu Glu Asp Pro Thr Phe Arg Val Ser Thr Asn Glu		
	435	440
Glu Thr Gly Gln Thr Ile Ile Ser Gly Met Gly Glu Leu His Leu Asp		
	450	455
Ile Leu Arg Asp Arg Met Ile Arg Glu Phe Arg Val Glu Ala Asn Val		
465	470	475
Gly Lys Pro Gln Val Ser Tyr Lys Glu Thr Ile Thr Lys Thr Ser Asn		
	485	490
Ser Glu Thr Lys Tyr Val Lys Gln Ser Gly Gly Arg Gly Gln Tyr Ala		
	500	505
His Val Cys Leu Glu Ile Glu Pro Asn Glu Pro Gly Lys Gly Asn Glu		
	515	520
Val Val Ser Lys Ile Val Gly Gly Val Ile Pro Lys Glu Tyr Ile Pro		
	530	535
Ala Val Ile Lys Gly Val Glu Glu Gly Leu Asn Ser Gly Val Leu Ala		
545	550	555
Gly Tyr Gly Leu Val Asp Val Lys Val Ser Ile Val Phe Gly Ser Tyr		
	565	570
His Glu Val Asp Ser Ser Glu Met Ala Phe Lys Ile Cys Gly Ser Met		
	580	585
Ala Val Lys Glu Ala Cys Arg Lys Ala Leu Pro Val Ile Leu Glu Pro		
	595	600
Ile Met Lys Val Thr Val Ile Thr Pro Glu Asp His Leu Gly Asp Val		
	610	615
Ile Gly Asp Leu Asn Arg Arg Arg Gly Lys Ile Leu Gly Gln Glu Ser		
625	630	635
Ser Arg Asn Met Ala Gln Val Ser Ala Glu Val Pro Leu Ser Glu Met		
	645	650
Phe Gly Tyr Met Thr Ser Leu Arg Ser Leu Thr Ser Gly Arg Ala Thr		
	660	665
Ser Thr Met Glu Pro Ala Phe Phe Ala Lys Val Pro Gln Lys Ile Gln		
	675	680
Glu Glu Ile Val Lys Lys		685
690		

(2) INFORMATIONS POUR LA SEQ ID NO: 1043:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1007507..1007821

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1043:

Met	Lys	Gln	Gln	Lys	Gln	Arg	Ile	Arg	Ile	Arg	Leu	Lys	Gly	Phe	Asp	1	5	10	15
Gln	Gly	Gln	Leu	Asp	Gln	Ser	Thr	Ala	Asn	Ile	Val	Glu	Thr	Ala	Lys	20	25	30	
Arg	Thr	Gly	Ala	Arg	Val	Val	Gly	Pro	Ile	Pro	Leu	Pro	Thr	Lys	Arg	35	40	45	
Glu	Val	Tyr	Thr	Val	Leu	Arg	Ser	Pro	His	Val	Asp	Lys	Lys	Ser	Arg	50	55	60	
Glu	Gln	Phe	Glu	Ile	Arg	Thr	His	Lys	Arg	Leu	Ile	Asp	Ile	Leu	Asp	65	70	75	80
Pro	Thr	Gly	Lys	Thr	Ile	Asp	Ala	Leu	Lys	Met	Leu	Ser	Leu	Pro	Ala	85	90	95	
Gly	Val	Asp	Ile	Lys	Ile	Lys	Ala	Ala								100	105		

(2) INFORMATIONS POUR LA SEQ ID NO: 1044:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 299 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1007802..1008698

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1044:

Ile	Leu	Arg	Ser	Arg	Leu	Pro	Asn	Ser	Phe	Asp	Leu	Lys	Met	Ser	Leu	1	5	10	15
Phe	Ser	Lys	Phe	Lys	Ala	Gln	Trp	Met	Phe	Leu	His	Ser	Arg	Glu	Leu	20	25	30	
Cys	Ser	Ser	Thr	Ser	Asp	Ile	Gly	Asn	Thr	Cys	Ser	Asp	Pro	Val	Phe	35	40	45	
Gln	Ile	Leu	Cys	Asn	Pro	Val	Arg	Ser	Glu	Ile	Ser	Tyr	Lys	Val	Gly	50	55	60	
Asp	Ser	Leu	Gly	Val	Phe	Pro	Thr	Asn	Pro	Ser	Thr	Leu	Val	Asp	Ser	65	70	75	80
Val	Leu	Asp	Ala	Leu	Gln	Tyr	Gly	Pro	Arg	Ser	Pro	Val	Val	Ser	Arg	85	90	95	
His	Ala	Asp	Ser	Val	Leu	Pro	Leu	His	Glu	Phe	Leu	Thr	Ser	Tyr	Val	100	105	110	
Asp	Leu	Asp	Lys	Ile	Pro	Lys	Ser	Leu	Arg	Pro	Phe	Phe	Pro	Gly	Asp	115	120	125	
Leu	Asp	Asp	Thr	Trp	Ser	Leu	Ala	Glu	Ala	Ile	Leu	Val	Tyr	Gln	Pro	130	135	140	
Arg	Ile	Pro	Phe	Glu	Glu	Phe	Ile	Arg	Ser	Ala	Met	Pro	Leu	Leu	Pro				

145		150		155		160									
Arg	Phe	Tyr	Ser	Ile	Ala	Ser	Ser	Pro	Thr	Cys	Ser	His	Gly	Lys	Leu
			165					170						175	
Glu	Leu	Leu	Val	Arg	Cys	Val	Ser	Phe	Gln	Gly	Lys	Thr	Gln	Leu	Arg
			180					185					190		
Tyr	Gly	Leu	Cys	Ser	Ala	Phe	Leu	Cys	Lys	Asp	Leu	Gln	Glu	Gly	Glu
		195					200				205				
Ser	Phe	Arg	Gly	Phe	Ile	Gln	Pro	Thr	Arg	His	Phe	Thr	Leu	Glu	Gln
	210				215						220				
Lys	Asn	Phe	Gly	Lys	Pro	Leu	Ile	Met	Ile	Gly	Ala	Gly	Thr	Gly	Ile
225					230					235					240
Ala	Pro	Tyr	Lys	Gly	Phe	Leu	Gln	His	Arg	Ile	Tyr	His	Gln	Asp	Val
			245						250				255		
Gly	Ser	Asn	Ile	Leu	Phe	Phe	Gly	Glu	Arg	Phe	Glu	Lys	Ser	Asn	Phe
		260					265				270				
Tyr	Tyr	Arg	Ala	Phe	Ser	Pro	Gly	Ala	Asp	Arg	Phe	Arg	Lys	Thr	Pro
		275				280					285				
Val	Ile	His	Ser	Leu	Phe	Gln	Arg	Phe	Arg	Val					
	290					295									

(2) INFORMATIONS POUR LA SEQ ID NO: 1045:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 87 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1009121..1009381)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1045:

Ile	Tyr	Arg	Val	Gly	Ile	Gly	Gln	Asp	Ser	His	Arg	Phe	Leu	Pro	Asp
1				5				10						15	
Glu	Asp	Pro	Lys	Pro	Cys	Ile	Leu	Gly	Gly	Ile	Ile	Phe	Glu	Asn	Thr
			20					25					30		
Pro	Gly	Phe	Glu	Ala	Asn	Ser	Asp	Gly	Asp	Val	Val	Phe	His	Ala	Ile
		35				40						45			
Cys	Asn	Ala	Phe	Ser	Ser	Val	Thr	His	Lys	Gly	Ile	Leu	Gly	Gly	Leu
	50					55					60				
Ala	Asp	Glu	Leu	Leu	Lys	Thr	Lys	Gly	Ile	Thr	Asp	Ser	Val	Val	Tyr
65					70					75					80
Leu	Gln	Glu	Leu	Ser	Pro	Leu									
						85									

(2) INFORMATIONS POUR LA SEQ ID NO: 1046:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 469 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1010648..1012054

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1046:

Leu 1	Asp	His	Leu	Leu 5	His	Ala	Phe	Pro	Ser 10	Ile	Gly	Gln	Ser	Ile 15	Val
Gln	Glu	Leu	Lys 20	Ser	Gln	Arg	Ser	Arg 25	Leu	Lys	Met	Ile	Ala	Ser	Glu
Asn	Phe	Ser	Ser 35	Leu	Ser	Val	Gln 40	Leu	Ala	Met	Gly	Asn 45	Leu	Leu	Thr
Asp	Lys 50	Tyr	Cys	Glu	Gly	Ser 55	Pro	Phe	Lys	Arg	Phe 60	Tyr	Ser	Cys	Cys
Glu 65	Asn	Val	Asp	Ala	Ile 70	Glu	Trp	Glu	Cys	Ala	Glu 75	Thr	Ala	Lys	Glu 80
Leu	Phe	Gly	Ala	Glu 85	Ser	Ala	Phe	Val 90	Gln	Pro	His	Ser	Gly	Ala 95	Asp
Ala	Asn	Leu	Leu 100	Ala	Ile	Met	Ser 105	Ile	Ile	Thr	Gln	Lys 110	Ile	Gln	Ser
Pro	Ala	Val	Gln 115	Gln	Leu	Gly	Tyr 120	Lys	Thr	Ile	Asn	Asp 125	Leu	Pro	Glu
Gln	Glu 130	Tyr	Glu	Ala	Leu	Lys 135	Ala	Glu	Met	Ala	Gln 140	His	Lys	Cys	Leu
Gly 145	Pro	Ser	Leu	Asn 150	Ser	Gly	Gly	His	Leu	Thr	His 155	Gly	Thr	Val	Arg 160
Met	Asn	Ile	Met 165	Ser	Lys	Leu	Met	His 170	Cys	Leu	Pro	Tyr	Glu	Val 175	Asn
Leu	Asp	Thr	Glu 180	Leu	Phe	Asp	Tyr 185	Asp	Glu	Ile	Ala	Lys 190	Xaa	Ala	Lys
Glu	His	Lys 195	Pro	Thr	Val	Leu 200	Ile	Ala	Gly	Tyr	Ser 205	Ser	Tyr	Ser	Arg
Arg	Phe 210	Asn	Phe	Ala	Thr	Leu 215	Lys	Gln	Ile	Ala	Glu 220	Asp	Cys	Gly	Ala
Val 225	Leu	Trp	Val	Asp 230	Met	Ala	His	Phe	Ala	Gly	Leu 235	Val	Ala	Gly	Gly 240
Val	Phe	Val	Gly 245	Glu	Glu	Asn	Pro	Met 250	Pro	Tyr	Ala	Asp	Ile	Val 255	Thr
Thr	Thr	Thr	His 260	Lys	Thr	Leu	Arg	Gly 265	Pro	Arg	Gly	Gly 270	Leu	Val	Leu
Ala	Lys	Xaa 275	Glu	Tyr	Ala	Asn	Thr 280	Leu	Asn	Lys	Ala	Cys 285	Leu	Xaa	Met
Met	Gly 290	Gly	Pro	Leu	Pro	His 295	Val	Ile	Ala	Ala	Lys 300	Ala	Ile	Ala	Leu
Lys 305	Glu	Ala	Met	Thr 310	Ile	Asn	Phe	Arg	Lys	Tyr	Ala 315	His	Lys	Val	Val 320
Glu	Asn	Ala	Gln 325	Thr	Leu	Ala	Glu	Val 330	Phe	Gln	Arg	Asn	Gly	Leu 335	Arg
Leu	Leu	Thr 340	Gly	Thr	Asp	Asn 345	His	Met	Leu	Ile	Ile 350	Asp	Leu	Leu	Thr
Ser	Leu	Gly 355	Val	Pro	Gly	Arg 360	Ile	Ala	Glu	Asp	Met 365	Leu	Thr	Ser	Val
Gly	Ile 370	Ala	Val	Asn	Arg	Asn 375	Thr	Ile	Pro	Ser	Asp 380	Ala	Ser	Gly	Gln
Trp 385	Lys	Thr	Ser 390	Gly	Ile	Arg	Leu	Gly	Thr	Pro	Ala 395	Leu	Thr	Thr	Leu 400
Gly	Met	Gly	Ser 405	Ala	Glu	Met	Glu	Glu 410	Val	Ala	Asn	Ile	Ile	Val 415	Lys
Val	Leu	Arg	Asn 420	Ile	Thr	Val	Arg 425	Ser	Asn	Ala	Glu	Ser 430	Gly	Ser	Ser
Lys	Ser	Glu	Gly	Glu	Leu	Ser	Glu	Gly	Ile	Ala	Gln	Glu	Ala	Arg	Glu

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1047:

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1048:

Gly Asn Ala Ser Leu Val Gly Asp Ser Met Pro Glu Gly Glu Met Met  
1 5 10 15



```

His Lys Leu Gln Asp Val Ile Asp Arg Lys Leu Leu Asp Ser Arg Arg
      20                      25                      30
Ile Phe Phe Ser Glu Pro Val Thr Glu Lys Ser Ala Ala Glu Ala Ile
      35                      40                      45
Lys Lys Leu Trp Tyr Leu Glu Leu Thr Asn Pro Gly Gln Pro Ile Val
      50                      55                      60
Phe Val Ile Asn Ser Pro Gly Gly Ser Val Asp Ala Ser Phe Ala Val
      65                      70                      75                      80
Trp Asp Gln Ile Lys Met Ile Ser Ser Pro Leu Thr Thr Val Val Thr
      85                      90                      95
Gly Leu Ala Ala Ser Thr Gly Ser Val Leu Ser Leu Cys Ala Val Pro
      100                     105                     110
Gly Arg Arg Phe Ala Thr Pro His Ala Arg Ile Met Ile Thr Lys Pro
      115                     120                     125
Ser Ile Gly Gly Thr Ile Thr Gly Gln Ala Thr Asp Leu Asp Ile His
      130                     135                     140
Ala Arg Glu Xaa Leu Lys Thr Lys Ala Arg Ile Ile Asp Val Tyr Val
      145                     150                     155                     160
Glu Ala Thr Gly Gln Ser Pro Glu Val Ile Glu Lys Ala Ile Asp Arg
      165                     170                     175
Asp Met Trp Met Ser Ala Asn Glu Ala Met Glu Phe Gly Leu Leu Asp
      180                     185                     190
Gly Ile Ser Leu Leu Phe
      195

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1049:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 90 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1012593..1012862

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1049:

```

Ser Asn Gly Val Trp Thr Val Arg Trp Asp Phe Ser Ser Leu Leu Thr
1      5      10      15
Thr Cys Arg Tyr Leu Leu Tyr Ser Gly Ala Gly Asn Ser Phe Ile Leu
      20      25      30
Gly Glu Ser Met Pro Ser Leu Glu Asp Val Leu Phe Leu Cys Gln Glu
      35      40      45
Glu Met Val Asp Gly Phe Leu Cys Val Glu Ser Ser Glu Ile Ala Asp
      50      55      60
Ala Lys Leu Thr Val Phe Asn Ser Asp Gly Ser Ile Ala Ser Met Cys
      65      70      75      80
Gly Asn Gly Leu Gln Ser Gln Trp Arg Thr
      85      90

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1050:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 210 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1012811..1013440

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1050:

Trp	Ile	Tyr	Arg	Val	Tyr	Val	Arg	Glu	Trp	Val	Ala	Val	Ala	Met	Ala
1				5					10					15	
His	Val	Ala	Gln	Cys	Phe	Gly	Leu	Glu	Asp	Val	Ser	Ile	Glu	Thr	Glu
			20					25					30		
Arg	Gly	Val	Tyr	Gln	Gly	Lys	Phe	Phe	Ser	Met	Asn	Arg	Val	Leu	Val
		35				40					45				
Asp	Met	Thr	Leu	Pro	Asp	Trp	Lys	Lys	Ala	Glu	Arg	Lys	Leu	Thr	His
	50				55				60						
Val	Leu	Pro	Gly	Met	Pro	Glu	Gln	Val	Phe	Phe	Ile	Asp	Thr	Gly	Val
65				70					75					80	
Pro	His	Val	Val	Val	Phe	Val	Ser	Asp	Leu	Ser	Lys	Val	Pro	Val	Gln
				85					90					95	
Glu	Trp	Gly	Ser	Phe	Leu	Arg	Tyr	His	Glu	Asp	Phe	Ala	Pro	Glu	Gly
			100					105					110		
Val	Asn	Val	Asp	Phe	Val	Gln	Arg	Lys	Lys	Asp	Asp	Leu	Leu	Leu	Val
		115					120					125			
Tyr	Thr	Tyr	Glu	Arg	Gly	Cys	Glu	Arg	Glu	Thr	Leu	Ser	Cys	Gly	Thr
	130				135						140				
Gly	Met	Leu	Ala	Ser	Ala	Leu	Val	Ala	Ala	Asp	Ile	Phe	Ser	Leu	Gly
145				150						155				160	
Gln	Asp	Phe	Ser	Ile	Ala	Val	Cys	Ser	Arg	Ser	Arg	Asn	Leu	Ile	Lys
				165					170					175	
Ile	Phe	Ser	Glu	Lys	Gly	Lys	Val	Phe	Leu	Glu	Gly	Pro	Val	Ser	Leu
			180					185					190		
Leu	Asn	Arg	Ser	Glu	Asn	Phe	Gly	Trp	Leu	Glu	Pro	Lys	Ser	Arg	Arg
		195					200					205			
Phe	Gly														
	210														

(2) INFORMATIONS POUR LA SEQ ID NO: 1051:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 200 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1013456...1014055

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1051:

His	Lys	Arg	Glu	Leu	Leu	Ser	Asn	Arg	Ala	Ser	Pro	Ile	Leu	Glu	Pro
1				5					10					15	
Met	Thr	Thr	Tyr	Pro	Val	Pro	Gln	Asn	Pro	Leu	Leu	Leu	Arg	Val	Leu
			20				25						30		
Arg	Leu	Met	Asp	Ala	Phe	Ser	Lys	Ser	Asp	Asp	Glu	Arg	Asp	Phe	Tyr
		35					40					45			

```

Leu Asp Arg Val Xaa Gly Phe Ile Leu Tyr Ile Asp Leu Asp Lys Asp
 50                      55                      60
Gln Glu Asp Leu Asp Lys Ile Tyr Gln Glu Leu Glu Glu Asn Ala Asp
65                      70                      75                      80
Arg Tyr Cys Leu Ile Pro Lys Leu Thr Phe Tyr Glu Ile Lys Lys Ile
                      85                      90                      95
Met Glu Thr Phe Val Asn Glu Lys Ile Tyr Asp Ile Asp Thr Lys Glu
                      100                     105                     110
Lys Phe Leu Glu Ile Val Gln Ser Lys Asn Ala Arg Glu Gln Phe Gln
                      115                     120                     125
Glu Phe Leu Tyr Asp His Glu Thr Glu Gln Glu Lys Trp Gln Gln Phe
130                      135                      140
Tyr Val Glu Arg Ser Arg Ile Arg Ile Ile Glu Trp Leu Arg Asn Asn
145                      150                      155                      160
Gln Phe Gln Phe Val Phe Glu Glu Asp Leu Asp Phe Ser Lys His Ile
                      165                      170                      175
Leu Glu Gln Leu Lys Val His Leu Phe Asp Ala Lys Val Ser Lys Glu
                      180                     185                     190
Leu Thr Gln Ala Arg His Phe Phe
                      195                     200

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1052:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1013977...1014489

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1052:

```

Ala His Phe Arg Thr Thr Glu Gly Thr Ser Ile Arg Cys Gln Gly Ile
 1                      5                      10                      15
Glu Arg Val Asn Thr Gly Ala Ser Leu Leu Asn Lys Ser Lys Val
                      20                      25                      30
Tyr Tyr Ser Asn Glu Ala Leu Asn Pro Arg Pro Lys Arg Gly Arg Pro
                      35                      40                      45
Pro Lys Gln Ser Ala Lys Val Glu Ala Glu Thr Thr Ile Ser Asn Asp
50                      55                      60
Ile Tyr Thr Lys Val Pro Ser Ala Ala Arg Arg Phe Leu Phe Leu Pro
65                      70                      75                      80
Glu Ile Thr Ser Pro Ser Ser Leu Thr Phe Ser Glu Lys Phe Asp Thr
                      85                      90                      95
Glu Glu Glu Phe Leu Ala His Leu Arg Gly Gly Gly Arg Leu Glu Asp
                      100                     105                     110
Gln Leu Asn Leu Ala Lys Phe Ser Glu Arg Phe Asp Ser Leu Arg Glu
115                      120                      125
Leu Ser Ala Lys Leu Gly Tyr Asp Ser Asp Gly Glu Thr Gly Asp Phe
130                      135                      140
Phe Asn Glu Glu Tyr Asp Asp Glu Glu Glu Glu Ile Lys Pro Lys Lys
145                      150                      155                      160
Thr Thr Lys Arg Gly Arg Lys Lys Ser Arg Ser
                      165                     170

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1053:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 232 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1014529..1015224)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1053:

```

Asn Ser Leu Glu Thr Ile Met Thr Asp Phe His Asp Lys Pro Asn Ile
1          5          10          15
Gln Ile Met Phe Asp Ser Leu Ala Pro Thr Tyr Asp Lys Ile Asn Gly
          20          25          30
Ile Leu Ser Leu Gly Leu His Ile Ala Trp Asn Asn Ala Leu Val Ser
          35          40          45
Leu Leu Gly Glu Thr Asn His Leu Leu Asp Leu Cys Ala Gly Thr Gly
          50          55          60
Arg Val Ala Leu Ser Tyr Val Gln Asn Tyr Pro Arg Ala Ser Ala Thr
65          70          75          80
Leu Val Asp Phe Ser Thr Lys Met Leu Glu Asn Val Gln Lys Arg His
          85          90          95
Pro Ser Ala Pro Phe Ser Tyr Ile Thr Ser Asp Val Thr His Leu Pro
          100          105          110
Leu Pro Asp Asn Thr Phe Arg Leu Ala Ser Met Ala Tyr Gly Leu Arg
          115          120          125
Asn Leu Ser Tyr Pro Leu Glu Ala Leu Arg Glu Val Tyr Arg Val Leu
          130          135          140
Gln Pro Gly Gly His Leu Gly Ile Leu Glu Leu Thr Arg Pro Ala Thr
145          150          155          160
Tyr Asn Pro Val Tyr Leu Leu His Lys Leu Tyr Leu Asn Leu Val Val
          165          170          175
Pro Ser Val Gly Arg Phe Tyr Ser Gly Asn Ser Tyr Ala Tyr Ser Tyr
          180          185          190
Leu Lys Glu Ser Ile Arg Asp Leu Pro Arg Met Pro Leu Ser Lys Gln
          195          200          205
Ser Phe Met Gln Arg Ile Tyr Ala Leu Ser Gly Asn Ala Asn Tyr Phe
          210          215          220
Leu Ala Gln Gln Pro Phe Gly Phe
225          230

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1054:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 286 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1015145..1016002)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1054:

Arg	Asp	Val	Pro	Ser	His	Asn	Thr	Thr	Trp	Ser	Tyr	Pro	Met	Leu	Ser
1				5					10					15	
Gln	Phe	Gln	Asp	Arg	Leu	Asn	Ile	Gly	Cys	Val	Arg	Tyr	Val	Asn	Ala
			20					25					30		
Leu	Pro	Phe	Ser	Ser	Gly	Leu	Ser	Gln	Ala	Pro	Gly	Val	Ser	Leu	Leu
		35				40						45			
Met	Asp	Thr	Pro	Thr	Asn	Leu	Val	Pro	Lys	Leu	Leu	Ser	Arg	Glu	Ile
	50				55						60				
Asp	Tyr	Ala	Leu	Thr	Ser	Val	Ala	Ala	Thr	Phe	Ser	Ser	Ser	Leu	His
65					70					75					80
Arg	Val	Ser	Ser	Phe	Gly	Ile	Ala	Ala	Tyr	Lys	Lys	Ile	Leu	Ser	Val
				85					90					95	
Asn	Leu	His	Ala	Thr	Ser	Gln	Phe	Phe	Ala	Lys	Glu	Ala	Pro	His	Ile
			100					105					110		
Ala	Ala	Thr	Lys	Glu	Ser	Leu	Ser	Ser	Ile	Leu	Leu	Leu	Arg	Val	Leu
		115					120					125			
Cys	Glu	Asn	Leu	Trp	Asn	Ile	Pro	Phe	Pro	Ser	Val	Thr	Leu	Leu	Ser
	130				135						140				
Ser	Asp	Ser	Ile	Leu	Thr	Gln	Ala	Glu	His	Tyr	Asp	Ala	Leu	Leu	Leu
145					150					155					160
Ile	Gly	Asp	Thr	Ala	Leu	Arg	His	Pro	Ile	Ile	Pro	Gly	Phe	His	Thr
			165						170					175	
Tyr	Asp	Leu	Ala	Ala	Ser	Trp	Tyr	Asp	Leu	Thr	Ala	Lys	Pro	Phe	Val
		180						185					190		
Phe	Ala	Gly	Ile	Leu	Ser	Leu	Ser	Ser	Thr	Ile	Ser	Phe	Gln	Leu	Gln
		195					200					205			
Gln	Glu	Phe	Ser	Ser	Thr	Leu	Asn	Tyr	Phe	Gln	Asn	His	Lys	Glu	Asp
	210					215					220				
Ile	Thr	Ser	Lys	Ala	Ala	Ala	Leu	Leu	Lys	Leu	Pro	Glu	Ser	Leu	Met
225					230					235					240
Gln	Glu	Tyr	Tyr	Thr	Leu	Cys	Arg	Tyr	Glu	Leu	Ser	Glu	Glu	Asp	Phe
				245					250					255	
Ala	Gly	Leu	Glu	Gln	Phe	Arg	Asp	Tyr	Tyr	Asp	Arg	Leu	Pro	Arg	Gln
		260						265					270		
Ala	Lys	Tyr	Pro	Asn	His	Val	Arg	Phe	Ser	Cys	Ala	Tyr	Leu		
		275					280					285			

## (2) INFORMATIONS POUR LA SEQ ID NO: 1055:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1015939..1016994)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1055:

Leu	Phe	Asp	Asp	Tyr	Leu	Ser	Gly	Ala	Arg	Leu	Ser	Glu	Lys	Gln	Ala
1				5					10					15	
Leu	Gln	Leu	Leu	Leu	Val	Asp	Ala	Glu	Asp	Gln	Gln	Ala	Leu	Trp	Ser
			20					25					30		
Phe	Ala	Asp	Leu	Ile	Arg	Ala	Asn	Arg	Val	Gly	Asp	Thr	Val	Phe	Tyr

(2) INFORMATIONS POUR LA SEQ ID NO: 1056:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 174 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1017245..1017766)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1056:

Arg Glu Thr Cys Val Phe Gly Phe Val Ala Gly Gly Leu Asp Asp Arg  
1 5 10 15  
Asn Leu Tyr Asn His Phe Phe Asp Ser Asp Gln Gln Gln Tyr Ser Pro  
20 25 30

(i) CARACTERISTIQUES DE LA SEQUENCE:  
(A) LONGUEUR: 174 acides aminés  
(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1017245..1017766)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1056:

Arg Glu Thr Cys Val Phe Gly Phe Val Ala Gly Gly Leu Asp Asp Arg  
1 5 10 15  
Asn Leu Tyr Asn His Phe Phe Asp Ser Asp Gln Gln Gln Tyr Ser Pro  
20 25 30

```

Gly Leu Thr Ala Val Ile Cys Asn Lys Tyr Ser Arg Asp Ser Leu Leu
   35                               40                               45
Glu Ala Leu Tyr Gln Arg Gln Cys Tyr Ala Thr Thr Gly Gln Arg Ile
   50                               55                               60
Ile Val Asn Phe Gln Ile Thr Ser Ala Pro Met Gly Ser Glu Leu Ser
  65                               70                               75                               80
Thr Ala Ile Lys Pro Gly Leu Val Ile Asn Arg His Ile Ser Gly Tyr
   85                               90                               95
Val Ala Gly Thr Ala Lys Ile Ala Ser Ile Glu Ile Ile Arg Asn Gly
  100                               105                               110
Asp Ile Leu His Pro Phe His Pro Asp Gly Asn Asn Phe Glu Tyr Glu
  115                               120                               125
Tyr Asp Asp Leu Ser Pro Phe Ala Gln Val Thr Leu Lys Asp Pro Gln
  130                               135                               140
Asn Gly Ala Pro Phe Ala Phe Tyr Tyr Leu Arg Val Thr Gln Glu Asn
  145                               150                               155                               160
Gly Ala Met Ala Leu Ser Ser Pro Xaa Trp Ile Asp Leu Asn
                               165                               170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1057:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 332 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1017916..1018911)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1057:

```

Lys Arg Leu Pro Arg Ile Leu Trp Leu Gln Lys Leu Cys Met Leu Pro
 1                               5                               10                               15
Glu Ala Ile Ser Leu Leu Ser Asn Leu Leu Ser Leu Val Met Trp Lys
 20                               25                               30
Leu Gly Thr Leu Ser Leu Leu Phe Leu Ala Pro Leu Pro Thr Ser Leu
 35                               40                               45
Lys Arg Thr Leu Gln Val Met Val Leu Asn Tyr Leu Leu Asn Ala Val
 50                               55                               60
Asn Leu Ser Leu Phe Met Leu Thr His Gln Gly Lys Asp Leu Leu Lys
 65                               70                               75                               80
Asp Pro Asp Ile Phe Thr Met Asp Ile Arg Gly Asn Val Leu Lys Asn
   85                               90                               95
Ile Arg Ile Phe Ala Pro Ser Tyr Val Ile Lys Asn Lys Arg Phe Asp
 100                               105                               110
Ile Thr Val Arg Phe Glu Asp Glu Phe Gly Asn Leu Thr Asn Phe Ser
 115                               120                               125
Pro Glu Glu Thr His Ile Glu Leu Ser Tyr Glu His Leu Arg Glu Asn
 130                               135                               140
Leu Asn Trp Gln Leu Phe Ile Pro Glu Thr Gly Phe Val Ile Leu Pro
 145                               150                               155                               160
Asn Leu Tyr Phe Asn Glu Pro Gly Ile Tyr Arg Ile Gln Leu Arg Asn
 165                               170                               175
Gln Ala Thr Lys Glu Val Phe Thr Ser Ala Pro Ile Lys Cys Phe Ala
 180                               185                               190
Glu Thr Ser Ser His Leu Leu Trp Gly Leu Leu His Gly Glu Ser Asp

```

		195				200				205					
Arg	Val	Asp	Ser	Glu	Gly	Asn	Ile	Glu	Ser	Cys	Leu	Arg	Tyr	Phe	Arg
	210					215					220				
Asp	Asp	Cys	Ala	Leu	Asn	Phe	Phe	Ala	Thr	Ser	Ser	Phe	Glu	Ile	Gln
225					230					235					240
Asp	Gly	Leu	Thr	Pro	Glu	Thr	Ile	Lys	Thr	Ile	Asn	Gln	Thr	Val	Ala
				245					250					255	
Asp	Phe	Asn	Glu	Glu	Asp	Arg	Phe	Ile	Ala	Leu	Ser	Gly	Ala	Gln	Tyr
			260					265					270		
Leu	Ser	Glu	Glu	Pro	Gly	Glu	Gly	Ile	Arg	Glu	Val	Leu	Leu	Met	Lys
		275					280					285			
Glu	Pro	Lys	Ser	Pro	Gly	Lys	His	Lys	Glu	Cys	Lys	Leu	Phe	Pro	Leu
	290					295					300				
Ser	Lys	Leu	Tyr	Lys	Gln	Ser	Thr	Ser	His	Glu	Leu	Ile	Ser	Ile	Pro
305					310					315					320
Gln	Leu	His	Cys	Phe	Lys	Glu	Ile	Trp	Ile	Gln	Phe				
				325					330						

(2) INFORMATION POUR LA SEQ ID NO: 1058:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1018580..1019191)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1058:

Arg	Ser	Ser	Val	Lys	His	Ala	Lys	Ala	Lys	Phe	Leu	Gln	Ile	Lys	Asp
1				5					10					15	
Phe	Leu	Val	Thr	Arg	Thr	Tyr	Ile	Leu	Val	Ala	Met	Arg	Arg	Ser	Val
			20					25					30		
Cys	Tyr	Val	Thr	Pro	Ser	Val	Ala	Arg	Ala	Gly	Gln	Ile	Ser	Thr	Trp
		35				40						45			
Arg	Phe	Glu	Tyr	Ser	Ser	Ala	Asn	Phe	Leu	Pro	Glu	Gly	Thr	Leu	Leu
	50					55					60				
Lys	Phe	Asp	Leu	Gly	Ile	Asp	Gly	Arg	Pro	Ile	Asp	Trp	Glu	Ile	Pro
65					70					75					80
Ser	Ile	Asp	Leu	Ser	Gln	Pro	Cys	Asn	Thr	Ile	Tyr	Leu	Glu	Thr	Pro
				85					90					95	
Ser	Glu	Asp	Ile	Val	Ala	Ala	Lys	Ala	Val	Tyr	Ala	Pro	Gly	Gly	Tyr
			100					105					110		
Ile	Pro	Thr	Phe	Glu	Phe	Thr	Leu	Pro	Cys	Asp	Val	Glu	Ala	Gly	Asp
		115					120					125			
Thr	Phe	Ser	Ile	Ile	Leu	Gly	Ser	Pro	Asn	Phe	Pro	Gln	Glu	Asp	
	130					135				140					
Ser	Ser	Gly	Asn	Gly	Ala	Gln	Leu	Phe	Thr	Gln	Arg	Arg	Lys	Pro	Phe
145					150					155					160
Ser	Leu	Tyr	Val	Asp	Pro	Ser	Gly	Lys	Gly	Ser	Phe	Glu	Arg	Ser	Arg
				165					170					175	
Tyr	Leu	His	Asn	Gly	Tyr	Gln	Arg	Lys	Cys	Ile	Lys	Lys	Tyr	Pro	Asp
			180					185					190		
Phe	Cys	Ser	Phe	Leu	Cys	Asp	Gln	Lys	Gln	Thr	Leu				
		195					200								



(2) INFORMATIONS POUR LA SEQ ID NO: 1059:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1019831..1020199)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1059:

Arg	Leu	Ser	Leu	Met	Asn	Thr	Asp	Leu	Gln	Lys	Ala	Phe	Val	Ser	Met
1				5					10					15	
Glu	Asp	Ile	Val	Glu	Glu	Ile	Phe	Gly	Glu	Ile	Ala	Asp	Glu	Tyr	Asp
			20					25					30		
Asp	Gln	Glu	Asp	Val	His	Tyr	Lys	Xaa	Ile	Gly	Asn	Ala	Trp	Ile	Val
		35					40				45				
Asp	Gly	Arg	Met	Asn	Ile	Ser	Asp	Ala	Glu	Glu	Cys	Phe	Gly	Leu	His
	50					55					60				
Ile	Glu	His	Glu	Ser	Ser	Tyr	Asp	Thr	Leu	Gly	Gly	Tyr	Val	Phe	His
65					70					75				80	
Lys	Leu	Gly	Ala	Val	Pro	Glu	Lys	Gly	Met	Lys	Ile	Tyr	Tyr	Glu	Asp
			85					90						95	
Phe	Ala	Ile	Asp	Ile	Leu	Ser	Cys	Ser	Asp	Arg	Ser	Val	Glu	Lys	Met
			100					105					110		
Lys	Ile	Thr	Pro	Arg	Arg	Arg	Lys	Pro	Leu	Ser					
		115					120								

(2) INFORMATIONS POUR LA SEQ ID NO: 1060:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1020114..1021007)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1060:

Ala	Ser	Ser	Leu	Phe	Val	Asp	Ser	Pro	Asn	Asn	Phe	Phe	Tyr	Arg	Ser
1				5					10					15	
Trp	Leu	Phe	Ser	Pro	Leu	Ile	Met	Leu	Tyr	Ile	Leu	Leu	Ala	Ile	Ile
			20					25					30		
Val	Leu	Phe	Leu	Phe	Leu	Gly	Ser	Ala	Thr	His	Arg	Arg	Ala	Ser	Ile
		35				40					45				
Ser	Ala	Tyr	Gly	Gly	Glu	Gly	Leu	Pro	Pro	Phe	Ser	Ser	Cys	Pro	Lys
	50				55					60					
Val	Leu	Pro	Leu	Leu	Cys	Leu	Ile	Tyr	Gly	Met	Leu	Gly	Ala	Pro	Val
65					70				75					80	
Tyr	Gln	Tyr	Ile	His	Asn	Phe	Phe	Ser	Leu	Ser	Pro	Ser	Ile	Phe	Trp

				85					90					95					
Leu	Ile	Phe	Leu	Ser	Leu	Ala	Leu	Val	Ile	Tyr	Lys	Phe	Leu	Pro	Leu				
			100					105					110						
Cys	Pro	Gly	Tyr	Ser	Asp	Asp	Ser	Phe	Ser	Tyr	Lys	Val	Ser	Ser	Ser				
		115					120					125							
Thr	Val	Lys	Thr	Leu	Glu	Asn	Cys	Leu	Ala	Gly	Phe	Lys	Thr	Pro	Ser				
	130					135					140								
Ile	Thr	Ala	Met	Gln	Gln	Thr	Pro	Pro	Pro	Glu	Pro	Pro	Asn	Glu	Leu				
145					150					155					160				
Ser	Thr	Asn	Ile	Ser	Cys	Leu	Asn	His	Met	Ile	Ala	Arg	Glu	Ile	Met				
			165						170					175					
Thr	Pro	Lys	Ala	Asp	Ile	Phe	Ala	Leu	Gln	Gly	Asp	Thr	Pro	Ile	Ser				
			180					185						190					
Gln	Ala	Phe	Pro	Leu	Ile	Ile	Asp	Glu	Gly	Tyr	Ser	Arg	Ile	Pro	Leu				
		195					200					205							
Phe	Thr	Lys	Ser	Ile	Asp	Asp	Ile	Thr	Gly	Met	Val	Leu	Val	Lys	Asp				
	210					215					220								
Leu	Ser	Pro	Val	Tyr	Tyr	Lys	Asp	Pro	His	Thr	Ser	Gln	Pro	Leu	Ser				
225					230					235					240				
Ser	Ile	Ala	Tyr	Pro	Pro	Leu	Tyr	Thr	Pro	Glu	Ile	Arg	Arg	Ala	Ser				
			245					250						255					
Leu	Leu	Leu	Gln	Glu	Phe	Xaa	Gln	Lys	Arg	Cys	His	Leu	Ala	Ile	Val				
			260				265						270						
Val	Asn	Glu	Tyr	Gly	Phe	Thr	Glu	Gly	Leu	Cys	Leu	Tyr	Gly	Arg	Tyr				
	275						280					285							
Arg	Arg	Arg	Asn	Leu	Trp	Arg	Asn	Cys	Arg										
	290					295													

(2) INFORMATIONS POUR LA SEQ ID NO: 1061:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 165 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1021075..1021569)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1061:

Val	Ile	Phe	Phe	Leu	Leu	Ile	Leu	Asp	Arg	Ser	Ser	Pro	Gln	Ile	Phe				
1				5				10				15							
Ile	Ser	Asn	Glu	Gln	Gln	Asp	Val	Ser	Ile	Asp	Leu	Gln	Ser	Ala	Gln				
		20					25				30								
Arg	Leu	Val	Val	Leu	Phe	Leu	Glu	Leu	Gln	Lys	Val	Ser	Thr	Asp	Gln				
	35					40					45								
Val	Tyr	Val	Tyr	Phe	Leu	Asp	Asp	Thr	Ala	Leu	Ala	Gln	Leu	His	Asp				
	50				55					60									
Glu	Gln	Phe	Ser	Asp	Pro	Ser	Leu	Thr	Asp	Thr	Ile	Thr	Leu	Pro	Ile				
65				70				75						80					
Asp	Lys	Pro	Gly	Ile	Ala	Ser	Phe	Pro	His	Val	Leu	Gly	Glu	Ala	Phe				
			85				90					95							
Val	Ser	Pro	Lys	Ala	Ala	Met	Arg	Phe	Leu	Glu	Gln	Tyr	Thr	Glu	Asp				
		100				105						110							
Gln	Leu	Tyr	His	Glu	Ile	Ser	Arg	Tyr	Val	Val	His	Ser	Leu	Leu	His				
	115					120						125							

```

Met Leu Gly Tyr Asp Asp Gln Thr Asp Glu Asp Lys Arg Ile Met Gln
  130                      135                      140
Glu Gln Glu Asp Val Ser Leu Ser Phe Leu Ala Glu His Gln Ala Leu
145                      150                      155                      160
Leu Arg Pro Ala Val
                      165

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1062:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1022097..1022411)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1062:

```

Gln Gln Ser Leu Gly Leu Asn Gln Asp Pro Leu Asn Lys Val Val Met
  1                      5                      10                      15
Val Pro Phe Pro Asn Arg Glu Val Leu Cys Ile Gly Leu Val Ala Gly
                20                      25                      30
Glu Ala Pro Thr Thr Cys Ser Gln Asp Ala Asp Asp Pro Met Ile Thr
        35                      40                      45
Val Phe Ile Pro Thr Thr Pro Asn Pro Thr Ser Gly Phe Leu Thr Leu
  50                      55                      60
Phe Lys Lys Ser Asp Ile Thr Phe Leu Asp Met Lys Ile Glu Asp Ala
65                      70                      75                      80
Phe Lys Tyr Val Ile Ser Cys Gly Val Leu Asn Ser Asp Pro Cys Ala
                85                      90                      95
Thr Ser Pro Phe Ile His Pro Gln Phe
                100                      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1063:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1023347..1023667

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1063:

```

Met Glu Pro Tyr Ala Val Ile Gln Thr Gly Asn Lys Gln Tyr Gln Val
  1                      5                      10                      15
Arg Lys Gly Asp Val Ile Asp Val Glu Leu Leu Asp Gly Ile Ser Glu
                20                      25                      30
Glu Asn Lys Glu Val Leu Phe Gln Asp Val Leu Phe Thr Phe Asp Gly
        35                      40                      45
Glu Lys Ala Ser Val Gly Ala Pro Thr Val Gly Asn Ala Val Val Lys

```

```

      50              55              60
Gly Glu Leu Val Ser Phe Val Arg Gly Glu Lys Val Val Ala Tyr Lys
65              70              75              80
Tyr Lys Lys Arg Lys Asn Tyr His Lys Lys Ile Gly His Arg Gln Asn
      85              90              95
Tyr Leu Arg Val Lys Ile Ser Asp Leu Val Met
      100              105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1064:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 83 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1023701..1023949

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1064:

```

Met Ala His Lys Lys Gly Gln Gly Ala Ser Arg Asn Gly Arg Asp Ser
1              5              10              15
Glu Ser Lys Arg Leu Gly Leu Lys Val Gly Ala Gly Gln Arg Val Ser
      20              25              30
Thr Gly Ser Ile Leu Val Arg Gln Arg Gly Thr Lys Trp His Pro Ala
      35              40              45
Val Asn Val Gly Arg Gly Lys Asp Asp Thr Leu Phe Ala Leu Ala Asp
      50              55              60
Gly Ile Val Val Met Lys Lys Thr Asp Arg Thr Tyr Val Ser Val Ile
65              70              75              80
Pro Gln Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1065:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1024042..1024776

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1065:

```

Met Phe Val Asp Gln Ile Thr Leu Glu Leu Arg Ala Gly Lys Gly Gly
1              5              10              15
Asn Gly Val Val Ala Trp Arg Lys Glu Lys Tyr Leu Pro Lys Gly Gly
      20              25              30
Pro Tyr Gly Gly Asn Gly Gly Asn Gly Gly Ser Ile Leu Ile Glu Thr
      35              40              45
Val Thr Asn Met Tyr Ser Phe Glu Glu Tyr Arg Asn Leu Arg Phe Leu
      50              55              60

```

```

Lys Ala Asp Asp Gly Gln Ala Gly Ala Ser Asn Asn Arg Thr Gly Arg
65          70          75          80
Asn Gly Lys Asp Leu Val Leu Lys Val Pro Glu Gly Thr Leu Leu Arg
          85          90          95
Asp Ala Ala Thr Gly Glu Leu Ile His Asp Phe Thr Lys Asp Gly Glu
          100          105          110
Arg Ile Val Val Cys Gln Gly Gly Arg Gly Gly Lys Gly Asn Val Phe
          115          120          125
Phe Lys Thr Ser Thr Asn Arg Ala Pro Thr Lys Ala Thr Pro Gly Lys
          130          135          140
Pro Gly Glu Ile Arg Leu Val Glu Leu Glu Leu Lys Leu Ile Ala Asp
145          150          155          160
Ile Gly Leu Val Gly Phe Pro Asn Ala Gly Lys Ser Thr Leu Phe Asn
          165          170          175
Thr Leu Ala Arg Thr Glu Val Lys Val Gly Ala Tyr Pro Phe Thr Thr
          180          185          190
Leu His Pro Ser Leu Gly Leu Val His Gln Glu Gly Met Leu Tyr Gln
          195          200          205
Lys Thr Trp Ile Met Ala Asp Ile Pro Gly Ile Ile Glu Gly Ala Ser
          210          215          220
Gln Asn Arg Gly Leu Gly Leu Asp Phe Phe Gly Ile Leu Asn Val Arg
225          230          235          240
Asp Tyr Cys Tyr Ser
          245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1066:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 114 acides aminés.

(B) TYPE: acide aminé.

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1024704..1025045

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1066:

```

Arg Ser Val Ala Lys Pro Gly Ile Gly Ile Gly Phe Leu Arg His Ile
1          5          10          15
Glu Arg Thr Arg Leu Leu Leu Phe Val Ile Asp Ile Ser Gly Ile Glu
          20          25          30
Arg His Ser Pro Glu Gln Asp Leu Lys Ile Leu Met Gly Glu Leu Leu
          35          40          45
Ala Tyr Lys Glu Glu Leu Lys Asp Lys Asp Met Val Ile Ala Leu Asn
          50          55          60
Lys Ile Asp Gln Leu Leu Pro Asp Glu Arg Glu Arg Val Ala Leu
65          70          75          80
Leu Lys Gln Gln Phe Pro Asp Gln Glu Phe Ile Leu Leu Ser Gly Leu
          85          90          95
Thr Gly Glu Gly Val Asp Ala Leu Tyr Asp Leu Phe Lys Ser Lys Leu
          100          105          110
Ser Glu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1067:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 305 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1024967..1025881)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1067:

Asn	Phe	Arg	Lys	Ile	Leu	Leu	Gln	His	Phe	Trp	Glu	Met	Pro	Met	Ile	1	5	10	15
Ser	Ile	Leu	Cys	Ser	Leu	Phe	Pro	Pro	Leu	Leu	Phe	Pro	Ser	Leu	Leu	20	25	30	
Ala	Ala	Phe	Gly	Ala	Ser	Ile	Ala	Ala	Gly	Ile	Val	Gly	Ser	Tyr	Ile	35	40	45	
Val	Val	Lys	Arg	Ile	Val	Ser	Ile	Ser	Gly	Ser	Ile	Ala	His	Ser	Ile	50	55	60	
Leu	Gly	Gly	Val	Gly	Ile	Ala	Leu	Trp	Leu	Gln	Tyr	Gln	Phe	Asn	Leu	65	70	75	80
Pro	Ile	Ser	Pro	Leu	His	Gly	Ala	Ile	Ala	Ser	Ala	Ile	Phe	Val	Ala	85	90	95	
Ile	Cys	Ile	Gly	Asn	Val	His	Leu	Lys	Tyr	His	Glu	Arg	Glu	Asp	Ser	100	105	110	
Ile	Ile	Ser	Met	Ile	Trp	Ser	Ile	Gly	Met	Ala	Ile	Gly	Ile	Ile	Cys	115	120	125	
Ile	Ser	Lys	Leu	Pro	Ser	Phe	Asn	Ser	Glu	Leu	Ser	Asp	Phe	Leu	Phe	130	135	140	
Gly	Asn	Ile	Leu	Trp	Val	Thr	Pro	Gln	Asp	Leu	Tyr	Phe	Leu	Gly	Ile	145	150	155	160
Leu	Asp	Leu	Phe	Ile	Val	Ala	Thr	Val	Ser	Ile	Cys	His	Thr	Arg	Phe	165	170	175	
Leu	Ala	Leu	Cys	Phe	Asp	Glu	Lys	Tyr	Met	Ala	Leu	Asn	His	Tyr	Ser	180	185	190	
Ile	Lys	Thr	Trp	Tyr	Leu	Leu	Leu	Leu	Ile	Leu	Thr	Ala	Ile	Thr	Thr	195	200	205	
Val	Val	Leu	Met	Tyr	Val	Met	Gly	Val	Ile	Leu	Met	Leu	Ser	Met	Leu	210	215	220	
Val	Leu	Pro	Val	Ser	Ile	Ala	Cys	Arg	Phe	Ser	Tyr	Lys	Met	Ser	His	225	230	235	240
Ile	Ile	Tyr	Ile	Ala	Ser	Ile	Leu	Asn	Ile	Val	Cys	Ser	Phe	Leu	Gly	245	250	255	
Ile	Met	Leu	Ala	Tyr	Leu	Leu	Asp	Leu	Pro	Val	Gly	Pro	Val	Ile	Ala	260	265	270	
Ile	Leu	Met	Gly	Gly	Ala	Tyr	Ser	Leu	Ser	Leu	Leu	Leu	Asn	Arg	Ser	275	280	285	
Tyr	Asn	Ala	Ser	Thr	Pro	Ser	Pro	Val	Ser	Pro	Glu	Ser	Lys	Ile	Asn	290	295	300	
Ser																305			

(2) INFORMATIONS POUR LA SEQ ID NO: 1068:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé  
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1025839..1026546)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1068:

Met	Thr	Lys	Gln	Met	Leu	Leu	Glu	Asn	Val	Ser	Phe	Arg	Tyr	Gly	Lys
1			5					10						15	
Thr	Gly	Pro	Leu	Ile	Val	Asp	His	Val	Ser	Cys	Glu	Val	Tyr	Ser	Gly
		20					25						30		
Asp	Phe	Ile	Gly	Ile	Ile	Gly	Pro	Asn	Gly	Gly	Gly	Lys	Thr	Thr	Leu
		35				40						45			
Thr	Gln	Leu	Met	Leu	Arg	Leu	Leu	Gln	Pro	Val	Cys	Gly	Ser	Ile	Ser
	50					55					60				
Thr	Tyr	Ser	Val	Gln	Asp	His	Arg	Pro	Leu	Ser	Ile	Gly	Trp	Val	Pro
65				70					75						80
Gln	His	Phe	Ser	Tyr	Asp	Ala	Ala	Phe	Pro	Ile	Thr	Val	Lys	Glu	Thr
			85					90					95		
Val	Leu	Ser	Gly	Arg	Leu	Ala	Thr	Leu	Pro	Trp	Tyr	Gly	Arg	Tyr	Thr
			100					105					110		
Gln	Glu	Asp	His	Glu	Ala	Ala	Glu	Glu	Ala	Leu	Leu	Thr	Val	Asp	Leu
		115					120					125			
Ile	Asp	Tyr	Lys	Asp	Ser	Cys	Phe	Ser	His	Leu	Ser	Gly	Gly	Gln	Ile
	130					135					140				
Gln	Arg	Val	Leu	Leu	Ala	Arg	Ala	Leu	Ala	Ala	Arg	Pro	Glu	Phe	Leu
145					150					155					160
Leu	Leu	Asp	Glu	Pro	Thr	Ala	Asn	Ile	Asp	Pro	Val	Asn	Gln	Gln	Lys
			165					170					175		
Ile	Leu	Gln	Ile	Leu	Ser	Ala	Leu	Asn	Lys	His	Cys	Thr	Ile	Leu	Met
		180						185					190		
Ile	Thr	His	Asp	Leu	His	His	Thr	Ala	Gly	Cys	Phe	Asn	Arg	Val	Phe
	195						200					205			
Phe	Met	Asn	Lys	Thr	Leu	Thr	Thr	Leu	Ala	Asp	Thr	Thr	Thr	Ile	Ser
	210					215					220				
Glu	Arg	Phe	Cys	Cys	Asn	Thr	Phe	Gly	Arg	Cys	Pro				
225					230					235					

(2) INFORMATIONS POUR LA SEQ ID NO: 1069:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1026546..1027379)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1069:

Asp	Asn	Met	Arg	Leu	Leu	Phe	Leu	Leu	Leu	Phe	Ser	Leu	Gly	Ile	Thr
1				5					10					15	
Cys	Ser	Tyr	Gly	Asp	Glu	Val	Ser	Thr	Arg	Lys	Gln	Ile	Leu	Val	Ser

(2) INFORMATION POUR LA SEQ ID NO: 1070:

(A) LONGUEUR: 892 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1027929..1030604)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1070:

Arg	Asp	Ser	Arg	Arg	Thr	Val	Thr	Phe	Ser	Gly	Asn	Thr	Val	Ser	Ser
1				5					10					15	
Gln	Ser	Thr	Thr	Gly	Gln	Val	Ala	Gly	Gly	Ala	Ile	Tyr	Ser	Pro	Thr
			20					25					30		
Val	Thr	Ile	Ala	Thr	Pro	Val	Val	Phe	Ser	Lys	Asn	Ser	Ala	Thr	Asn
			35				40					45			
Asn	Ala	Asn	Asn	Ala	Thr	Asp	Thr	Gln	Arg	Lys	Asp	Thr	Phe	Gly	Gly
	50					55					60				
Ala	Ile	Gly	Ala	Thr	Ser	Ala	Val	Ser	Leu	Ser	Gly	Gly	Ala	His	Phe
65					70					75					80



Leu	Glu	Asn	Val	Ala	Asp	Leu	Gly	Ser	Ala	Ile	Gly	Leu	Val	Pro	Asp		
				85					90					95			
Thr	Gln	Asn	Thr	Glu	Thr	Val	Lys	Leu	Glu	Ser	Gly	Ser	Tyr	Tyr	Phe		
			100					105					110				
Glu	Lys	Asn	Lys	Ala	Leu	Lys	Arg	Ala	Thr	Ile	Tyr	Ala	Pro	Val	Val		
		115					120					125					
Ser	Ile	Lys	Ala	Tyr	Thr	Ala	Thr	Phe	Asn	Gln	Asn	Arg	Ser	Leu	Glu		
	130					135					140						
Glu	Gly	Ser	Ala	Ile	Tyr	Phe	Thr	Lys	Glu	Ala	Ser	Ile	Glu	Ser	Leu		
145					150					155					160		
Gly	Ser	Val	Leu	Phe	Thr	Gly	Asn	Leu	Val	Thr	Pro	Thr	Leu	Ser	Thr		
			165						170						175		
Thr	Thr	Glu	Gly	Thr	Pro	Ala	Thr	Thr	Ser	Gly	Asp	Val	Thr	Lys	Tyr		
			180					185					190				
Gly	Ala	Ala	Ile	Phe	Gly	Gln	Ile	Ala	Ser	Ser	Asn	Gly	Ser	Gln	Thr		
		195				200						205					
Asp	Asn	Leu	Pro	Leu	Lys	Leu	Ile	Ala	Ser	Gly	Gly	Asn	Ile	Cys	Phe		
	210					215					220						
Arg	Asn	Asn	Glu	Tyr	Arg	Pro	Thr	Ser	Ser	Asp	Thr	Gly	Thr	Ser	Thr		
225					230					235					240		
Phe	Cys	Ser	Ile	Ala	Gly	Asp	Val	Lys	Leu	Thr	Met	Gln	Ala	Ala	Lys		
			245						250					255			
Gly	Lys	Thr	Ile	Ser	Phe	Phe	Asp	Ala	Ile	Arg	Thr	Ser	Thr	Lys	Lys		
		260					265						270				
Thr	Gly	Thr	Gln	Ala	Thr	Ala	Tyr	Asp	Thr	Leu	Asp	Ile	Asn	Lys	Ser		
		275					280					285					
Glu	Asp	Ser	Glu	Thr	Val	Asn	Ser	Ala	Phe	Thr	Gly	Thr	Ile	Leu	Phe		
	290					295					300						
Ser	Ser	Glu	Leu	His	Glu	Asn	Lys	Ser	Tyr	Ile	Pro	Gln	Asn	Val	Val		
305					310					315					320		
Leu	His	Ser	Gly	Ser	Leu	Val	Leu	Lys	Pro	Asn	Thr	Glu	Leu	His	Val		
			325						330					335			
Ile	Ser	Phe	Glu	Gln	Lys	Glu	Gly	Ser	Ser	Leu	Val	Met	Thr	Pro	Gly		
		340					345						350				
Ser	Val	Leu	Ser	Asn	Gln	Thr	Val	Ala	Asp	Gly	Ala	Leu	Val	Ile	Asn		
	355						360					365					
Asn	Met	Thr	Ile	Asp	Leu	Ser	Ser	Val	Glu	Lys	Asn	Gly	Ile	Ala	Glu		
	370					375					380						
Gly	Asn	Ile	Phe	Thr	Pro	Glu	Leu	Arg	Ile	Ile	Asp	Thr	Thr	Thr			
385					390				395						400		
Ser	Gly	Ser	Gly	Gly	Thr	Pro	Ser	Thr	Asp	Ser	Glu	Ser	Asn	Gln	Asn		
			405						410					415			
Ser	Asp	Asp	Thr	Lys	Glu	Gln	Asn	Asn	Asn	Asp	Ala	Ser	Asn	Gln	Gly		
			420				425						430				
Glu	Ser	Ala	Asn	Gly	Ser	Ser	Ser	Pro	Ala	Val	Ala	Ala	Ala	His	Thr		
		435					440					445					
Ser	Arg	Thr	Arg	Asn	Phe	Ala	Ala	Ala	Ala	Thr	Ala	Thr	Pro	Thr	Thr		
	450					455					460						
Thr	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Ser	Asn	Gln	Val	Ile	Leu	Gly	Gly		
465					470					475					480		
Glu	Ile	Lys	Leu	Ile	Asp	Pro	Asn	Gly	Thr	Phe	Phe	Gln	Asn	Pro	Ala		
			485					490						495			
Leu	Arg	Ser	Asp	Gln	Gln	Ile	Ser	Leu	Leu	Val	Leu	Pro	Thr	Asp	Ser		
			500					505					510				
Ser	Lys	Met	Gln	Ala	Gln	Lys	Ile	Val	Leu	Thr	Gly	Asp	Ile	Ala	Pro		
		515					520					525					
Gln	Lys	Gly	Tyr	Thr	Gly	Thr	Leu	Thr	Leu	Asp	Pro	Asp	Gln	Leu	Gln		
	530					535					540						
Asn	Gly	Thr	Ile	Ser	Ala	Leu	Trp	Lys	Phe	Asp	Ser	Tyr	Arg	Gln	Trp		

545		550		555		560
Ala Tyr Val Pro Arg	Asp Asn His Phe Tyr	Ala Asn Ser Ile Leu Gly				
	565	570		575		
Ser Gln Met Ser Met	Val Thr Val Lys Gln Gly	Leu Leu Asn Asp Lys				
	580	585		590		
Met Asn Leu Ala Arg	Phe Asp Glu Val Ser Tyr	Asn Asn Leu Trp Ile				
	595	600		605		
Ser Gly Leu Gly Thr	Met Leu Ser Gln Val Gly Thr	Pro Thr Ser Glu				
	610	615		620		
Glu Phe Thr Tyr Tyr	Ser Arg Gly Ala Ser Val	Ala Leu Asp Ala Lys				
	625	630		635		640
Pro Ala His Asp Val	Ile Val Gly Ala Ala Phe	Ser Lys Met Ile Gly				
	645	650		655		
Lys Thr Lys Ser Leu	Lys Arg Glu Asn Asn Tyr Thr	His Lys Gly Ser				
	660	665		670		
Glu Tyr Ser Tyr Gln	Ala Ser Val Tyr Gly Gly	Lys Pro Phe His Phe				
	675	680		685		
Val Ile Asn Lys Lys	Thr Glu Lys Ser Leu Pro	Leu Leu Leu Gln Gly				
	690	695		700		
Val Ile Ser Tyr Gly	Tyr Ile Lys His Asp Thr	Val Thr His Tyr Pro				
	705	710		715		720
Thr Ile Arg Glu Arg	Asn Gln Gly Glu Trp Glu	Asp Leu Gly Trp Leu				
	725	730		735		
Thr Ala Leu Arg Val	Ser Ser Val Leu Arg Thr	Pro Ala Gln Gly Asp				
	740	745		750		
Thr Lys Arg Ile Thr	Val Tyr Gly Glu Leu Glu	Tyr Ser Ser Ile Arg				
	755	760		765		
Gln Lys Gln Phe Thr	Glu Thr Glu Tyr Asp Pro	Arg Tyr Phe Asp Asn				
	770	775		780		
Cys Thr Tyr Arg Asn	Leu Ala Ile Pro Met Gly	Leu Ala Phe Glu Gly				
	785	790		795		800
Glu Leu Ser Gly Asn	Asp Ile Leu Met Tyr Asn	Arg Phe Ser Val Ala				
	805	810		815		
Tyr Met Pro Ser Ile	Tyr Arg Asn Ser Pro Thr	Cys Lys Tyr Gln Val				
	820	825		830		
Leu Ser Ser Gly Glu	Gly Gly Glu Ile Ile Cys	Gly Val Pro Thr Arg				
	835	840		845		
Asn Ser Ala Arg Gly	Glu Tyr Ser Thr Gln Leu	Tyr Pro Gly Pro Leu				
	850	855		860		
Trp Thr Leu Tyr Gly	Ser Tyr Thr Ile Glu Ala	Asp Ala His Thr Leu				
	865	870		875		880
Ala His Met Met Asn	Cys Gly Ala Arg Met Ile Phe					
	885	890				

(2) INFORMATIONS POUR LA SEQ ID NO: 1071:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 914 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1030508..1033249)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1071:

Met	Lys	Phe	Leu	Ser	Ala	Thr	Ala	Val	Phe	Ala	Ala	Val	Leu	Ser	Ser	
1				5					10					15		
Val	Thr	Glu	Ala	Ser	Ser	Ile	Gln	Asp	Gln	Ile	Lys	Asn	Thr	Asp	Cys	
			20					25					30			
Asn	Val	Ser	Lys	Val	Gly	Tyr	Ser	Thr	Ser	Gln	Ala	Phe	Thr	Asp	Met	
		35					40					45				
Met	Leu	Ala	Asp	Asn	Thr	Glu	Tyr	Arg	Ala	Ala	Asp	Ser	Val	Ser	Phe	
	50					55					60					
Tyr	Asp	Phe	Ser	Thr	Ser	Ser	Gly	Leu	Pro	Arg	Lys	His	Leu	Ser	Ser	
65					70					75					80	
Ser	Ser	Glu	Ala	Ser	Pro	Thr	Thr	Glu	Gly	Val	Ser	Ser	Ser	Ser	Ser	
				85					90					95		
Gly	Glu	Asn	Thr	Glu	Asn	Ser	Gln	Asp	Ser	Ala	Pro	Ser	Ser	Gly	Glu	
			100					105					110			
Thr	Asp	Lys	Lys	Thr	Glu	Glu	Glu	Leu	Asp	Asn	Gly	Gly	Ile	Ile	Tyr	
		115					120					125				
Ala	Arg	Glu	Lys	Leu	Thr	Ile	Ser	Glu	Ser	Gln	Asp	Ser	Leu	Ser	Asn	
	130					135					140					
Pro	Ser	Ile	Glu	Leu	His	Asp	Asn	Ser	Phe	Phe	Phe	Gly	Glu	Gly	Glu	
145					150					155					160	
Val	Ile	Phe	Asp	His	Arg	Val	Ala	Leu	Lys	Asn	Gly	Gly	Ala	Ile	Tyr	
				165					170					175		
Gly	Glu	Lys	Glu	Val	Val	Phe	Glu	Asn	Ile	Lys	Ser	Leu	Leu	Val	Glu	
			180					185					190			
Val	Asn	Ile	Xaa	Xaa	Glu	Lys	Gly	Gly	Ser	Val	Tyr	Ala	Lys	Glu	Arg	
	195						200					205				
Val	Ser	Leu	Glu	Asn	Val	Thr	Glu	Ala	Thr	Phe	Ser	Ser	Asn	Gly	Gly	
	210					215					220					
Glu	Gln	Gly	Gly	Gly	Gly	Ile	Tyr	Ser	Glu	Gln	Asp	Met	Leu	Ile	Ser	
225					230					235					240	
Asp	Cys	Asn	Asn	Val	His	Phe	Gln	Gly	Asn	Ala	Ala	Gly	Ala	Thr	Ala	
				245					250					255		
Val	Lys	Gln	Cys	Leu	Asp	Glu	Glu	Met	Ile	Val	Leu	Leu	Thr	Glu	Cys	
			260					265					270			
Val	Asp	Ser	Leu	Ser	Glu	Asp	Thr	Leu	Asp	Ser	Thr	Pro	Glu	Thr	Glu	
	275						280					285				
Gln	Thr	Lys	Ser	Asn	Gly	Asn	Gln	Asp	Gly	Ser	Ser	Glu	Thr	Lys	Asp	
	290					295					300					
Thr	Gln	Val	Ser	Glu	Ser	Pro	Glu	Ser	Thr	Pro	Ser	Pro	Asp	Asp	Val	
305					310					315					320	
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Tyr	Thr	Glu	Lys	Ser	Leu	Thr	Ile	Thr	
				325					330					335		
Gly	Ile	Thr	Gly	Thr	Ile	Asp	Phe	Val	Ser	Asn	Ile	Ala	Thr	Asp	Ser	
			340					345					350			
Gly	Ala	Gly	Val	Phe	Thr	Lys	Glu	Asn	Leu	Ser	Cys	Thr	Asn	Thr	Asn	
	355						360					365				
Ser	Leu	Gln	Phe	Leu	Lys	Asn	Ser	Ala	Gly	Gln	His	Gly	Gly	Gly	Ala	
	370					375					380					
Tyr	Val	Thr	Gln	Thr	Met	Ser	Val	Thr	Asn	Thr	Thr	Ser	Glu	Ser	Ile	
385					390					395					400	
Thr	Thr	Pro	Pro	Leu	Val	Gly	Glu	Val	Ile	Phe	Ser	Glu	Asn	Thr	Ala	
				405					410					415		
Lys	Gly	His	Gly	Gly	Gly	Ile	Cys	Thr	Asn	Lys	Leu	Ser	Leu	Ser	Asn	
			420					425					430			
Leu	Lys	Thr	Val	Thr	Leu	Thr	Lys	Asn	Ser	Ala	Lys	Glu	Ser	Gly	Gly	
	435						440					445				
Ala	Ile	Phe	Thr	Asp	Leu	Ala	Ser	Ile	Pro	Thr	Thr	Asp	Thr	Pro	Glu	
	450					455					460					
Ser	Ser	Thr	Pro	Ser	Ser	Ser	Ser	Pro	Ala	Ser	Thr	Xaa	Glu	Val	Val	

465					470					475					480
Ala	Ser	Ala	Lys	Ile	Asn	Arg	Phe	Phe	Ala	Ser	Thr	Ala	Glu	Pro	Ala
				485					490					495	
Ala	Pro	Ser	Leu	Thr	Glu	Ala	Glu	Ser	Asp	Gln	Thr	Asp	Gln	Thr	Glu
			500					505					510		
Thr	Ser	Asp	Thr	Asn	Ser	Asp	Ile	Asp	Val	Ser	Ile	Glu	Asn	Ile	Leu
		515					520					525			
Asn	Val	Ala	Ile	Asn	Gln	Asn	Thr	Ser	Ala	Lys	Lys	Gly	Gly	Ala	Ile
	530					535					540				
Tyr	Gly	Lys	Lys	Ala	Lys	Leu	Ser	Arg	Ile	Asn	Asn	Leu	Glu	Leu	Ser
545					550					555					560
Gly	Asn	Ser	Ser	Gln	Asp	Val	Gly	Gly	Gly	Leu	Cys	Leu	Thr	Glu	Ser
				565					570					575	
Val	Glu	Phe	Asp	Ala	Ile	Gly	Ser	Leu	Leu	Ser	His	Tyr	Asn	Ser	Ala
			580					585					590		
Ala	Lys	Glu	Gly	Gly	Val	Ile	His	Ser	Lys	Thr	Val	Thr	Leu	Ser	Asn
		595					600					605			
Leu	Lys	Ser	Thr	Phe	Thr	Phe	Ala	Asp	Asn	Thr	Val	Lys	Ala	Ile	Val
	610					615					620				
Glu	Ser	Thr	Pro	Glu	Ala	Pro	Glu	Glu	Ile	Pro	Pro	Val	Glu	Gly	Glu
625					630					635					640
Glu	Ser	Thr	Ala	Thr	Glu	Asn	Pro	Asn	Ser	Asn	Thr	Glu	Gly	Ser	Ser
				645					650					655	
Ala	Asn	Thr	Asn	Leu	Glu	Gly	Ser	Gln	Gly	Asp	Thr	Ala	Asp	Thr	Gly
			660					665					670		
Thr	Gly	Val	Val	Asn	Asn	Glu	Ser	Gln	Asp	Thr	Ser	Asp	Thr	Gly	Asn
		675					680					685			
Ala	Glu	Ser	Gly	Glu	Gln	Leu	Gln	Asp	Ser	Thr	Gln	Ser	Asn	Glu	Glu
	690					695					700				
Asn	Thr	Leu	Pro	Asn	Ser	Ser	Ile	Asp	Gln	Ser	Asn	Glu	Asn	Thr	Asp
705					710					715					720
Glu	Ser	Ser	Asp	Ser	His	Thr	Glu	Glu	Ile	Thr	Asp	Glu	Ser	Val	Ser
				725					730					735	
Ser	Ser	Ser	Lys	Ser	Gly	Ser	Ser	Thr	Pro	Gln	Asp	Gly	Gly	Ala	Ala
			740					745					750		
Ser	Ser	Gly	Ala	Pro	Ser	Gly	Asp	Gln	Ser	Ile	Ser	Ala	Asn	Ala	Cys
		755					760					765			
Leu	Ala	Lys	Ser	Tyr	Ala	Ala	Ser	Thr	Asp	Ser	Ser	Pro	Val	Ser	Asn
	770					775						780			
Ser	Ser	Gly	Ser	Asp	Val	Thr	Ala	Ser	Ser	Asp	Asn	Pro	Asp	Ser	Ser
785					790					795					800
Ser	Ser	Gly	Asp	Ser	Ala	Gly	Asp	Ser	Glu	Gly	Pro	Thr	Glu	Pro	Glu
				805					810					815	
Ala	Gly	Ser	Thr	Thr	Glu	Thr	Pro	Thr	Leu	Ile	Gly	Gly	Gly	Ala	Ile
		</													

## (2) INFORMATIONS POUR LA SEQ ID NO: 1072:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1031733..1032086

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1072:

```

Ser Asp Ser Ala Ser Val Arg Glu Gly Ala Ala Gly Ser Ala Val Glu
1          5          10          15
Ala Lys Asn Arg Phe Ile Leu Ala Glu Ala Thr Thr Ser Xaa Val Leu
          20          25          30
Ala Gly Glu Glu Glu Gly Val Glu Asp Ser Gly Val Ser Val Val
          35          40          45
Gly Ile Asp Ala Arg Ser Val Lys Ile Ala Pro Pro Asp Ser Phe Ala
          50          55          60
Glu Phe Leu Val Arg Val Thr Val Phe Lys Leu Asp Lys Glu Ser Leu
65          70          75          80
Leu Val Gln Ile Pro Pro Pro Cys Pro Leu Ala Val Phe Ser Glu Lys
          85          90          95
Ile Thr Ser Pro Thr Arg Gly Gly Val Val Ile Leu Ser Leu Val Val
          100          105          110
Leu Val Thr Asp Met Val
          115

```

## (2) INFORMATIONS POUR LA SEQ ID NO: 1073:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1033456..1037037)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1073:

```

Leu Ile Thr His Gln Lys Asn Met Val Val Glu Pro Leu Leu Pro Lys
1          5          10          15
Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
          20          25          30
Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
          35          40          45
Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
          50          55          60
Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
65          70          75          80
Ala Tyr Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
          85          90          95
Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Asp Pro Val

```

			100				105				110				
Ala	Ser	Thr	Ala	Leu	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Val	Ser	Ser	Leu
115							120				125				
Thr	Leu	Leu	Ala	Ala	Ser	Ser	Gln	Ala	Ser	Pro	Ala	Thr	Ser	Asn	Glu
130							135				140				
Lys	Thr	Gln	Asp	Pro	Asn	Ala	Asp	Thr	Asp	Leu	Leu	Ile	Asp	Tyr	Val
145			150				155				160				
Val	Asp	Thr	Thr	Ile	Ser	Lys	Asn	Thr	Ala	Lys	Lys	Gly	Gly	Gly	Ile
			165				170				175				
Tyr	Ala	Lys	Lys	Ala	Lys	Met	Ser	Arg	Ile	Asp	Gln	Leu	Asn	Ile	Ser
			180				185				190				
Glu	Asn	Ser	Ala	Thr	Glu	Ile	Gly	Gly	Gly	Ile	Cys	Cys	Lys	Lys	Ser
195							200				205				
Leu	Lys	Leu	Asp	Ala	Leu	Val	Ser	Leu	Ser	Val	Thr	Glu	Asn	Leu	Val
210							215				220				
Gly	Lys	Glu	Gly	Gly	Gly	Leu	His	Ala	Lys	Thr	Val	Asn	Ile	Ser	Asn
225			230				235				240				
Leu	Lys	Ser	Gly	Phe	Ser	Phe	Ser	Asn	Asn	Lys	Ala	Asn	Ser	Ser	Ser
			245				250				255				
Thr	Gly	Val	Ala	Thr	Thr	Ala	Ser	Ala	Pro	Ala	Ala	Ala	Ala	Ala	Ser
260							265				270				
Leu	Gln	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Ser	Ser	Pro	Ala	Thr	Pro	Thr
275							280				285				
Tyr	Ser	Gly	Val	Val	Gly	Gly	Ala	Ile	Tyr	Gly	Glu	Gln	Phe	Thr	Phe
290							295				300				
Ser	Gln	Cys	Ser	Gly	Thr	Cys	Gln	Phe	Ser	Gly	Asn	Gln	Ala	Ile	Asp
305			310				315				320				
Asn	Asn	Pro	Ser	Gln	Ser	Ser	Leu	Asn	Val	Gln	Gly	Gly	Ala	Ile	Tyr
			325				330				335				
Ala	Lys	Thr	Ser	Leu	Ser	Ile	Arg	Ser	Ser	Asp	Ala	Gly	Thr	Ser	Tyr
340							345				350				
Ile	Phe	Ser	Gly	Asn	Ser	Val	Ser	Thr	Gly	Lys	Ser	Gln	Thr	Thr	Gly
355							360				365				
Gln	Ile	Ala	Gly	Gly	Ala	Ile	Tyr	Ser	Pro	Thr	Val	Thr	Leu	Asn	Cys
370							375				380				
Pro	Ala	Thr	Phe	Ser	Asn	Asn	Thr	Ala	Ser	Met	Ala	Thr	Pro	Lys	Thr
385			390				395				400				
Ser	Ser	Ser	Ser	Gly	Asn	Ser	Ile	Lys	Asp	Thr	Ile	Gly	Gly	Ala	Ile
			405				410				415				
Ala	Gly	Thr	Ala	Ile	Thr	Leu	Ser	Gly	Val	Ser	Arg	Phe	Ser	Gly	Asn
420							425				430				
Thr	Ala	Asp	Leu	Gly	Ala	Ala	Ile	Gly	Thr	Leu	Ala	Asn	Ala	Asn	Thr
435							440				445				
Pro	Arg	Ala	Thr	Ser	Gly	Ser	Gln	Asn	Ser	Ile	Thr	Glu	Lys	Ile	Thr
450							455				460				
Leu	Lys	Asn	Ser	Ser	Phe	Ile	Phe	Glu	Arg	Asn	Gln	Ala	Asn	Lys	Arg
465			470				475				480				
Gly	Ala	Ile	Tyr	Ser	Pro	Ser	Val	Ser	Ile	Lys	Gly	Asn	Asn	Ile	Thr
			485				490				495				
Phe	Asn	Gln	Asn	Thr	Ser	Thr	His	Asp	Gly	Ser	Ala	Ile	T		

Asn	Ile	Thr	Phe	Ser	Asn	Asn	Ser	Leu	Gln	Asn	Asn	Gln	Gly	Gly	Thr		
			580					585					590				
Pro	Ala	Ser	Lys	Phe	Cys	Ser	Ile	Ala	Gly	Tyr	Val	Lys	Leu	Ser	Leu		
		595					600					605					
Gln	Ala	Thr	Lys	Gly	Lys	Thr	Ile	Ser	Phe	Phe	Asp	Cys	Val	His	Thr		
	610					615					620						
Ser	Thr	Lys	Lys	Thr	Gly	Ser	Thr	Gln	Asn	Val	Tyr	Glu	Thr	Leu	Asp		
625					630					635					640		
Ile	Asn	Lys	Lys	Glu	Asn	Ser	Lys	Pro	Tyr	Thr	Gly	Thr	Ile	Val	Phe		
				645				650						655			
Ser	Ser	Glu	Leu	His	Glu	Asn	Lys	Ser	Tyr	Ile	Pro	Gln	Asn	Ala	Ile		
		660						665					670				
Leu	His	Asn	Gly	Thr	Leu	Val	Leu	Lys	Glu	Lys	Thr	Glu	Leu	His	Val		
	675						680					685					
Val	Ser	Phe	Glu	Gln	Lys	Glu	Gly	Ser	Lys	Leu	Ile	Met	Glu	Pro	Gly		
	690					695				700							
Ala	Val	Leu	Ser	Asn	Gln	Asn	Ile	Ala	Asn	Gly	Ala	Leu	Ala	Ile	Asn		
705					710					715					720		
Gly	Leu	Thr	Ile	Asp	Leu	Ser	Ser	Met	Gly	Thr	Pro	Gln	Ala	Gly	Glu		
				725					730					735			
Ile	Phe	Ser	Pro	Pro	Glu	Leu	Arg	Ile	Val	Ala	Thr	Thr	Ser	Ser	Ala		
		740						745					750				
Ser	Gly	Arg	Ser	Gly	Val	Ser	Arg	Ser	Ile	Pro	Thr	Asn	Pro	Lys	Gly		
	755					760						765					
Ile	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Ser	Ala	Ala	Thr	Thr	Pro	Thr	Met		
	770				775						780						
Ser	Glu	Asn	Lys	Val	Phe	Leu	Thr	Gly	Asp	Leu	Thr	Leu	Ile	Asp	Pro		
785					790				795					800			
Asn	Gly	Asn	Phe	Tyr	Gln	Asn	Pro	Met	Leu	Gly	Ser	Asp	Leu	Asp	Val		
			805						810					815			
Pro	Leu	Ile	Lys	Leu	Pro	Thr	Asn	Thr	Ser	Asp	Val	Gln	Val	Tyr	Asp		
			820					825					830				
Leu	Thr	Leu	Ser	Gly	Asp	Leu	Phe	Pro	Gln	Lys	Gly	Tyr	Met	Gly	Thr		
	835						840					845					
Trp	Thr	Leu	Asn	Ser	Asn	Pro	Gln	Thr	Gly	Lys	Leu	Gln	Ala	Arg	Trp		
	850				855						860						
Thr	Phe	Asp	Thr	Tyr	Arg	Arg	Trp	Val	Tyr	Ile	Pro	Arg	Asp	Asn	His		
865					870					875				880			
Phe	Tyr	Ala	Asn	Ser	Ile	Leu	Gly	Ser	Gln	Asn	Ser	Met	Ile	Val	Val		
			885						890					895			
Lys	Gln	Gly	Leu	Ile	Asn	Asn	Met	Leu	Asn	Asn	Ala	Arg	Phe	Asp	Asp		
		900						905					910				
Ile	Ala	Tyr	Asn	Asn	Phe	Trp	Val	Ser	Gly	Val	Gly	Thr	Phe	Leu	Ala		
	915					920						925					
Gln	Gln	Gly	Thr	Pro	Leu	Ser	Glu	Glu	Phe	Ser	Tyr	Tyr	Ser	Arg	Gly		
	930					935					940						
Thr	Ser	Val	Ala	Ile	Asp	Ala	Lys	Pro	Arg	Gln	Asp	Phe	Ile	Leu	Gly		
945					950					955				960			
Ala	Ala	Phe	Ser	Lys	Met	Val	Gly	Lys	Thr	Lys	Ala	Ile	Lys	Lys	Met		
			965						970					975			
His	Asn	Tyr	Phe	His	Lys	Gly	Ser	Glu	Tyr	Ser	Tyr	Gln	Ala	Ser	Val		
		980						985					990				
Tyr	Gly	Gly	Lys	Phe	Leu	Tyr	Phe	Leu	Leu	Asn	Lys	Gln	His	Gly	Trp		
	995						1000					1005					
Ala	Leu	Pro	Phe	Leu	Ile	Gln	Gly	Val	Val	Ser	Tyr	Gly	His	Ile	Lys		
	1010					1015					1020						
His	Asp	Thr	Thr	Ile	Leu	Tyr	Pro	Ser	Ile	His	Glu	Arg	Asn	Lys	Gly		
1025					1030					1035					1040		
Asp	Trp	Glu	Asp	Ile	Gly	Trp	Leu	Ala	Asp	Leu	Arg	Ile	Ser	Met	Asp		

				1045					1050					1055	
Leu	Lys	Glu	Pro	Ser	Lys	Asp	Ser	Ser	Lys	Arg	Ile	Thr	Val	Tyr	Gly
			1060						1065					1070	
Glu	Leu	Glu	Tyr	Ser	Ser	Ile	Arg	Gln	Lys	Gln	Phe	Thr	Glu	Ile	Asp
		1075						1080					1085		
Tyr	Asp	Pro	Arg	His	Phe	Asp	Asp	Cys	Ala	Tyr	Arg	Asn	Leu	Ser	Leu
	1090						1095					1100			
Pro	Val	Gly	Cys	Ala	Val	Glu	Gly	Ala	Ile	Met	Asn	Cys	Asn	Ile	Leu
1105					1110					1115					1120
Met	Tyr	Asn	Lys	Leu	Ala	Leu	Ala	Tyr	Met	Pro	Ser	Ile	Tyr	Arg	Asn
			1125						1130					1135	
Asn	Pro	Val	Cys	Lys	Tyr	Arg	Val	Leu	Ser	Ser	Asn	Glu	Ala	Gly	Gln
		1140							1145				1150		
Val	Ile	Cys	Gly	Val	Pro	Thr	Arg	Thr	Ser	Ala	Arg	Ala	Glu	Tyr	Ser
		1155					1160					1165			
Thr	Gln	Leu	Tyr	Leu	Gly	Pro	Phe	Trp	Thr	Leu	Tyr	Gly	Asn	Tyr	Thr
	1170					1175						1180			
Ile	Asp	Val	Gly	Met	Tyr	Thr	Tyr	Arg	Lys						
1185						1190									

(2) INFORMATIONS POUR LA SEQ ID NO: 1074:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 79 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1035674..1035910

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1074:

Asp	Pro	Leu	Val	Ala	Leu	Gly	Val	Phe	Ala	Leu	Ala	Arg	Val	Pro	Ile
1				5					10					15	
Ala	Ala	Pro	Lys	Ser	Ala	Val	Phe	Pro	Glu	Asn	Arg	Glu	Thr	Pro	Asp
			20					25					30		
Arg	Val	Met	Ala	Val	Pro	Ala	Met	Ala	Pro	Pro	Met	Val	Ser	Leu	Ile
		35					40					45			
Glu	Phe	Pro	Glu	Asp	Glu	Glu	Val	Phe	Gly	Val	Ala	Ile	Glu	Ala	Val
	50					55					60				
Leu	Leu	Glu	Asn	Val	Ala	Gly	Gln	Phe	Asn	Val	Thr	Val	Gly	Glu	
65					70						75				

(2) INFORMATIONS POUR LA SEQ ID NO: 1075:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 111 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1036175..1036507



## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1075:

Val	Gly	Val	Ala	Gly	Asp	Asp	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Cys	Arg
1				5				10						15	
Glu	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Glu	Ala	Val	Val	Ala	Thr	Pro	Val
			20					25					30		
Asp	Glu	Glu	Phe	Ala	Leu	Leu	Phe	Glu	Lys	Glu	Lys	Pro	Asp	Phe	Arg
		35					40					45			
Leu	Glu	Ile	Phe	Thr	Val	Leu	Ala	Cys	Lys	Pro	Pro	Pro	Ser	Phe	Pro
	50					55					60				
Thr	Arg	Phe	Ser	Val	Thr	Asp	Lys	Glu	Thr	Arg	Ala	Ser	Ser	Phe	Lys
65					70					75					80
Asp	Phe	Leu	Gln	Gln	Ile	Pro	Pro	Pro	Ile	Ser	Val	Ala	Glu	Phe	Ser
			85					90						95	
Glu	Ile	Phe	Ser	Trp	Ser	Met	Arg	Asp	Ile	Leu	Ala	Phe	Leu	Ala	
			100					105					110		

## (2) INFORMATIONS POUR LA SEQ ID NO: 1076:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 542 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1036967..1038592)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1076:

Leu	Asn	Phe	Ser	Arg	Val	Gly	Thr	Ser	Ser	Ser	Thr	Thr	Phe	Thr	Glu
1				5				10						15	
Thr	Val	Gly	Glu	Ala	Gly	Ala	Glu	Tyr	Ile	Val	Ser	Ser	Asn	Ala	Ser
			20					25					30		
Phe	Thr	Lys	Phe	Thr	Asn	Ile	Pro	Thr	Thr	Asn	Thr	Thr	Thr	Pro	Thr
		35					40					45			
Asn	Ser	Asn	Ser	Ser	Ser	Ser	Asn	Arg	Glu	Thr	Ala	Ser	Val	Ser	Lys
	50					55					60				
Asp	Ser	Asp	Ser	Thr	Thr	Thr	Thr	Pro	Asp	Pro	Lys	Gly	Gly	Gly	Xaa
65					70				75						80
Phe	Tyr	Asn	Ala	His	Ser	Gly	Val	Leu	Ser	Phe	Met	Thr	Arg	Ser	Gly
			85					90						95	
Thr	Glu	Gly	Ser	Leu	Thr	Leu	Ser	Glu	Ile	Lys	Met	Thr	Gly	Glu	Gly
			100					105					110		
Gly	Ala	Ile	Phe	Ser	Gln	Gly	Glu	Leu	Leu	Phe	Thr	Asp	Leu	Thr	Gly
		115					120					125			
Leu	Thr	Ile	Gln	Asn	Asn	Leu	Ser	Gln	Leu	Ser	Gly	Gly	Ala	Ile	Phe
	130					135					140				
Gly	Gly	Ser	Thr	Ile	Ser	Leu	Ser	Gly	Ile	Thr	Lys	Ala	Thr	Phe	Ser
145					150				155						160
Ser	Asn	Ser	Ala	Glu	Val	Pro	Ala	Pro	Val	Lys	Lys	Pro	Thr	Lys	Pro
			165					170						175	
Glu	Ala	Gln	Thr	Ala	Gly	Glu	Thr	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Gly
		180						185					190		
Asn	Asp	Ser	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Ala	Glu	Pro	Ala	Ala
		195					200						205		

Ala	Asn	Leu	Gln	Ser	His	Phe	Ile	Cys	Ala	Thr	Ala	Thr	Pro	Ala	Ala
210						215					220				
Gln	Thr	Asp	Thr	Glu	Thr	Ser	Thr	Pro	Ser	His	Lys	Pro	Gly	Ser	Gly
225					230					235					240
Gly	Ala	Ile	Tyr	Ala	Lys	Gly	Asp	Leu	Thr	Ile	Ala	Asp	Ser	Gln	Lys
				245					250					255	
Val	Leu	Phe	Ser	Ile	Asn	Lys	Ala	Thr	Lys	Asp	Gly	Gly	Ala	Ile	Phe
			260					265					270		
Ala	Glu	Lys	Asp	Val	Ser	Phe	Glu	Asn	Ile	Thr	Ser	Leu	Lys	Val	Gln
	275						280					285			
Thr	Asn	Gly	Ala	Glu	Glu	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Gly	Asp
290						295					300				
Leu	Ser	Ile	Gln	Ser	Ser	Lys	Gln	Ser	Leu	Phe	Asn	Ser	Asn	Tyr	Ser
305					310					315					320
Lys	Gln	Gly	Gly	Gly	Ala	Leu	Tyr	Val	Glu	Gly	Asn	Ile	Asn	Phe	Gln
				325					330					335	
Asp	Leu	Glu	Glu	Ile	Arg	Ile	Lys	Tyr	Asn	Lys	Ala	Gly	Thr	Phe	Lys
			340					345					350		
Thr	Lys	Lys	Ile	Thr	Leu	Pro	Ser	Lys	Ala	Gln	Ala	Ser	Ala	Gly	Asn
	355						360					365			
Ala	Asp	Ala	Trp	Ala	Ser	Ser	Ser	Pro	Gln	Ser	Ser	Ser	Gly	Ala	Thr
370						375				380					
Thr	Val	Ser	Asp	Ser	Gly	Asp	Ser	Ser	Ser	Gly	Ser	Asn	Ser	Asp	Thr
385					390					395					400
Ser	Lys	Thr	Val	Pro	Val	Thr	Ala	Lys	Gly	Gly	Gly	Leu	Tyr	Thr	Asp
				405					410					415	
Lys	Asn	Leu	Ser	Ile	Thr	Asn	Ile	Thr	Gly	Ile	Ile	Glu	Ile	Ala	Ile
		420						425				430			
Asn	Lys	Ala	Thr	Asp	Val	Gly	Gly	Ala	Tyr	Val	Lys	Gly	Thr	Leu	
	435					440					445				
Thr	Cys	Lys	Asn	Ser	His	Arg	Leu	Gln	Phe	Leu	Lys	Asn	Ser	Ser	Asp
450						455					460				
Lys	Gln	Gly	Gly	Gly	Ile	Tyr	Gly	Glu	Asp	Asn	Ile	Thr	Leu	Ser	Asn
465					470					475					480
Leu	Thr	Gly	Lys	Thr	Leu	Phe	Gln	Glu	Asn	Thr	Ala	Lys	Lys	Glu	Gly
				485					490					495	
Gly	Gly	Leu	Phe	Ile	Lys	Gly	Thr	Asp	Lys	Ala	Leu	Thr	Met	Thr	Gly
		500						505					510		
Leu	Asp	Ser	Phe	Cys	Leu	Ile	Asn	Asn	Thr	Ser	Glu	Lys	His	Gly	Gly
	515						520					525			
Gly	Ala	Phe	Val	Thr	Gln	Arg	Asn	Leu	Ser	Asp	Leu	His	Leu		
530						535					540				

## REVENDECATIONS

1. Séquence nucléotidique de séquence SEQ ID N° 1 du  
génomè de *Chlamydia trachomatis* LGV2.
- 5 2. Séquence nucléotidique de *Chlamydia trachomatis*,  
caractérisée en ce qu'elle est choisie parmi :
  - a) une séquence nucléotidique comportant au moins 99,9 %  
d'identité avec la séquence SEQ ID N° 1 ;
  - 10 b) une séquence nucléotidique homologue à la séquence SEQ  
ID N° 1 ;
  - c) une séquence nucléotidique complémentaire de la séquence  
SEQ ID N° 1 ou complémentaire d'une séquence nucléotidique  
telle que définie en a), ou b), et une séquence  
15 nucléotidique de leur ARN correspondant ;
  - d) une séquence nucléotidique de fragment représentatif de  
la séquence SEQ ID N° 1, ou de fragment représentatif de  
séquence nucléotidique telle que définie en a), b) ou c) ;
  - e) une séquence nucléotidique comprenant une séquence telle  
20 que définie en a), b), c) ou d) ;
  - f) une séquence nucléotidique susceptible d'être obtenue à  
partir d'une séquence nucléotidique telle que définie en  
a), b), c), d) ou e) ; et
  - g) une séquence nucléotidique modifiée d'une séquence  
25 nucléotidique telle que définie en a), b), c), d), e) ou  
f) .
3. Séquence nucléotidique selon la revendication 2,  
caractérisée en ce qu'elle est choisie parmi les séquences  
30 ORF2 à ORF1076.
4. Séquence nucléotidique caractérisée en ce qu'elle  
comprend une séquence nucléotidique choisie parmi :
  - a) une séquence nucléotidique selon la revendication 3 ;
  - 35 b) une séquence nucléotidique homologue comportant au moins  
80 % d'identité avec une séquence nucléotidique selon la  
revendication 3 ou telle que définie en a) ;

- c) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence selon la revendication 3 ou telle que définie en a) ou b) ;
- d) une séquence nucléotidique de fragment représentatif d'une séquence selon la revendication 3 ou d'une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique susceptible d'être obtenue à partir d'une séquence selon la revendication 3 ou telle que définie en a), b), c) ou d) ; et
- f) une séquence nucléotidique modifiée d'une séquence selon la revendication 3 ou telle que définie en a), b), c), d) ou e).

5. Polypeptide codé par une séquence nucléotidique selon l'une des revendications 2 à 4.

6. Polypeptide selon la revendication 5, caractérisé en ce qu'il est codé par un fragment représentatif correspondant à une séquence ORF d'une séquence nucléotidique selon l'une des revendications 1 à 4.

7. Polypeptide de *Chlamydia trachomatis*, caractérisé en ce qu'il est choisi parmi les séquences SEQ ID N°2 à SEQ ID N°1076.

8. Polypeptide caractérisé en ce qu'il comprend un polypeptide choisi parmi :

- a) un polypeptide selon l'une des revendications 5 à 7 ;
- b) un polypeptide homologue à un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a) ;
- c) un fragment d'au moins 5 acides aminés d'un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a) ou b) ;
- d) un fragment biologiquement actif d'un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a), b) ou c) ; et

e) un polypeptide modifié d'un polypeptide selon l'une des revendications 5 à 7 ou tel que défini en a), b), c) ou d).

5 9. Séquence nucléotidique codant pour un polypeptide selon la revendication 8.

10 10. Vecteur de clonage, et/ ou d'expression, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 2 à 4, et 9.

15

Figure 1.

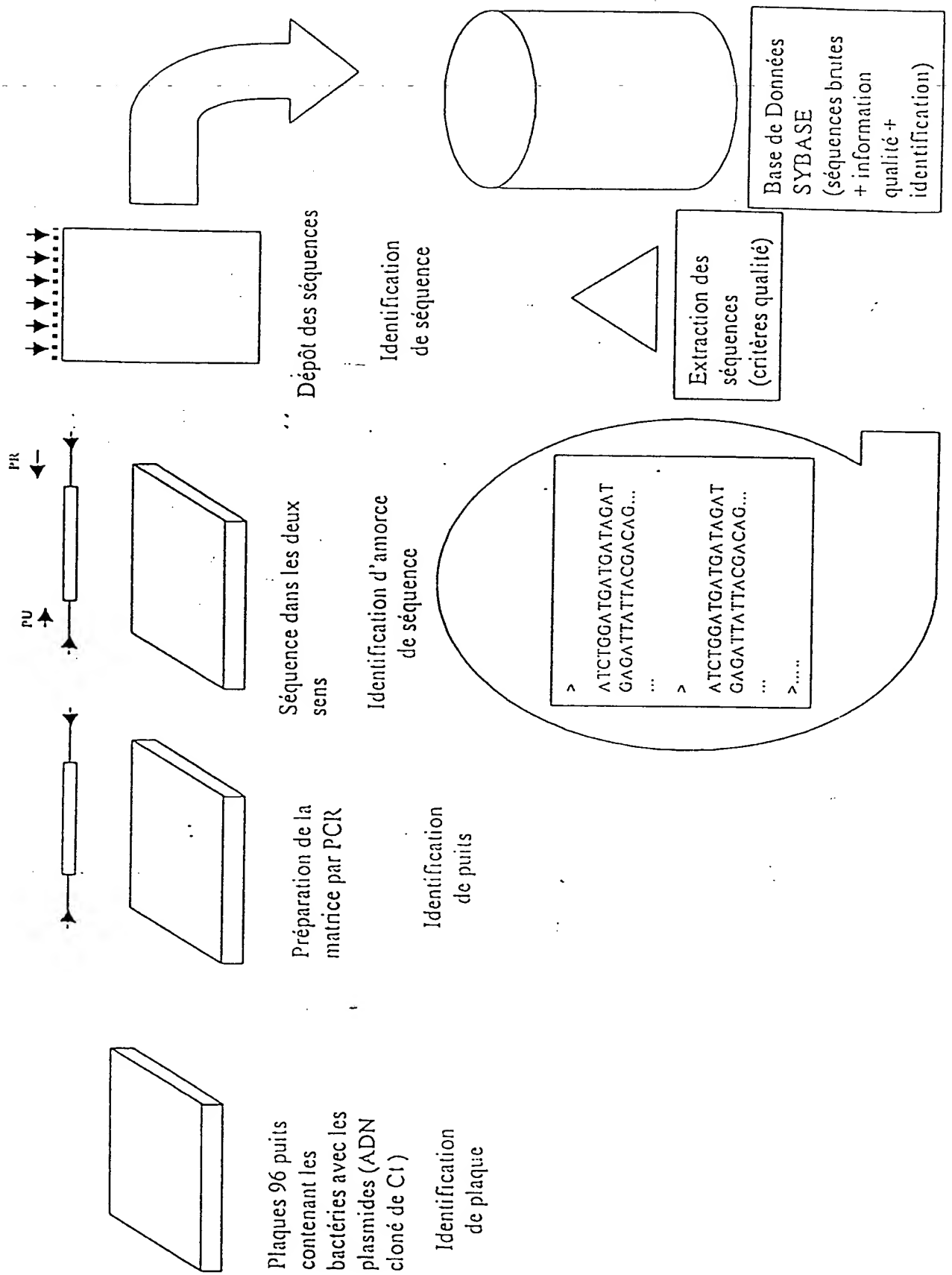


Figure 2.

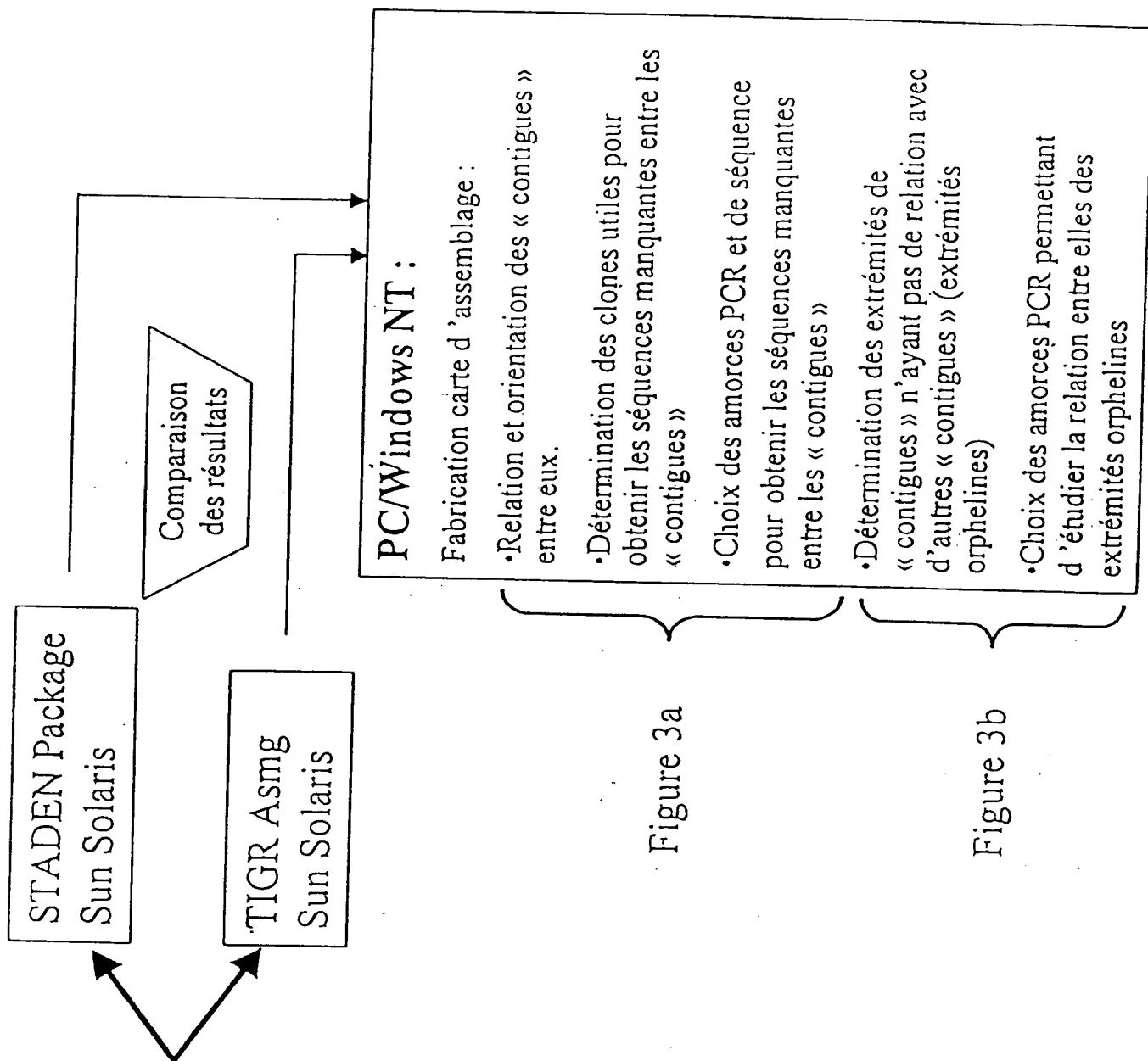
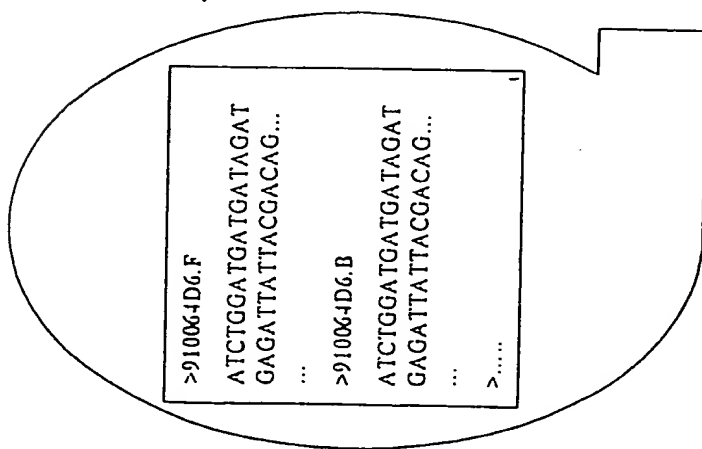
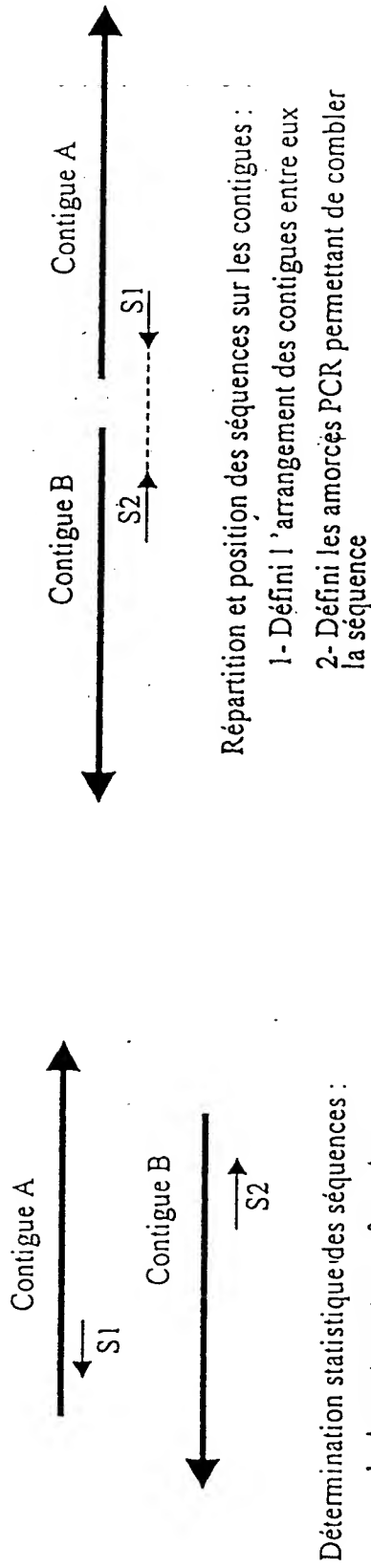


Figure 3a

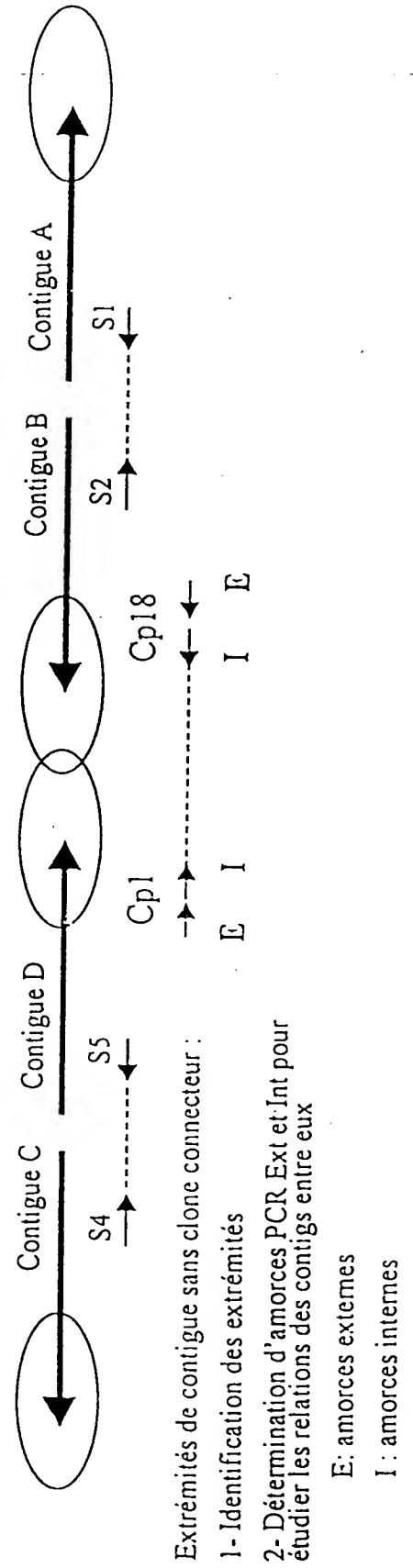
Figure 3b

Figure 3.

a.



b.





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